

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 0.439826 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-11

Perfect score: 15

Sequence: 1 RXRS 4

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUTS\_COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	4	2	US-08-387-942C-14
2	15	100.0	4	3	US-08-894-173-17
3	15	100.0	4	3	US-09-398-193-17
4	15	100.0	4	4	US-09-443-780C-82
5	15	100.0	4	4	US-09-079-723-263
6	15	100.0	5	2	US-08-637-759B-84
7	15	100.0	5	3	US-08-871-355A-84
8	15	100.0	5	3	US-08-894-173-40
9	15	100.0	5	3	US-09-398-193-40
10	15	100.0	5	3	US-09-201-945-84
11	15	100.0	5	4	US-09-638-202A-79
12	15	100.0	5	4	US-09-638-202A-85
13	15	100.0	5	4	US-09-638-202A-87
14	15	100.0	5	4	US-09-638-202A-91
15	15	100.0	5	4	US-09-367-777-130
16	15	100.0	5	4	US-09-367-791A-106
17	15	100.0	5	4	US-09-096-749A-79
18	15	100.0	5	4	US-09-096-749A-85
19	15	100.0	5	4	US-09-096-749A-87
20	15	100.0	5	4	US-09-096-749A-91
21	15	100.0	5	4	US-09-637-614-79
22	15	100.0	5	4	US-09-637-614-85
23	15	100.0	5	4	US-09-637-614-87
24	15	100.0	5	4	US-09-637-614-91
25	15	100.0	5	4	US-09-933-999A-24
26	15	100.0	5	4	US-09-933-999A-29
27	15	100.0	6	1	US-08-030-077-3

28	15	100.0	6	1	US-08-064-111C-4	Sequence 4, Appli
29	15	100.0	6	1	US-08-537-069-9	Sequence 9, Appli
30	15	100.0	6	1	US-08-537-069-10	Sequence 10, Appli
31	15	100.0	6	1	US-08-537-069-11	Sequence 11, Appli
32	15	100.0	6	1	US-08-537-069-12	Sequence 12, Appli
33	15	100.0	6	1	US-08-537-069-13	Sequence 13, Appli
34	15	100.0	6	2	US-08-733-505A-4	Sequence 4, Appli
35	15	100.0	6	2	US-08-733-505A-5	Sequence 5, Appli
36	15	100.0	6	2	US-08-733-505A-7	Sequence 7, Appli
37	15	100.0	6	2	US-08-387-942C-12	Sequence 12, Appli
38	15	100.0	6	3	US-08-843-659-6	Sequence 6, Appli
39	15	100.0	6	4	US-08-171-384A-6	Sequence 6, Appli
40	15	100.0	6	4	US-09-122-144-8	Sequence 8, Appli
41	15	100.0	6	4	US-09-579-894-3	Sequence 3, Appli
42	15	100.0	7	1	US-08-537-069-14	Sequence 14, Appli
43	15	100.0	7	3	US-09-049-691-68	Sequence 68, Appli
44	15	100.0	7	3	US-09-049-691-70	Sequence 70, Appli
45	15	100.0	7	3	US-09-258-754-393	Sequence 393, App

## ALIGNMENTS

RESULT 1  
US-08-387-942C-14  
; Sequence 14, Application US/08387942C  
; Patent No. 5939289  
; GENERAL INFORMATION:  
; APPLICANT: ERTESVAG, HELGA  
; APPLICANT: VALLA, SVEIN  
; APPLICANT: SKJAK-BRAEK, GUDMUND  
; APPLICANT: LARSEN, BJORN  
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP  
; STREET: P.O. BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,942C  
; FILING DATE: 09-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1809-106P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-205-8000  
; TELEFAX: 703-205-8050  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-387-942C-14

Query Match 100.0%; Score 15; DB 2; Length 4;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4  
|:|

Db 1 RARS 4

## RESULT 2

US-08-894-173-17  
; Sequence 17, Application US/08894173A  
; Patent No. 6090612  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Adenylate cyclase and uses therefor  
; FILE REFERENCE: P14716C  
; CURRENT APPLICATION NUMBER: US/08/894,173A  
; CURRENT FILING DATE: 1997-08-13  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Mouse  
; OTHER INFORMATION: STRANDEDNESS : Single  
; FEATURE:  
; OTHER INFORMATION: TOPOLOGY : Linear  
; FEATURE:  
; OTHER INFORMATION: MOLECULE TYPE : Peptide  
; FEATURE:  
; OTHER INFORMATION: HYPOTHETICAL : NO  
; FEATURE:  
; OTHER INFORMATION: ANTI-SENSE : NO  
; US-08-894-173-17

Query Match 100.0%; Score 15; DB 3; Length 4;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4

|:|

Db 1 RARS 4

## RESULT 3

US-09-398-193-17  
; Sequence 17, Application US/09398193  
; Patent No. 6197581  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Adenylate cyclase and uses therefor  
; FILE REFERENCE: P24360-  
; CURRENT APPLICATION NUMBER: US/09/398,193  
; CURRENT FILING DATE: 1999-09-17  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Mouse  
; FEATURE:  
; OTHER INFORMATION: STRANDEDNESS : Single  
; FEATURE:  
; OTHER INFORMATION: TOPOLOGY : Linear  
; FEATURE:  
; OTHER INFORMATION: MOLECULE TYPE : Peptide  
; FEATURE:  
; OTHER INFORMATION: HYPOTHETICAL : NO  
; FEATURE:  
; OTHER INFORMATION: ANTI-SENSE : NO  
; US-09-398-193-17

Query Match 100.0%; Score 15; DB 3; Length 4;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4

Db |:|  
1 RRSR 4

## RESULT 4

US-09-443-780C-82  
; Sequence 82, Application US/09443780C  
; Patent No. 6699973  
; GENERAL INFORMATION:  
; APPLICANT: O'Mahony, Daniel J  
; APPLICANT: Seveso, Michela  
; TITLE OF INVENTION: Antibodies To Peptides That Target GIT Receptors And Related Metho  
; FILE REFERENCE: E1067/20037  
; CURRENT APPLICATION NUMBER: US/09/443,780C  
; CURRENT FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: US 60/109,036  
; PRIOR FILING DATE: 1998-11-19  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 82  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: binding 4 mer fragment L-form  
; US-09-443-780C-82

Query Match 100.0%; Score 15; DB 4; Length 4;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4

|:|

Db 1 RRSR 4

## RESULT 5

US-09-079-723-263  
; Sequence 263, Application US/09079723  
; Patent No. 6703362  
; GENERAL INFORMATION:  
; APPLICANT: Alvarez, Vernon L.  
; APPLICANT: O'Mahony, Daniel J.  
; APPLICANT: Lambkin, Imelda J.  
; APPLICANT: Singleton, Judith  
; APPLICANT: Patterson, Catherine A.  
; APPLICANT: Cagney, Gerard M.  
; APPLICANT: Belinka, Benjamin A.  
; APPLICANT: Carter, John M.  
; TITLE OF INVENTION: RANDOM PEPTIDES THAT BIND TO GASTRO-  
; TITLE OF INVENTION: INTESTINAL TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA: US/09/079,723  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-219  
; TELECOMMUNICATION INFORMATION:



; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 263:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-079-723-263

Query Match 100.0%; Score 15; DB 4; Length 4;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4  
|:|  
DB 1 RVRS 4

RESULT 6  
US-08-637-759B-84  
; Sequence 84, Application US/08637759B  
; Patent No. 5876931  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 03-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 84:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-637-759B-84

Query Match 100.0%; Score 15; DB 2; Length 5;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4  
|:|

DB 1 RRRS 4  
RESULT 7  
US-08-871-355A-84  
; Sequence 84, Application US/08871355A  
; Patent No. 6013669  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 84:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-871-355A-84

Query Match 100.0%; Score 15; DB 3; Length 5;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4  
|:|  
DB 1 RRRS 4

RESULT 8  
US-08-894-173-40  
; Sequence 40, Application US/08894173A  
; Patent No. 6090612  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Adenylate cyclase and uses therefor  
; FILE REFERENCE: P14716C  
; CURRENT APPLICATION NUMBER: US/08/894.173A  
; CURRENT FILING DATE: 1997-08-13  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 5  
; TYPE: PRT

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; ORGANISM: Mouse
; FEATURE:
; OTHER INFORMATION: STRANDEDNESS : Single
; FEATURE:
; OTHER INFORMATION: TOPOLOGY : Linear
; FEATURE:
; OTHER INFORMATION: MOLECULE TYPE : Peptide
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL : NO
; FEATURE:
; OTHER INFORMATION: ANTI-SENSE : NO
;
US-08-894-173-40
Query Match          100.0%; Score 15; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
Db 2 RSRS 5

RESULT 9
US-09-398-193-40
; Sequence 40, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; OTHER INFORMATION: STRANDEDNESS : Single
; FEATURE:
; OTHER INFORMATION: TOPOLOGY : Linear
; FEATURE:
; OTHER INFORMATION: MOLECULE TYPE : Peptide
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL : NO
; FEATURE:
; OTHER INFORMATION: ANTI-SENSE : NO
;
US-09-398-193-40
Query Match          100.0%; Score 15; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
Db 2 RSRS 5

RESULT 10
US-09-201-945-84
; Sequence 84, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
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; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
;
US-09-201-945-84
Query Match          100.0%; Score 15; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
Db 1 RRRS 4

RESULT 11
US-09-638-202A-79
; Sequence 79, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koleda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,202A
; FILING DATE: 11-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnine
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
```

TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 79:  
US-09-638-202A-79

Query Match 100.0%; Score 15; DB 4; Length 5;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4  
|:|  
DB 2 RXRS 5

RESULT 12  
US-09-638-202A-85  
; Sequence 85, Application US/09638202A  
; Patent No. 6462189  
; GENERAL INFORMATION:  
; APPLICANT: Koieda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/638,202A  
; FILING DATE: 11-Aug-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/096,749  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 85:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 85:  
US-09-638-202A-85

Query Match 100.0%; Score 15; DB 4; Length 5;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RXRS 4  
|:|  
DB 2 RXRS 5

RESULT 13  
US-09-638-202A-87  
; Sequence 87, Application US/09638202A  
; Patent No. 6462189  
; GENERAL INFORMATION:  
; APPLICANT: Koieda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/638,202A  
; FILING DATE: 11-Aug-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/096,749  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:  
US-09-638-202A-87

Query Match 100.0%; Score 15; DB 4; Length 5;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4  
|:|  
DB 2 RXRS 5

RESULT 14  
US-09-638-202A-91  
; Sequence 91, Application US/09638202A  
; Patent No. 6462189  
; GENERAL INFORMATION:  
; APPLICANT: Koieda, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.

STREET: 121 South Eighth Street, Ste. 1600  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/638,202A  
FILING DATE: 11-Aug-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/096,749  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Ann S. Viksnins  
REGISTRATION NUMBER: 37,748  
REFERENCE/DOCKET NUMBER: 109.034US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (612) 373-6900  
TELEFAX: (612) 339-3061  
INFORMATION FOR SEQ ID NO: 91:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 91:  
US-09-638-202A-91

Query Match 100.0%; Score 15; DB 4; Length 5;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4  
|:|  
Db 2 RYRS 5

RESULT 15  
US-09-367-777-130  
; Sequence 130, Application US/0936777  
; Patent No. 6562598  
; GENERAL INFORMATION:  
; APPLICANT: Himmelspach, Michele  
; Pfleiderer, Michael  
; Falkner, Falko-Gunter  
; Bibl, Johann  
; Dörner, Friedrich  
; Schlokat, Uwe  
; TITLE OF INVENTION: Factor X Deletion Mutants  
; and Analogues Thereof  
; NUMBER OF SEQUENCES: 145  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/367,777  
FILING DATE: 10-No. 6562598-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AT A 336/97  
FILING DATE: 27-FEB-1997  
APPLICATION NUMBER: WO PCT/AT98/00046  
FILING DATE: 27-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 20695D-000900US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 130:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 130:  
US-09-367-777-130

Query Match 100.0%; Score 15; DB 4; Length 5;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4  
|:|  
Db 2 RKRS 5

Search completed: March 8, 2005, 05:53:48  
Job time : 1.43983 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 1.85451 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-11  
Perfect score: 15  
Sequence: 1 RXRS 4

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	4	2	AAR22517 Peptide o
2	15	100.0	4	2	Aaw74084 Fragment
3	15	100.0	4	2	Aay34297 Consensus
4	15	100.0	4	2	Aay34295 Consensus
5	15	100.0	4	5	Aag68362 Tomato mo
6	15	100.0	4	5	Aag68364 Tomato mo
7	15	100.0	4	5	Abg78063 ITALY, LO
8	15	100.0	4	6	Abp55115 Human pot
9	15	100.0	4	8	Adm72392 cAMP and
10	15	100.0	4	8	Adr45631 Human STM
11	15	100.0	5	2	Aaw56878 Enzyme in
12	15	100.0	5	2	Aay21060 Human p53
13	15	100.0	5	2	Aay34296 Consensus
14	15	100.0	5	2	Aay34298 Consensus
15	15	100.0	5	2	Aaw98065 Sorting s
16	15	100.0	5	2	Aaw98060 Staphyloc
17	15	100.0	5	2	Aaw94174 BC loop s
18	15	100.0	5	3	Aab10342 Human and
19	15	100.0	5	3	Aab11071 S. apyoge
20	15	100.0	5	3	Aab11076 S. pyogen
21	15	100.0	5	5	Abb94435 Ubiquitin
22	15	100.0	5	5	Abb94441 Ubiquitin
23	15	100.0	5	5	Abb94443 Ubiquitin
24	15	100.0	5	5	Abb94447 Ubiquitin
25	15	100.0	5	6	Aae36595 Staphyloc

26	15	100.0	5	6	AAE36600	Staphyloc
27	15	100.0	5	6	ABU64640	Motif-ape
28	15	100.0	5	6	ABU61779	S. aureus
29	15	100.0	5	6	ABU61774	S. aureus
30	15	100.0	5	6	ABR55100	MMP subet
31	15	100.0	5	7	ADI10968	Cell surf
32	15	100.0	5	7	ADI10841	Cell surf
33	15	100.0	5	7	ADI10848	Cell surf
34	15	100.0	5	7	ADI10554	Cell surf
35	15	100.0	5	7	ADI10838	Cell surf
36	15	100.0	5	7	ADI10844	Cell surf
37	15	100.0	5	7	ADI10846	Cell surf
38	15	100.0	5	7	ADI10553	Cell surf
39	15	100.0	5	7	ADI10552	Cell surf
40	15	100.0	5	7	ADI10555	Cell surf
41	15	100.0	5	7	ADI10842	Cell surf
42	15	100.0	5	7	ADI10849	Cell surf
43	15	100.0	5	8	ADI32462	Phage dis
44	15	100.0	5	8	ADI32466	Phage dis
45	15	100.0	5	8	ADI32454	Phage dis

## ALIGNMENTS

## RESULT 1

AAR22517  
ID AAR22517 standard; peptide; 4 AA.

AC AAR22517;

XX 20-NOV-1992 (first entry)

XX Peptide or peptide-analogue kininogenase inhibitor.

XX Kininogenase inhibitor; kallikrein; antiinflammatory; antiasthmatic;

KW antiallergic; hay fever; antispasmodic; smooth muscle spasm;

KW antihypotensive; hypotension; oedema; pain; analgesia; irritation.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "D-Arg"

FT Modified-site 4 /note= "Ser-NH2"

XX WO9204371-A.

XX 19-MAR-1992.

XX 02-SEP-1991; 91WO-GB001479.

XX 07-SEP-1990; 90GB-00019558.

XX (FERR ) FERRING PEPTIDE RES.

XX Szelke M, Evans DM, Jones DM;

XX WPI, 1992-114296/14.

XX New di:peptide analogues not exceeding size of hexa:peptide - are kininogenase inhibitors for treating inflammatory disorders and hypertension, etc.

XX Disclosure; Page 21; 70pp; English.

XX The peptide is one specific example of a group of highly generic peptide analogues not exceeding the size of a hexapeptide, based on the known amino acid sequence of the kininogens at cleavage site 1, which analogues have sufficient similarity to the cleavage site sequence to bind to the active site of the kininogenase but are not hydrolysable and therefore remain bound, inactivating the enzyme. The kininogenase inhibitors are

CC useful for the treatment or prophylaxis of inflammatory disorders (esp.  
 CC allergic inflammation disorders such as asthma and hay fever), smooth  
 CC muscle spasms, hypotension, oedema, pain and irritation

XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 15; DB 2; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4  
 | : | |  
 Db 1 RFRS 4

RESULT 2  
 AAW74084  
 ID AAW74084 standard; peptide; 4 AA.  
 XX AC AAW74084;  
 XX  
 DT 04-MAY-1999 (first entry)  
 XX  
 DE Fragment of gastro-intestinal transport receptor binding peptide.  
 XX  
 KW Gastro-intestinal transport receptor; binding protein; hSI; HPT1; D2H;  
 KW hPEPT1; human; GI tract receptor; sucrose-isomaltase complex;  
 KW intestinal peptide-associated transporter; hypertension; diabetes;  
 KW osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris;  
 KW therapeutic agent delivery; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09851325-A2.  
 XX  
 PD 19-NOV-1998.  
 XX  
 PF 15-MAY-1998; 98WO-US010088.  
 XX  
 PR 15-MAY-1997; 97US-0046595P.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (ELAN-) ELAN CORP PLC.  
 XX  
 PI Alvarez VL, Mahony DJ, Lambkin IJ, Patterson CA, Singleton J;  
 PI Belinka BA, Carter JM, Cagney GM;  
 XX WPI; 1999-009568/01.  
 XX  
 PT New proteins that bind specifically to receptors in the gastro-intestinal  
 PT tract and related nucleic acid - chimaeras and antibodies, used to  
 PT deliver therapeutic or diagnostic agents to, or through, the  
 PT gastrointestinal tract, e.g. insulin or leuprolide.  
 XX  
 PS Claim 20; Page 237; 294pp; English.  
 XX  
 CC This sequence represents a fragment of a protein of the invention. The  
 CC invention relates to purified proteins (I) that bind specifically to at  
 CC least one of the gastro-intestinal (GI) tract receptors human intestinal  
 CC peptide-associated transporter (HPT1), hPEPT1, D2H and human sucrose-  
 CC isomaltase complex (hSI). (I) provide active transport of therapeutic  
 CC agents through human and animal GI tissue (into the blood) for in vivo  
 CC delivery, particularly for treatment or prevention of hypertension,  
 CC diabetes, osteoporosis, haemophilia, anaemia, cancer, migraine, or angina  
 CC pectoris. Specifically they are used to deliver insulin or leuprolide,  
 CC but many other suitable therapeutic agents are disclosed, including genes  
 CC or inhibitory nucleic acid, imaging agents and antigens. (I) may also  
 CC provide targeting to the GI tract. Other uses of (I) are: (i) to  
 CC determine the level of specified receptors in a sample (in a binding  
 CC assay); and (ii) to screen for molecules that bind (I). Immunogenic  
 CC analogues or derivatives of (I) are used to raise antibodies and in  
 CC immunoassays. The antibodies are used to locate, detect and measure (I),  
 CC e.g. for imaging, monitoring treatment, tissue analysis etc., also for

CC peptide purification and immobilisation  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 15; DB 2; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4  
 | : | |  
 Db 1 RFRS 4

RESULT 3  
 AAY34297  
 ID AAY34297 standard; peptide; 4 AA.  
 XX AC AAY34297;  
 XX  
 DT 19-NOV-1999 (first entry)  
 XX  
 DE Consensus binding site for antibody ABX-CBL.  
 XX  
 KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site.  
 XX  
 OS Synthetic.  
 XX  
 PN W09945031-A2.  
 XX  
 PD 10-SEP-1999.  
 XX  
 PF 03-MAR-1999; 99WO-US004583.  
 XX  
 PR 03-MAR-1998; 98US-00034607.  
 PR 03-FEB-1999; 99US-00244253.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
 XX WPI; 1999-540816/45.  
 XX  
 PT New monoclonal antibody, used for treating e.g. graft versus host  
 PT disease, cancers, autoimmune diseases and inflammatory diseases.  
 XX  
 PS Claim 24; Page 131; 245pp; English.  
 XX  
 CC This sequence represents a consensus binding site for the antibody of the  
 CC invention. The antibody is a monoclonal antibody (Mab) with an isotype on  
 CC that fixes complement and a variable region that binds to the epitope on  
 CC CD147 bound by the IGM Mab ABX-CBL, providing that the antibody is not  
 CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells  
 CC or rearing or activated monocytes. The products and methods can be used  
 CC for treating diseases involving activated T-cells or B-cells or  
 CC monocytes, e.g. graft versus host disease (GVHD), organ transplant  
 CC rejection diseases (e.g. renal transplant, ocular transplant), cancers  
 CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and  
 CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases  
 CC (e.g. arthritis)  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 15; DB 2; Length 4;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4  
 | : | |  
 Db 1 RFRS 4

RESULT 4  
AAY34295  
ID AAY34295 standard; peptide; 4 AA.  
XX  
AC AAY34295;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE Consensus binding site for antibody ABX-CBL.  
XX  
KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocytic; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 2 /note= "unspecified amino acid"  
XX  
PN WO9945031-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 03-MAR-1999; 99WO-US004583.  
XX  
PR 03-MAR-1998; 98US-00034607.  
PR 03-FEB-1999; 99US-00244253.  
XX  
PA (ABGE-) ABGENIX INC.  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX  
DR WPI; 1999-540816/45.  
XX  
XX New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX  
PS Claim 24; Page 131; 245pp; English.  
XX  
CC This sequence represents a consensus binding site for the antibody of the  
CC invention. The antibody is a monoclonal antibody (Mab) with an isotype  
CC that fixes complement and a variable region that binds to the epitope on  
CC CD147 bound by the IGM Mab ABX-CBL, providing that the antibody is not  
CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells  
CC or resting or activated monocytes. The products and methods can be used  
CC for treating diseases involving activated T-cells or B-cells or  
CC monocytes, e.g. graft versus host disease (GVHD), organ transplant  
CC rejection diseases (e.g. renal transplant, ocular transplant), cancers  
CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and  
CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases  
CC (e.g. arthritis)  
XX  
SQ Sequence 4 AA;  
XX  
Query Match 100.0%; Score 15; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RXRS 4  
Db 1 RXRS 4  
XX  
RESULT 5  
AAG68362  
ID AAG68362 standard; peptide; 4 AA.  
XX  
AC AAG68362;  
XX

XX  
DT 01-MAR-2002 (first entry)  
XX  
DE Tomato mosaic virus related peptide #2.  
XX  
KW Tomato mosaic virus; vaccine K; low-virulent vaccine K genome;  
KW point mutation; replicase; motor protein; plant virus genome;  
KW genetic engineering; viral disease; plant.  
XX  
OS Tomato mosaic virus.  
XX  
PN CN1306090-A.  
XX  
PD 01-AUG-2001.  
XX  
PF 14-JAN-2000; 2000CN-00100211.  
XX  
PR 14-JAN-2000; 2000CN-00100211.  
XX  
PA (MICR-) INST MICROBIOLOGY CHINESE ACAD SCI.  
XX  
PI Qiu B, Yang G, Tian B;  
XX  
DR WPI; 2002-000227/01.  
XX  
PT Low-virulent vaccine K genom sequence of tomato mosaic.  
XX  
PS Example 7; Page 10 (Disclosure); 22pp; Chinese.  
XX  
CC The present invention describes the genome separated and cloned from  
CC tomato mosaic virus, which is modified into low-virulent vaccine K genome  
CC by point mutation. The nucleotide sequence of its coded replicase and  
CC motor protein has the mutation, so it can be used to modify the plant  
CC virus genome and prepare genetically engineered vaccine for effectively  
CC preventing and treating the viral diseases of plants. The present  
CC sequence represents a peptide which is used in an example from the  
CC present invention  
XX  
SQ Sequence 4 AA;  
XX  
Query Match 100.0%; Score 15; DB 5; Length 4;  
Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RXRS 4  
Db 1 RXRS 4  
XX  
RESULT 6  
AAG68364  
ID AAG68364 standard; peptide; 4 AA.  
XX  
AC AAG68364;  
XX  
DT 01-MAR-2002 (first entry)  
XX  
DE Tomato mosaic virus related peptide #4.  
XX  
KW Tomato mosaic virus; vaccine K; low-virulent vaccine K genome;  
KW point mutation; replicase; motor protein; plant virus genome;  
KW genetic engineering; viral disease; plant.  
XX  
OS Tomato mosaic virus.  
XX  
PN CN1306090-A.  
XX  
PD 01-AUG-2001.  
XX  
PF 14-JAN-2000; 2000CN-00100211.  
XX  
PR 14-JAN-2000; 2000CN-00100211.  
XX





OS Homo sapiens;  
 XX WO200281657-A2.  
 XX  
 XX PD 17-OCT-2002.  
 XX  
 XX PF 01-APR-2002; 2002WO-US009743.  
 XX  
 XX PR 30-MAR-2001; 2001US-00820923.  
 XX  
 XX PA (PEKE ) PE CORP NY.  
 XX PA (BEAS/) BEASLEY E M.  
 XX PA (WEIM/) WEI M.  
 XX PA (KETC/) KETCHUM K A.  
 XX PA (DFRA/) DI FRANCESCO V.  
 XX  
 XX PI Beasley EM, Wei M, Ketchum KA, Di Francesco V;  
 XX  
 XX DR WPI; 2003-058533/05.  
 XX  
 XX PT Novel isolated human transporter peptide useful for treating disorder  
 PT characterized by absence of, in appropriate or unwanted expression of the  
 PT transporter protein, and as immunogens to raise antibodies.  
 XX  
 XX PS Disclosure; Fig 2A; 75pp; English.  
 XX  
 XX CC The present sequence is that of a cAMP- and cGMP-dependent protein kinase  
 CC phosphorylation site located at amino acid residues 120-123 of a novel  
 CC human transporter protein (see ABP55112) of the invention. Unique peptide  
 CC sequences from the transporter protein, and nucleic acids encoding them,  
 CC can be used as models for the development of human therapeutic targets,  
 CC aid in the identification of therapeutic proteins, and serve as targets  
 CC for the development of therapeutic agents that modulate transporter  
 CC activity in cells and tissues that express the transporter  
 XX  
 XX SQ Sequence 4 AA;  
 XX  
 XX Query Match 100.0%; Score 15; DB 6; Length 4;  
 XX Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 RXRS 4  
 XX Db ||||  
 XX 1 RRRS 4  
 XX  
 XX RESULT 9  
 XX ADM72392  
 XX ID ADM72392 standard; peptide; 4 AA.  
 XX AC ADM72392;  
 XX  
 XX DT 01-JUL-2004 (first entry)  
 XX  
 XX DE cAMP and cGMP-dependent protein phosphorylation site.  
 XX  
 XX KW Plant; nematode-regulated polypeptide; calcium dependent protein kinase;  
 KW CDPK; nematode-responsive transcription factor 1; NRTF1;  
 KW nematode-responsive protein; NRP; caffeic acid 7-O-methyltransferase;  
 KW 7OM; inositol 5-phosphatase; IPP; nematocidal; gene therapy;  
 KW nematode resistance; enzyme.  
 XX  
 XX OS Synthetic.  
 XX  
 XX PN WO2004029222-A2.  
 XX  
 XX PD 08-APR-2004.  
 XX  
 XX PF 30-SEP-2003; 2003WO-US031029.  
 XX  
 XX PR 30-SEP-2002; 2002US-0414771P.  
 XX  
 XX PA (PION-) PIONEER HI-BRED INT INC.

XX Hu X, Lu G;  
 XX WPI; 2004-316104/29.  
 XX  
 XX PT New isolated nucleic acid molecules encoding nematode-responsive  
 PT proteins, useful for conferring or improving nematode resistance in  
 PT plants.  
 XX  
 XX PS Disclosure; SEQ ID NO 30; 143pp; English.  
 XX  
 XX CC The invention relates to pathogen-responsive genes that encode a nematode  
 CC regulated polypeptides. The proteins of the invention include calcium  
 CC dependent protein kinase (CDPK), nematode-responsive transcription factor  
 CC 1 (NRTF1), nematode-responsive protein (NRP), caffeic acid 7-O-  
 CC methyltransferase (7OM) or inositol 5-phosphatase (IPP) polypeptides. The  
 CC nucleic acid molecule encoding the polypeptides are operably linked to a  
 CC promoter that drives expression in a host cell. The composition and  
 CC methods are useful for conferring or improving nematode resistance in  
 CC plants. The present sequence represents a cAMP and cGMP-dependent protein  
 CC phosphorylation site peptide fragment.  
 XX  
 XX SQ Sequence 4 AA;  
 XX  
 XX Query Match 100.0%; Score 15; DB 8; Length 4;  
 XX Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 RXRS 4  
 XX Db ||||  
 XX 1 RRRS 4  
 XX  
 XX RESULT 10  
 XX ADR45631  
 XX ID ADR45631 standard; peptide; 4 AA.  
 XX AC ADR45631;  
 XX  
 XX DT 02-DEC-2004 (first entry)  
 XX  
 XX DE Human STMST-2 cGMP-dependent protein kinase phosphorylation site #4.  
 XX  
 XX KW Human; ITALY; Lysyl Oxidase Related-2; LOR-2; STRIFE; TRASH;  
 KW Brain-derived Signaling Factor; BDSF; Leucine-rich Surface Glycoprotein;  
 KW LRSG; Seven Transmembrane Signal Transducer; STMST; cancer; obesity;  
 KW gastritis; diarrhoea; constipation; haemorrhoid; asthma; anaemia;  
 KW thrombocytopaenia; graft-versus-host disease; allergy; cystic fibrosis;  
 KW hypogonadism; cardiovascular disorder; arthritis; osteoarthritis;  
 KW arteriosclerosis; hypertension; bacterial infection; psoriasis;  
 KW diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;  
 KW Parkinson's disease; systemic lupus erythematosus;  
 KW Chediak-Higashi syndrome; AIDS; tuberculosis; viral infection; malaria;  
 KW goitre; infertility; endometriosis; wound; muscular disorder;  
 KW Interleukin ten Associated Locus Yang.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN US2004176296-A1.  
 XX  
 XX PD 09-SEP-2004.  
 XX  
 XX PF 22-MAR-2004; 2004US-00806018.  
 XX  
 XX PR 27-JAN-1998; 98US-00014195.  
 XX PR 27-JAN-1998; 98US-00014348.  
 XX PR 27-MAR-1998; 98US-00049799.  
 XX PR 21-APR-1998; 98US-00063950.  
 XX PR 29-MAY-1998; 98US-00086892.  
 XX PR 29-MAY-1998; 98US-00087121.  
 XX PR 27-JAN-1999; 99US-0117580P.  
 XX PR 25-MAR-1999; 99US-00276400.  
 XX PR 21-APR-1999; 99US-00296208.

```

PR 23-NOV-1999; 99US-00448076.
PR 27-JAN-2000; 2000WO-US002125.
PR 28-APR-2000; 2000US-00561381.
PR 28-APR-2000; 2000US-00561810.
PR 28-SEP-2000; 2000US-00672721.
PR 13-FEB-2001; 2001US-00782980.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Holtzman DA, McCarthy SA, Macbeth KJ, Busfield SJ, Pan Y;
PI White D, Khodadoust MW, Gu W;
XX
XX WPI; 2004-661401/64.
XX
XX New ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG and STMST polypeptide and
PT encoding nucleic acid molecule, useful in diagnosing or treating cancer,
PT diabetes, psoriasis, hepatitis and Alzheimer's disease.
XX
XX Example 13; SEQ ID NO 103; 259pp; English.
XX
XX The invention relates to an isolated Interleukin Ten Associated Locus
CC Yang (ITALY), Lysoyl Oxidase Related-2 (LOR-2), STRIFE, TRASH, Brain-
CC derived Signaling Factor (BDSF), Leucine-rich Surface Glycoprotein (LRSG)
CC and Seven Transmembrane Signal Transducer (STMST) nucleic acid molecule
CC and their encoded proteins. Also included are a host cell which contains
CC any of the above nucleic acids, a non-human mammalian host cell
CC containing any of the above nucleic acids, an isolated polypeptide
CC encoded by the isolated nucleic acid molecule as cited above (or their
CC complement), an antibody which selectively binds with the polypeptide, a
CC method for producing the polypeptide, a method for detecting the presence
CC of a polypeptide in a sample, a method for detecting the presence of any
CC of the above nucleic acids in a sample, a kit comprising a compound which
CC selectively binds with a polypeptide or a compound which selectively
CC hybridises with the nucleic acid molecule cited above (and instructions
CC for use), a method for identifying a compound which binds with a
CC polypeptide, a method for modulating the activity of a polypeptide, a
CC method for identifying a compound which modulates the activity of a
CC polypeptide, and a method of making an antibody substance which
CC selectively binds with the polypeptide. The nucleic acid molecules and
CC the encoded polypeptides and compositions are useful in diagnosing,
CC preventing, and treating cancer, obesity, gastritis, diarrhoea,
CC constipation, haemorrhoids, asthma, anaemia, thrombocytopaenia, graft-
CC versus-host reactions, allergic reactions, cystic fibrosis, hypogonadism,
CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease, systemic lupus erythematosus, Chediak-Higashi syndrome, AIDS,
CC tuberculosis, viral infections, malaria, goitre, infertility,
CC endometriosis, wounds, or muscular disorders. The present sequence
CC represents motif/domain/region identified in one of the novel proteins of
CC the invention.
XX
XX SQ Sequence 4 AA;
Query Match 100.0%; Score 15; DB 8; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RXRS 4
Db 1 RRRS 4
|:|
|:|
RESULT 11
AAW56878
ID AAW56878 standard; peptide; 5 AA.
XX
XX AC AAW56878;
XX
XX 28-JUL-1998 (first entry)
XX
XX DE Enzyme inhibitor peptide SEQ ID NO:79.
XX

```

---

```

KW Enzyme inhibitor; t-PA; u-PA; chymotrypsin; serine protease; active;
KW latent; substrate subtraction phage display peptide library;
XX identification; kinase; phosphatase; serpin.
OS Homo sapiens.
XX WO9747314-A1.
XX
XX 18-DEC-1997.
XX
XX 10-JUN-1997; 97WO-US009760.
XX
XX 10-JUN-1996; 96US-0019495P.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Madison EL, Ke S;
XX
XX WPI; 1998-062746/06.
XX
XX Substrate subtraction phage display peptide libraries - used to
PT distinguish between active and latent forms of enzyme, e.g. serine
PT protease.
XX
XX Claim 25; Page 66; 138pp; English.
XX
XX The present sequence represents an enzyme inhibitor peptide used in the
CC method of the invention to distinguish between t-PA and u-PA. The present
CC invention describes a substrate subtraction library for the
CC identification of peptide substrates selective between a first enzyme
CC (E1) and a second enzyme (E2), comprising a collection of different
CC peptides, substantially lacking peptides that are effective substrates
CC for E1. Also described are: (1) a method (M1) for identifying peptide
CC substrates selective between a first enzyme (E1) and a second enzyme (E2)
CC ; (2) a compound comprising the amino acid sequence of a peptide
CC identified by M1; (3) a polypeptide for use as an enzyme inhibitor
CC comprising one of 237 amino acid sequences (see AAW56801 to AAW56947, and
CC AAW56949 to AAW57038); (4) a recombinant DNA vector comprising DNA (I)
CC encoding a protease inhibitor including the sequence identified by the M1
CC ; (5) a prokaryotic or eukaryotic cell containing the vector of (4); (6)
CC an antibody (Ab) immunoreactive with at least one of the peptides
CC identified by M1; and (7) a diagnostic assay for distinguishing between
CC active and latent forms of protease inhibitors, that uses (Ab). The
CC library and method are used for distinguishing between active and latent
CC forms of enzyme inhibitors, e.g. proteases, kinases and phosphatases.
CC (Ab) are used for affinity purification of recombinant peptides and in
CC the identification of naturally occurring protease inhibitors. Enzyme-
CC inhibiting peptides identified can be used to treat a serpin deficiency
CC or a disorder of serine proteases
XX
XX SQ Sequence 5 AA;
Query Match 100.0%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RXRS 4
Db 1 RGRS 4
|:|
|:|
RESULT 12
AAAY21060
ID AAY21060 standard; protein; 5 AA.
XX
XX AC AAY21060;
XX
XX 22-JUL-1999 (first entry)
XX
XX DE Human p53 cellular tumour antigen mutant protein fragment 7.
XX
XX KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;

```

KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; MSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX  
 PN W09845322-A2.  
 XX  
 PD 15-OCT-1998.  
 XX  
 XX 02-APR-1998; 98WO-IB000705.  
 XX  
 XX 10-APR-1997; 97US-0043163P.  
 XX  
 XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
 PA (UYUT-) RIJKSUNIV UTRECHT.  
 XX  
 PI Van Leeuwen FW, Grosveld FG, Burbach JPH;  
 XX  
 DR WPI; 1998-609901/51.  
 DR N-PSDB; AAX75765.  
 XX  
 XX Diagnosing disease by detecting frameshift mutations in RNA or  
 PT corresponding protein mutations - used to diagnose cancer and  
 PT neurological diseases, particularly Alzheimer's disease, and also for  
 PT treatment and prevention with specific ribozymes or wild-type RNA.  
 XX  
 PS Disclosure; Fig 14; 258pp; English.  
 XX  
 CC This invention describes a novel method for the diagnosis of a disease  
 CC caused by, or associated with, an RNA molecule that has a frameshift  
 CC mutation. The method is used to diagnose age-related diseases, especially  
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 CC and many others listed) or susceptibility to these disorders. The method  
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
 CC at an early stage. It is based on the observation that disease may be  
 CC caused by mutations in RNA rather than DNA. The invention describes the  
 CC use of neuronal system RNA molecules, specifically proteins including  
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
 CC proteins tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
 CC protein-C (HMGP-C) and neuroendocrine specific protein A  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 15; DB 2; Length 5;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RXRS 4  
 Db 1 RPRS 4  
 RESULT 13  
 AAY34296  
 ID AAY34296 standard; peptide; 5 AA.  
 XX  
 AC AAY34296;  
 XX  
 DT 19-NOV-1999 (first entry)

XX Consensus binding site for antibody ABX-CBL.  
 DE  
 XX  
 KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 2 /note= "unspecified amino acid"  
 FT  
 XX W09945031-A2.  
 XX  
 PD 10-SEP-1999.  
 XX  
 XX 03-MAR-1999; 99WO-US004583.  
 XX  
 XX 03-MAR-1998; 98US-00034607.  
 PR 03-FEB-1999; 99US-00244253.  
 XX  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
 XX  
 XX WPI; 1999-540816/45.  
 DR  
 XX New monoclonal antibody, used for treating e.g. graft versus host  
 PT disease, cancer, autoimmune diseases and inflammatory diseases.  
 FT  
 XX  
 PS Claim 24; Page 131; 245pp; English.  
 XX  
 CC This sequence represents a consensus binding site for the antibody of the  
 CC invention. The antibody is a monoclonal antibody (MAB) with an isotype  
 CC that fixes complement and a variable region that binds to the epitope on  
 CC CD147 bound by the IGM MAB ABX-CBL, providing that the antibody is not  
 CC CBL1. The MAB can selectively kill activated T-cells, activated B-cells  
 CC or resting or activated monocytes. The products and methods can be used  
 CC for treating diseases involving activated T-cells or B-cells or  
 CC monocytes, e.g. graft versus host disease (GVHD), organ transplant  
 CC rejection diseases (e.g. renal transplant, ocular transplant), cancers  
 CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and  
 CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases  
 CC (e.g. arthritis)  
 CC  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 15; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RXRS 4  
 Db 1 RXRS 4  
 RESULT 14  
 AAY34298  
 ID AAY34298 standard; peptide; 5 AA.  
 XX  
 AC AAY34298;  
 XX  
 DT 19-NOV-1999 (first entry)  
 XX  
 XX Consensus binding site for antibody ABX-CBL.  
 DE  
 XX  
 KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site.

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XX OS Synthetic.
XX PN WO9945031-A2.
XX PD 10-SEP-1999.
XX PF 03-MAR-1999; 99WO-US004583.
XX PR 03-MAR-1998; 98US-00034607.
XX PR 03-FEB-1999; 99US-00244253.
XX PA (ABGE-) ABGENIX INC.
XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;
XX WPI; 1999-540816/45.
XX New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX Claim 24; Page 131; 245pp; English.
XX This sequence represents a consensus binding site for the antibody of the
CC invention. The antibody is a monoclonal antibody (Mab) with an isotype
CC that fixes complement and a variable region that binds to the epitope on
CC CD147 bound by the IGM Mab ABX-CBL, providing that the antibody is not
CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells
CC or resting or activated monocytes. The products and methods can be used
CC for treating diseases involving activated T-cells or B-cells or
CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
CC rejection diseases (e.g. renal transplant, ocular transplant) cancers
CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
CC (e.g. arthritis)
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4
Db 1 RVRS 4

RESULT 15
AAW98065
XX ID AAW98065 standard; peptide; 5 AA.
XX AC AAW98065;
XX 21-JUN-1999 (first entry)
XX DT
XX DE Sorting signal charged tail.
XX KW Sortase-transamidase; Gram-positive bacterium; peptidoglycan; antibiotic;
XX screening; peptide display; protein display; infection; diagnosis;
XX therapy; vaccine; sorting signal; proteinase.
XX OS Synthetic.
XX PN WO9909145-A1.
XX PD 25-FEB-1999.
XX PF 03-AUG-1998; 98WO-US016229.
XX PR 14-AUG-1997; 97US-0055662P.
XX PA (REGC ) UNIV CALIFORNIA.

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XX PI Schneewind O, Mazmanian S, Ton-That H;
XX DR WPI; 1999-190156/16.
XX New isolated sortase-transamidase enzyme - obtained from Staphylococcus
PT aureus, used to develop products for treating infections or for
PT displaying polypeptides on gram-positive bacteria.
XX Disclosure; Page 16; 98pp; English.
XX This synthetic peptide is useable as the charged tail portion of a sorting
CC signal. Novel sortase-transamidase (S-T) enzymes of the invention (see
CC AAW98038 and AAW98040) catalyse a reaction that covalently cross-links
CC the C-terminus of a protein having a sorting signal to the peptidoglycan
CC of a Gram-positive bacterium. The sorting signal has: (a) a motif (see
CC AAW98037) that is cleaved by the S-T; (b) a hydrophobic domain (see
CC AAW98045-50) of at least 31 amino acids carboxyl to the motif; and (c) a
CC charged tail region (see AAW98051-66). Novel isolated S-T enzymes are
CC utilised in methods of surface display of peptides and proteins, and can
CC also be utilised in the production of vaccines against antigens that can
CC be covalently bound to the surfaces of Gram-positive bacteria, and in
CC methods for the diagnosis and treatment of bacterial infections
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4
Db 1 RSRSS 4

Search completed: March 8, 2005, 06:16:59
Job time : 3.85451 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 0.355347 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-13

Perfect score: 23

Sequence: 1 RXRSH 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	42	1	WIBP17
2	23	100.0	42	2	gene 1.1 protein -
3	23	100.0	46	1	hypothetical prote
4	23	100.0	46	1	ribosomal protein
5	23	100.0	46	2	50S ribosomal prot
6	23	100.0	46	2	50S ribosomal subu
7	23	100.0	46	2	hypothetical prote
8	23	100.0	47	1	ribosomal protein
9	23	100.0	47	2	50S ribosomal prot
10	23	100.0	50	2	aspartic proteinas
11	23	100.0	51	2	ribosomal protein
12	23	100.0	58	2	hypothetical prote
13	23	100.0	63	2	hypothetical prote
14	23	100.0	68	2	hypothetical prote
15	23	100.0	68	2	hypothetical prote
16	23	100.0	92	2	protamine 2 precur
17	23	100.0	100	2	hypothetical prote
18	23	100.0	102	2	hypothetical prote
19	23	100.0	105	2	hypothetical prote
20	23	100.0	108	2	hypothetical prote
21	23	100.0	114	2	phytochrome - Meso
22	23	100.0	115	2	protamine 2 precur
23	23	100.0	118	2	hypothetical prote
24	23	100.0	118	2	hypothetical prote
25	23	100.0	119	2	hypothetical prote
26	23	100.0	123	2	hypothetical prote
27	23	100.0	124	2	hypothetical prote
28	23	100.0	125	2	hypothetical prote
29	23	100.0	127	2	hypothetical prote

30	23	100.0	129	2	T03248
31	23	100.0	130	2	calmodulin-binding
32	23	100.0	130	2	hypothetical prote
33	23	100.0	131	1	hypothetical prote
34	23	100.0	132	2	spermatid transiti
35	23	100.0	132	2	conserved hypothet
36	23	100.0	133	2	hypothetical prote
37	23	100.0	134	2	hypothetical 2b pr
38	23	100.0	136	2	hypothetical prote
39	23	100.0	139	2	finger protein (cl
40	23	100.0	141	2	hypothetical prote
41	23	100.0	141	2	unknown protein en
42	23	100.0	141	2	hypothetical prote
43	23	100.0	141	2	hypothetical prote
44	23	100.0	141	2	hypothetical prote
45	23	100.0	141	2	unknown protein en

ALIGNMENTS

RESULT 1

WIBP17

gene 1.1 protein - phase T7

C:Species: phase T7

C>Date: 28-Feb-1981 #sequence revision 01-Sep-1981 #text\_change 09-Jul-2004

C:Accession: E43002; E43004; A93851; S42290; A04404

R:Dunn, J.J.; Thompson, K.

submitted to the Nucleic Acid Sequence Database, September 1982

A:Reference number: A94615

A:Accession: E43002

A:Molecule type: DNA

A:Residues: 1-42 <DUN>

A:Cross-references: UNIPROT:P03779

R:Dunn, J.J.; Studier, F.W.

J. Mol. Biol. 148, 303-330, 1981

A:Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the be

A:Reference number: A92866; MUID:82078034; PMID:7310871

A:Accession: E43004

A:Molecule type: DNA

A:Residues: 1-42 <DU2>

A:Cross-references: GB:V01127; NID:g15498; PIDN:CAA24334.1; PID:g15506

R:Saito, H.; Tabor, S.; Tamanoi, F.; Richardson, C.C.

Proc. Natl. Acad. Sci. U.S.A. 77, 3917-3921, 1980

A:Reference number: A93851; MUID:81054683; PMID:6254001

A:Accession: A93851

A:Molecule type: DNA

A:Residues: 1-42 <SAI>

A:Cross-references: GB:V01126; NID:g15495; PIDN:CAA24324.1; PID:g15496

R:Dunn, J.J.; Studier, F.W.

J. Mol. Biol. 166, 477-535, 1983

A:Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 ge

A:Reference number: S42283; MUID:83241725; PMID:6864790

A:Accession: S42290

A:Molecule type: DNA

A:Residues: 1-42 <DUW>

A:Cross-references: EMBL:V01146; NID:g431187; PIDN:CAA24391.1; PID:g15570

C:Comment: The function of this early gene protein is unknown.

C:Genetics:

A:Gene: 1.1

A:Map position: 15.02-15.33

C:Superfamily: phase T7 gene 1.1 protein

Query Match 100.0%; Score 23; DB 1; Length 42;

Best Local Similarity 80.0%; Pred. No. 81;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5

|||

Db 31 RDRSH 35

## RESULT 2

F82691  
hypothetical protein XF1351 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: F82691  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A02515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: F82691  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-42 <SIM>  
A:Cross-references: UNIPROT:Q9PDM8; GB:AE0033967; GB:AE0033849; NID:g9106347; PIDN:AAF8416  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briñones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Roes, A.J. de M.; de Roes Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1351

Query Match 100.0%; Score 23; DB 2; Length 42;

Best Local Similarity 80.0%; Pred. No. 81;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5

Db 24 KTRSH 28

## RESULT 3

R5EC34  
ribosomal protein L34 [validated] - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C>Date: 12-Aug-1981 #sequence\_revision 12-Aug-1991 #text\_change 09-Jul-2004  
C:Accession: C21915; A02836; S11620; H65172  
R:Hansen, F.G.; Hansen, E.B.; Aclung, T.  
EMBO J. 1, 1043-1048, 1982  
A:Title: The nucleotide sequence of the dnaA gene promoter and of the adjacent rpmH gene  
A:Reference number: A21915; MUID:84236082; PMID:6329723  
A:Accession: C21915  
A:Molecule type: DNA  
A:Residues: 1-46 <HAN>  
A:Cross-references: UNIPROT:P02437; GB:J01602; NID:q145758; PIDN:AAB59148.1; PID:gl45759  
R:Chen, R.

Hoppe-Seyler's Z. Physiol. Chem. 357, 873-886, 1976

A:Title: The sequence determination of a protein in a micro scale: the sequence analysis  
A:Reference number: A02836; MUID:76258983; PMID:783033

A:Accession: A02836

A:Molecule type: protein

A:Residues: 1-46 <CHE>

A:Experimental source: strain K12

R:Kashiwagi, K.; Igarashi, K.

Biochim. Biophys. Acta 911, 180-190, 1987

A:Title: Nonspecific inhibition of Escherichia coli ornithine decarboxylase by various  
A:Reference number: S11620; MUID:87101185; PMID:3542048

A:Accession: S11620

A:Molecule type: protein

A:Residues: 1-46 <KAS>

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: H65172  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-46 <BLAT>  
A:Cross-references: GB:AE000447; GB:U00096; NID:q2367266; PIDN:AAC76726.1; PID:gl790138;  
A:Experimental source: strain K-12, substrain MG1655  
R:Arnold, R.J.; Reilly, J.P.  
Anal. Biochem. 269, 105-112, 1999  
A:Title: Observation of Escherichia coli ribosomal proteins and their posttranslational n  
A:Reference number: A59071; MUID:99196679; PMID:10094780  
A:Contents: annotation; mass spectrographic analysis  
A:Note: no post-translational modifications were observed in mass spectrographic analysis  
C:Genetics:  
A:Gene: rpmH  
A:Map position: 83 min  
C:Complex: the ribosome is composed of the large (50S) and small (30S) subunit; the large  
S rRNA and 22 distinct proteins  
C:Complex: large subunit ribosomal proteins: L1 (PIR:R5EC1), L3 (PIR:R5EC3), L2 (PIR:R5EC  
(PIR:R5EC11), L13 (PIR:R5EC13), L14 (PIR:R5EC14), L15 (PIR:R5EC15), L16 (PIR:R5EC16), L1:  
C:Function:  
A:Pathway: protein biosynthesis  
A:Superfamily: Escherichia coli ribosomal protein L34  
C:Keywords: protein biosynthesis; ribosome  
F:1-46/Product: ribosomal protein L34 #status experimental <MAT>

Query Match 100.0%; Score 23; DB 1; Length 46;

Best Local Similarity 80.0%; Pred. No. 88;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5

Db 12 RNRSH 16

## RESULT 4

AH0957  
50s ribosomal protein L34 [imported] - Salmonella enterica subsp. enterica serovar Typhi  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AH0957  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AH0957  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-46 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD03156.1; PID:gl6504791; GSPDB:GN00176  
C:Genetics:  
A:Gene: rpmH  
A:Superfamily: Escherichia coli ribosomal protein L34

Query Match 100.0%; Score 23; DB 2; Length 46;

Best Local Similarity 80.0%; Pred. No. 88;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5

Db 12 RNRSH 16

## RESULT 5

H86054

50S ribosomal subunit protein L34 [imported] - Escherichia coli (strain O157:H7, substra

C:Species: Escherichia coli  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: H86054  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouasis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: H86054  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-46 <STO>  
 A:Cross-references: UNIPROT:P02437; GB:AE005174; NID:G12518542; PIDN:AA058900.1; GSPDB:C  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: rpmH  
 C:Superfamily: Escherichia coli ribosomal protein L34

Query Match 100.0%; Score 23; DB 2; Length 46;  
 Best Local Similarity 80.0%; Pred. No. 88;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
 |::|||  
 Db 12 RNRSH 16

RESULT 6  
 F91208  
 50S ribosomal subunit protein L34 [imported] - Escherichia coli (strain O157:H7, substra  
 C:Species: Escherichia coli  
 C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C:Accession: F91208  
 R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: F91208  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-46 <HAY>  
 A:Cross-references: UNIPROT:P02437; GB:BA000007; PIDN:BA038061.1; PID:G13364113; GSPDB:C  
 A:Experimental source: strain O157:H7, substrain RIMD 0509952  
 C:Genetics:  
 A:Gene: ECS4638  
 C:Superfamily: Escherichia coli ribosomal protein L34

Query Match 100.0%; Score 23; DB 2; Length 46;  
 Best Local Similarity 80.0%; Pred. No. 88;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
 |::|||  
 Db 12 RNRSH 16

RESULT 7  
 D71317  
 hypothetical protein TP0504 - syphilis spirochete  
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
 C>Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
 C:Accession: D71317  
 R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
 raon, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo  
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
 Science 281, 375-388, 1998  
 A>Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
 A:Reference number: A71250; MUID:98332770; PMID:9665876  
 A:Accession: D71317  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-46 <COL>

A:Cross-references: UNIPROT:O83517; GB:AE001226; GB:AE000520; NID:G33222785; PIDN:AA06549;  
 A:Experimental source: strain Nichols  
 C:Genetics:  
 A:Gene: TP0504

Query Match 100.0%; Score 23; DB 2; Length 46;  
 Best Local Similarity 80.0%; Pred. No. 88;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
 |::|||  
 Db 10 RARSH 14

RESULT 8  
 JC1154  
 ribosomal protein L34 - Buchnera aphidicola  
 C:Species: Buchnera aphidicola  
 C>Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
 C:Accession: JC1154  
 R:Lai, C.Y.; Baumann, P.  
 Gene 113, 175-181, 1992  
 A>Title: Genetic analysis of an aphid endosymbiont DNA fragment homologous to the rnpA-  
 A:Reference number: JC1154; MUID:92241666; PMID:1572539  
 A:Accession: JC1154  
 A:Molecule type: DNA  
 A:Residues: 1-47 <LAI>  
 A:Cross-references: UNIPROT:P29437; GB:M80817; NID:G144144; PIDN:AAA73148.1; PID:G144148  
 C:Genetics:  
 A:Gene: rpmH  
 C:Superfamily: Escherichia coli ribosomal protein L34  
 C:Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 23; DB 1; Length 47;  
 Best Local Similarity 80.0%; Pred. No. 90;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
 |::|||  
 Db 12 RNRSH 16

RESULT 9  
 EB4931  
 50S ribosomal protein L34 [imported] - Buchnera sp. (strain APS)  
 C:Species: Buchnera sp.  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 17-May-2002  
 C:Accession: EB4931  
 R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
 Nature 407, 81-86, 2000  
 A>Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. At  
 A:Reference number: AB4930; MUID:20445173; PMID:10993077  
 A:Accession: EB4931  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-47 <STO>  
 A:Cross-references: GB:AF000398; GSPDB:GN00144  
 A:Experimental source: strain APS  
 C:Genetics:  
 A:Gene: rpmH; BU013  
 C:Superfamily: Escherichia coli ribosomal protein L34

Query Match 100.0%; Score 23; DB 2; Length 47;  
 Best Local Similarity 80.0%; Pred. No. 90;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
 |::|||  
 Db 12 RNRSH 16

RESULT 10  
 JT0399

aspartic proteinase (EC 3.4.23.-) NM1 - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 12-Apr-1995  
C:Accession: J70399  
R:Lu, Q.; Wolfe, K.H.; McConnell, D.J.  
Gene 71, 135-146, 1988  
A:Title: Molecular cloning of multiple bovine aspartyl protease genes.  
A:Reference number: J70397; MUID:89108032; PMID:3145907  
A:Accession: J70399  
A:Molecule type: DNA  
A:Residues: 1-50 <LUQ>  
C:Superfamily: peptin  
C:Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion; stomach

Query Match 100.0%; Score 23; DB 2; Length 50;  
Best Local Similarity 80.0%; Pred. No. 95;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5  
|:|:|  
Db 32 RXRSH 36  
|:|:|

RESULT 11  
E69082  
ribosomal protein L39 - Methanobacterium thermoautotrophicum (strain Delta H)  
C:Species: Methanobacterium thermoautotrophicum  
C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: E69082  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional genome  
A:Reference number: A69000; MUID:98037514; PMID:9371463  
A:Accession: E69082  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-51 <MTH>  
A:Cross-references: UNIPROT:Q27650; GB:AE000920; GB:AE000666; NID:g2622729; PIDN:AAB8608  
A:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH1613  
C:Superfamily: rat ribosomal protein L39

Query Match 100.0%; Score 23; DB 2; Length 51;  
Best Local Similarity 80.0%; Pred. No. 97;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5  
|:|:|  
Db 34 RXRSH 38  
|:|:|

RESULT 12  
AI3030  
hypothetical protein Atu3853 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AI3030  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AI3030  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-58 <KUR>  
A:Cross-references: UNIPROT:Q8U975; GB:AE008689; PIDN:AAL44663.1; PID:g17742289; GSPDB:G

A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu3853  
A:Map position: linear chromosome

Query Match 100.0%; Score 23; DB 2; Length 58;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5  
|:|:|  
Db 50 RLRSH 54  
|:|:|

RESULT 13  
B70638  
hypothetical protein Rv1950c - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: B70638  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: B70638  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-63 <COL>  
A:Cross-references: UNIPROT:P95264; GB:Z84498; GB:AL123456; NID:g3261701; PIDN:CAB06511.1  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: Rv1950c

Query Match 100.0%; Score 23; DB 2; Length 63;  
Best Local Similarity 80.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5  
|:|:|  
Db 38 RNRSH 42  
|:|:|

RESULT 14  
S72952  
hypothetical protein - Mycobacterium leprae  
C:Species: Mycobacterium leprae  
C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S72952  
R:Smith, D.R.; Robinson, K.  
submitted to the EMBL Data Library, November 1993  
A:Description: Mycobacterium leprae cosmid L247.  
A:Reference number: S72589  
A:Accession: S72952  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-68 <SML>  
A:Cross-references: UNIPROT:Q49883; EMBL:U00021; NID:g467141; PIDN:AAA50912.1; PID:g467141  
C:Genetics:  
A:Start codon: GTG

Query Match 100.0%; Score 23; DB 2; Length 68;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5  
|:|:|  
Db 26 RLRSH 30  
|:|:|

RESULT 15



G65037  
hypochemical protein b2596 - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: G65037  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Accession: G65037  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-68 <BLAT>  
A:Cross-references: UNIPROT:P76595; GB:AE000346; GB:U00096; NID:G2367141; PIDN:AAC75645.  
A:Experimental source: strain K-12, substrain MG1655

Query Match 100.0%; Score 23; DB 2; Length 68;  
Best Local Similarity 80.0%; Pred.No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5  
|:|  
Db 18 RYRSH 22

Search completed: March 8, 2005, 06:39:19  
Job time : 2.40535 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 1.86725 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-13  
Perfect score: 23  
Sequence: 1 RXRSH 5

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	23	100.0	35	2 Q7BQA7	Q7bqa7 mycobacteri
2	23	100.0	41	2 O60686	O60686 homo sapien
3	23	100.0	42	1 V11_BFT7	P03779 bacterioph
4	23	100.0	42	2 Q6WY56	Q6wy56 bacterioph
5	23	100.0	42	2 Q6WYGO	Q6wygo bacterioph
6	23	100.0	42	2 Q9PDM8	Q9pdm8 xylella fas
7	23	100.0	45	2 Q7U525	Q7u525 synechococc
8	23	100.0	45	2 Q7V0S1	Q7v0s1 prochloroco
9	23	100.0	45	2 Q8EKT3	Q8ekt3 shewanella
10	23	100.0	46	1 RL34_ECOLI	P02437 escherichia
11	23	100.0	46	1 RL34_YERPE	O829u5 versinia pe
12	23	100.0	46	1 Y504_TREPA	O83517 treponema p
13	23	100.0	46	2 Q663T0	Q663t0 yersinia ps
14	23	100.0	46	2 Q7MXZ2	Q7mxz2 photorhabdu
15	23	100.0	46	2 Q6CYR2	P57129 buchnera ap
16	23	100.0	47	1 RL34_BUCAI	P29437 buchnera ap
17	23	100.0	47	1 RL34_BUCBP	Q29b35 buchnera ap
18	23	100.0	47	1 RL34_BUCBP	Q29b35 buchnera ap
19	23	100.0	51	1 RL39_METTH	O27650 methanobact
20	23	100.0	53	2 Q6Z7G2	Q6z7g2 oryza sativ
21	23	100.0	57	2 Q7YVK1	Q7yvk1 trypanosoma
22	23	100.0	58	2 Q8U975	O8u975 agrobacteri
23	23	100.0	59	2 Q8VWS3	Q8vws3 narcissus p
24	23	100.0	60	2 Q8YSD3	Q8yds3 oryza sativ
25	23	100.0	62	1 HSP1_PLATE	O18748 planigale t
26	23	100.0	62	2 Q8EIF5	Q8eif5 homo sapien
27	23	100.0	62	2 Q63326	Q63326 rattus norv
28	23	100.0	63	1 RL32_ACHLA	Q81395 acholeplasm
29	23	100.0	63	2 P95264	P95264 mycobacteri
30	23	100.0	63	2 Q7Z82	Q7cz82 mycobacteri
31	23	100.0	64	2 Q6W4W0	Q6w4w0 homo sapien

32	23	100.0	66	2 Q6DTY1	Q6dty1 homo sapien
33	23	100.0	66	2 Q6L982	Q6l982 homo sapien
34	23	100.0	66	2 Q6Z9W1	Q6z9w1 oryza sativ
35	23	100.0	66	2 Q62BX6	Q62bx6 burkholderi
36	23	100.0	67	2 Q91ER3	Q91er3 cydia pomon
37	23	100.0	68	2 Q96GH5	Q96gh5 homo sapien
38	23	100.0	68	2 Q9M676	Q9m676 cucumis mel
39	23	100.0	68	2 Q49883	Q49883 mycobacteri
40	23	100.0	68	2 P76595	P76595 escherichia
41	23	100.0	68	2 Q8C1N3	Q8c1n3 mus musculu
42	23	100.0	70	2 Q6EP25	Q6epz5 oryza sativ
43	23	100.0	70	2 Q67720	Q67720 human adeno
44	23	100.0	72	2 Q7N4I3	Q7n4i3 photorhabdu
45	23	100.0	72	2 Q7U2F8	Q7u2f8 mycobacteri

ALIGNMENTS

RESULT 1  
Q7BQA7 PRELIMINARY; PRT; 35 AA.  
AC Q7BQA7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Alkanal monooxygenase-like protein (Fragment).  
OS Mycobacterium phlei.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1771;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 354;  
RA Kim B.-K., Choi K.-P., Daniels L.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 354;  
RA Kim B.-K., Choi K.-P., Purwantini E., Bae Y.-M., Cho P., Kang S.-A.,  
RA Simpson D.R., Daniels L.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF152397; AAR92169.1; -.  
KW GO; GO:0004497; F:monooxygenase activity; IEA.  
FT NON TER 1  
SQ SEQUENCE 35 AA; 4068 MW; 87A1P4A0990C209F CRC64;  
Query Match 100.0%; Score 23; DB 2; Length 35;  
Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RXRSH 5  
Db 22 RLRSH 26  
RESULT 2  
O60686 PRELIMINARY; PRT; 41 AA.  
AC O60686;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DE Erythroid alpha-spectrin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99224641; PubMed=10215350;

```
RA Galluzzi L., Patardini M., Magnani M., Nicolas G., Lecomte M.C.,
RA Harper S., Speicher D.W.;
RT "cDNA sequence of the human erythroid alpha-spectrin: identification
RL of a base deletion in the sequence database.";
DR Blood 93:2421-2422(1999).
FT EMBL; AF060556; AAC15757.1; -.
SQ SEQUENCE 41 AA; 4677 MW; EAA3BFF0EB3CD36D CRC64;

Query Match 100.0%; Score 23; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 21 RGRSH 25

RESULT 3
V11_BPT7 STANDARD; PRT; 42 AA.
AC P03779;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gene 1.1 protein.
GN Name=1.1;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83241725; PubMed=6864790;
RA Dunn J.J., Studier F.W.;
RT "Complete nucleotide sequence of bacteriophage T7 DNA and the
RT locations of T7 genetic elements.";
RL J. Mol. Biol. 166:477-535(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82078034; PubMed=7310871;
RA Dunn J.J., Studier F.W.;
RT "Nucleotide sequence from the genetic left end of bacteriophage T7 DNA
RT to the beginning of gene 4.";
RL J. Mol. Biol. 148:303-330(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81054683; PubMed=6254001;
RA Saito H., Tabor S., Tananai F., Richardson C.C.;
RT "Nucleotide sequence of the primary origin of bacteriophage T7 DNA
RT replication: relationship to adjacent genes and regulatory elements.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3917-3921(1980).
CC -!- FUNCTION: Function of this early gene protein is unknown.
CC -----
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CC -----
DR EMBL; V01146; CAA24391.1; -.
DR EMBL; V01126; CAA24324.1; -.
DR EMBL; V01127; CAA24334.1; -.
DR PIR; E43002; W1BP17.
KW Early protein.
SQ SEQUENCE 42 AA; 5181 MW; 26FDF241A530F76F CRC64;

Query Match 100.0%; Score 23; DB 1; Length 42;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RA Galluzzi L., Patardini M., Magnani M., Nicolas G., Lecomte M.C.,
RA Harper S., Speicher D.W.;
RT "cDNA sequence of the human erythroid alpha-spectrin: identification
RL of a base deletion in the sequence database.";
DR Blood 93:2421-2422(1999).
FT EMBL; AF060556; AAC15757.1; -.
SQ SEQUENCE 41 AA; 4677 MW; EAA3BFF0EB3CD36D CRC64;

Query Match 100.0%; Score 23; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 21 RGRSH 25

RESULT 3
V11_BPT7 STANDARD; PRT; 42 AA.
AC P03779;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gene 1.1 protein.
GN Name=1.1;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83241725; PubMed=6864790;
RA Dunn J.J., Studier F.W.;
RT "Complete nucleotide sequence of bacteriophage T7 DNA and the
RT locations of T7 genetic elements.";
RL J. Mol. Biol. 166:477-535(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82078034; PubMed=7310871;
RA Dunn J.J., Studier F.W.;
RT "Nucleotide sequence from the genetic left end of bacteriophage T7 DNA
RT to the beginning of gene 4.";
RL J. Mol. Biol. 148:303-330(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81054683; PubMed=6254001;
RA Saito H., Tabor S., Tananai F., Richardson C.C.;
RT "Nucleotide sequence of the primary origin of bacteriophage T7 DNA
RT replication: relationship to adjacent genes and regulatory elements.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3917-3921(1980).
CC -!- FUNCTION: Function of this early gene protein is unknown.
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CC -----
DR EMBL; V01146; CAA24391.1; -.
DR EMBL; V01126; CAA24324.1; -.
DR EMBL; V01127; CAA24334.1; -.
DR PIR; E43002; W1BP17.
KW Early protein.
SQ SEQUENCE 42 AA; 5181 MW; 26FDF241A530F76F CRC64;

Query Match 100.0%; Score 23; DB 1; Length 42;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 21 RGRSH 25

RESULT 3
V11_BPT7 STANDARD; PRT; 42 AA.
AC P03779;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gene 1.1 protein.
GN Name=1.1;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83241725; PubMed=6864790;
RA Dunn J.J., Studier F.W.;
RT "Complete nucleotide sequence of bacteriophage T7 DNA and the
RT locations of T7 genetic elements.";
RL J. Mol. Biol. 166:477-535(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82078034; PubMed=7310871;
RA Dunn J.J., Studier F.W.;
RT "Nucleotide sequence from the genetic left end of bacteriophage T7 DNA
RT to the beginning of gene 4.";
RL J. Mol. Biol. 148:303-330(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81054683; PubMed=6254001;
RA Saito H., Tabor S., Tananai F., Richardson C.C.;
RT "Nucleotide sequence of the primary origin of bacteriophage T7 DNA
RT replication: relationship to adjacent genes and regulatory elements.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3917-3921(1980).
CC -!- FUNCTION: Function of this early gene protein is unknown.
CC -----
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CC -----
DR EMBL; V01146; CAA24391.1; -.
DR EMBL; V01126; CAA24324.1; -.
DR EMBL; V01127; CAA24334.1; -.
DR PIR; E43002; W1BP17.
KW Early protein.
SQ SEQUENCE 42 AA; 5181 MW; 26FDF241A530F76F CRC64;

Query Match 100.0%; Score 23; DB 2; Length 42;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 31 RDRSH 35

RESULT 4
Q6WY56 PRELIMINARY; PRT; 42 AA.
ID Q6WY56
AC Q6WY56;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gene 1.1.
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990536; PubMed=14629033;
RA Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
RT viral genome.";
RL J. Mol. Evol. 57:241-248(2003).
DR EMBL; AY264778; AAP34125.1; -.
DR EMBL; AY264777; AAP34071.1; -.
SQ SEQUENCE 42 AA; 5162 MW; 26FDE29BC530F76F CRC64;

Query Match 100.0%; Score 23; DB 2; Length 42;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 31 RDRSH 35

RESULT 5
Q6WYGO PRELIMINARY; PRT; 42 AA.
ID Q6WYGO
AC Q6WYGO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gene 1.1.
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990536; PubMed=14629033;
RA Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
RT viral genome.";
RL J. Mol. Evol. 57:241-248(2003).
DR EMBL; AY264776; AAP34021.1; -.
DR EMBL; AY264775; AAP33970.1; -.
SQ SEQUENCE 42 AA; 5251 MW; 51E022AFABC0EFD8 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 42;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 31 RDRSH 35

RESULT 6
Q9PDM8 PRELIMINARY; PRT; 42 AA.
ID Q9PDM8
AC Q9PDM8;
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DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf1351;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Valverde R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.P., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Canagaro A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohlseil J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret P., Lambais M.R., Leite L.C.C.,
RA Lenos E.G.M., Lenos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menci C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa J.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva P.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terezzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AF003967; AAF84160.1; -.
DR PIR; P82691; P82691.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 42 AA; 4915 MW; 0F9E51F876F60C9E CRC64;

Query Match 100.0%; Score 23; DB 2; Length 42;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSX 5
DB 24 RTRSH 28

RESULT 7
ID Q7U525 PRELIMINARY; PRT; 45 AA.
AC Q7U525;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE 50S ribosomal protein L34.
GN Name=rp134; Synonyms=rpnh; OrderedLocusNames=SYNW1887;
OS Synecococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerding J.E., Regala W., Allen E.E., McCarren J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synecococcus.";
RL Nature 424:1037-1042(2003).
CC -1- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
DR EMBL; BX572093; CAE19642.1; -.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000271; Ribosomal_L34.
DR Pfam; PF00468; Ribosomal_L34; 1.
DR ProDom; PD003101; Ribosomal_L34; 1.
DR TIGRFAMs; TIGR01030; rpnh_bact; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 45 AA; 5400 MW; 3BE2FA307AA339B0 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSX 5
DB 22 RMRSH 26

RESULT 8
ID Q7V0S1 PRELIMINARY; PRT; 45 AA.
AC Q7V0S1;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE 50S ribosomal protein L34.
GN Name=rp134; Synonyms=rpnh; OrderedLocusNames=PMW1183;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=55919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerding J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman J.E., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation.";
RL Nature 424:1042-1047(2003).
CC -1- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
DR EMBL; BX572093; CAE19642.1; -.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000271; Ribosomal_L34.
DR Pfam; PF00468; Ribosomal_L34; 1.
DR ProDom; PD003101; Ribosomal_L34; 1.
DR TIGRFAMs; TIGR01030; rpnh_bact; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 45 AA; 5400 MW; 3BE2FA307AA339B0 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSX 5
DB 22 RMRSH 26

RESULT 9
ID Q8EKT3 PRELIMINARY; PRT; 45 AA.
AC Q8EKT3;
DT 01-MAR-2003 (TReMBLrel. 23, Created)

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DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Ribosomal protein L34.  
 GN Name=rpM; OrderedLocusNames=SO00007;  
 OS Shewanella oneidensis.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 CC Shewanellaceae; Shewanella.  
 OX NCBI\_TaxID=70863;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MR-1;  
 RX MEDLINE=22297686; PubMed=12369813; DOI=10.1038/nbr749;  
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
 RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,  
 RA Clayton R.A., Meyer T., Tesapin A., Scott J., Beanan M.J.,  
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,  
 RA Hatt D.H., Kolonay J.F., Madupu R., Peterson J.D., Unayam L.A.,  
 RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,  
 RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,  
 RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,  
 RA Venter J.C., Neillson K.H., Fraser C.M.,  
 RA "Genome sequence of the dissimilatory metal ion-reducing bacterium  
 RT Shewanella oneidensis.";  
 RL Nat. Biotechnol. 20:1118-1123(2002).  
 CC -!- SIMILARITY: Belongs to the L34P family of ribosomal proteins.  
 DR EMBL; AE015452; AAN53094.1; -;  
 DR TIGR; SO0007; -;  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
 DR GO; GO:0006412; P:protein biosynthesis; IEA.  
 DR InterPro; IPR000271; Ribosomal L34.  
 DR Pfam; PF00468; Ribosomal L34; 1.  
 DR ProDom; PD003101; Ribosomal\_L34; 1.  
 DR TIGRFAMs; TIGR01030; rpM\_bact; 1.  
 DR PROSITE; PS00784; RIBOSOMAL\_L34; 1.  
 KW Complete proteome; Ribonucleoprotein; Ribosomal protein.  
 SQ SEQUENCE 45 AA; 5125 MW; 54E7F791C32438C CRC64;

Query Match 100.0%; Score 23; DB 2; Length 45;  
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RKRS 5  
 |::|  
 Db 13 RKRS 17

RESULT 10  
 RL34 ECOLI STANDARD; PRT; 46 AA.  
 AC P02437;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE 50S ribosomal protein L34.  
 GN Name=rpM; Synonyms=rimA, ssaE;  
 GN OrderedLocusNames=B3703; c4627; 25194, ECs4638, STM3839, STV3939.1,  
 GN t3680, SF3761, S4010; ORFNames=STV3939A;  
 OS Escherichia coli,  
 OS Escherichia coli O6,  
 OS Escherichia coli O157:H7,  
 OS Salmonella typhimurium,  
 OS Salmonella typhi, and  
 OS Shigella flexneri.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562, 217992, 83334, 602, 601, 623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli;  
 RX MEDLINE=84236082; PubMed=6329723;  
 RA Hansen F.G., Hansen E.B., Atlung T.;

"The nucleotide sequence of the dnaA gene promoter and of the adjacent  
 rpmH gene, coding for the ribosomal protein L34, of Escherichia  
 coli.";  
 RL EMBL J. 1:1043-1048(1982).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli;  
 RX MEDLINE=86056995; PubMed=2415431; DOI=10.1016/0378-1119(85)90206-9;  
 RA Hansen F.G., Hansen E.B., Atlung T.;  
 RA "Physical mapping and nucleotide sequence of the rpmA gene that  
 RT encodes the protein component of ribonuclease P in Escherichia coli.";  
 RL Gene 38:85-93(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;  
 RX MEDLINE=93315143; PubMed=7686882;  
 RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;  
 RA "DNA sequence and analysis of 136 kilobases of the Escherichia coli  
 RT genome: organizational symmetry around the origin of replication.";  
 RL Genomics 16:551-561(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=O6.H1 / CFT073 / ATCC 700928 / UPEC;  
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.352529799;  
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
 RA Rasbo D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
 RA "Extensive mosaic structure revealed by the complete genome sequence  
 RT of uropathogenic Escherichia coli.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;  
 RX MEDLINE=21074935; PubMed=1208551; DOI=10.1038/35054089;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";  
 RL Nature 409:529-533(2001).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;  
 RX MEDLINE=21156231; PubMed=1258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
 RA Kubara S., Shiba T., Hattori M., Shinagawa H.;  
 RA "Complete genome sequence of enterohemorrhagic Escherichia coli  
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";  
 RL DNA Res. 8:11-22(2001).  
 RN [7]  
 RP SEQUENCE.  
 RC SPECIES=E.coli; STRAIN=K12;  
 RX MEDLINE=76258983; PubMed=783033;  
 RA Chen R.;  
 RA "The sequence determination of a protein in a micro scale: the  
 RT sequence analysis of ribosomal protein L34 of Escherichia coli.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:873-886(1976).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SCGCL1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RA "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 RT LT2.";

RL Nature 413:852-856 (2001).  
RN [9]  
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RC SPECIES=S.typhi; STRAIN=CT18;  
RX MEDLINE=2153497; PubMed=11677608; DOI=10.1038/35101607;  
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,  
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrell B.G.;  
RT "Complete genome sequence of a multiple drug resistant Salmonella  
RT enterica serovar Typhi CT18.";  
RL Nature 413:848-852 (2001).  
RN [10]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;  
RX MEDLINE=22531367; PubMed=12644504;  
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;  
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2  
RT and CT18.";  
RL J. Bacteriol. 185:2330-2337 (2003).  
RN [11]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;  
RX MEDLINE=2272406; PubMed=12384590; DOI=10.1093/nar/gkf566;  
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,  
RA Yang J., Yang F., Zhang J., Zhang J., Yang G., Wu H., Qu D., Dong J.,  
RA Sun L., Xue Y., Zhao Y., Gao Y., Zhu J., Kan B., Ping K., Chen S.,  
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,  
RA Yu J.;  
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity  
RT through comparison with genomes of Escherichia coli K12 and O157.";  
RL Nucleic Acids Res. 30:4432-4441 (2002).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;  
RX MEDLINE=22590274; PubMed=12704152;  
RA DOI=10.1128/JAI.71.5.2775-2786.2003;  
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,  
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,  
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,  
RA Schwartz D.C., Blattner F.R.;  
RT "Complete genome sequence and comparative genomics of Shigella  
RT flexneri serotype 2a strain 2457T.";  
RL Infect. Immun. 71:2775-2786 (2003).  
RN [13]  
RP MASS SPECTROMETRY.  
RC SPECIES=E.coli; STRAIN=K12 / ATCC 25404;  
RX MEDLINE=99196679; PubMed=10094780; DOI=10.1006/abio.1998.3077;  
RA Arnold R.J., Reilly J.P.;  
RT "Observation of Escherichia coli ribosomal proteins and their  
RT posttranslational modifications by mass spectrometry.";  
RL Anal. Biochem. 269:105-112 (1999).  
CC -1- MASS SPECTROMETRY: MW=5380.5; METHOD=MALDI; RANGE=1-46;  
CC -1- NOTE=Ref.13.  
CC -1- SIMILARITY: Belongs to the ribosomal protein L34P family.  
CC  
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CC  
DR EMBL; J01602; AAB59148.1; -  
DR EMBL; X01861; CAA25982.1; -  
DR EMBL; M11056; AAA24566.1; -

DR EMBL; L10328; AAA62054.1; -  
DR EMBL; U00096; AAC76726.1; -  
DR EMBL; AE016769; AAN83058.1; -  
DR EMBL; AP005601; AAG58900.1; -  
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DR EMBL; AL627280; CAD03156.1; -  
DR EMBL; AE016846; AAO71176.1; -  
DR EMBL; AE015383; AAN45204.1; -  
DR EMBL; AE016991; AAP18993.1; -  
DR PIR; C21915; R5EC34.  
DR PIR; F91208; F91208.  
DR PIR; H86054; H86054.  
DR ECHOBASE; EB0885; -  
DR EcoGene; EG10892; rpmH.  
DR StyGene; SG77777; rpmH.  
DR HAMAP; MF\_00391; -; 1.  
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DR Pfam; PF00468; Ribosomal\_L34; 1.  
DR ProDom; PD003101; Ribosomal\_L34; 1.  
DR TIGRFAMs; TIGR01030; rpmH\_bact; 1.  
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Query Match 100.0%; Score 23; DB 1; Length 46;  
Best Local Similarity 80.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 RXRS 5  
DB 12 RNRSH 16  
|:||||  
  
RESULT 11  
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AC Q829U5;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE S0S ribosomal protein L34.  
GN Name=rpmlH; OrderedLocNames=YPO4100, Y4114, YP4007;  
OS Versinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
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RP SEQUENCE FROM N.A.  
RC STRAIN=CO-92 / Biovar Orientalis;  
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;  
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,  
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.-M.,  
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,  
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,  
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";  
RL Nature 413:523-527 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KIMS / Biovar Mediaevalis;  
RX MEDLINE=22137863; PubMed=12142430;  
RX DOI=10.1128/JB.184.16.4601-4611.2002;  
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,  
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
RA Fetherston J.D., Lindler L.E., Babaker K.R., Plano G.V.,  
RA Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,  
RA Perry R.D.;  
RT "Genome sequence of Yersinia pestis KIM.";  
RL J. Bacteriol. 184:4601-4611 (2002).  
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RA Yang R.;
RC Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL -!- SIMILARITY: Belongs to the ribosomal protein L34P family.
CC -----
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CC -----
DR EMBL; AJ414160; CAC93549.1; -.
DR EMBL; AE014013; AAM87656.1; -.
DR EMBL; AE017142; AAS64146.1; -.
DR HMAP; MF_00391; -.
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DR Pfam; PF00468; Ribosomal_L34; 1.
DR ProDom; PD003101; Ribosomal_L34; 1.
DR TIGRFAMs; TIGR01030; rpmH_bact; 1.
DR PROSITE; PS00784; RIBOSOMAL_L34; 1.
KW Complete proteome; Ribosomal protein.
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Best Local Similarity 80.0%; Pred. No. 2.9e+02;
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Qy 1 RXRSH 5
Db 12 RNRSH 16

RESULT 12
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RT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein TP0504.
GN OrderedLocusNames=TP0504;
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
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RC STRAIN=Nichols;
RC MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
RA Utterback T.R., McDonald L.A., Artlich P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete";
RL Science 281:375-388 (1998).
CC -----
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DR EMBL; AE001226; AAC65493.1; -.
DR PIR; D71317; D71317.
DR TIGR; TP0504; -.
KW Complete proteome; Hypothetical protein.
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Db 10 RARSH 14

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AC Q663TO;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 50S ribosomal protein L34.
GN Name=rpMh; Synonyms=rmaA, ssaf; ORFNames=YPTB3945;
OS Versinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RC PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Verges L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francoise V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the genome evolution of Versinia pseudotuberculosis";
RT genome comparison with Versinia pseudotuberculosis";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
DR EMBL; BX936398; CAH23183.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR00271; Ribosomal_L34.
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DR ProDom; PD003101; Ribosomal_L34; 1.
DR TIGRFAMs; TIGR01030; rpmH_bact; 1.
DR PROSITE; PS00784; RIBOSOMAL_L34; 1.
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Query Match 100.0%; Score 23; DB 2; Length 46;
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Qy 1 RXRSH 5
Db 12 RNRSH 16

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DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 50S ribosomal protein L34.
GN Name=rpMh; OrderedLocusNames=plu4909;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
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RN SEQUENCE FROM N.A.
RC STRAIN=TT01;
RA MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Rude C., Chandler M., Charles J.-P.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguiet P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photobacterium
RT luminescens."
RL Nat. Biotechnol. 21:1307-1313(2003).
CC -!- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
DR EMBL; BX571875; CAB17281.1; -.
DR PhotoList; plu4909; -.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000271; Ribosomal_L34.
DR Pfam; PF00468; Ribosomal_L34; 1.
DR ProDom; PD003101; Ribosomal_L34; 1.
DR TIGRFAMs; TIGR01030; rpmH_bact; 1.
DR PROSITE; PS00784; RIBOSOMAL_L34; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 46 AA; 5410 MW; 600916E398938862 CRC64;

Query Match      100.0%; Score 23; DB 2; Length 46;
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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RXRSH 5
Db      12 RNRSH 16
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MEDLINE=22957627; PubMed=14528314;
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Taourit S., Bocs S., Boursaux-Rude C., Chandler M., Charles J.-P.,
Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
Medigue C., Lanois A., Powell K., Siguiet P., Vincent R., Wingate V.,
Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
"The genome sequence of the entomopathogenic bacterium Photobacterium
luminescens."
Nat. Biotechnol. 21:1307-1313(2003).
-!- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
EMBL; BX571875; CAB17281.1; -.
PhotoList; plu4909; -.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; P:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR000271; Ribosomal_L34.
Pfam; PF00468; Ribosomal_L34; 1.
ProDom; PD003101; Ribosomal_L34; 1.
TIGRFAMs; TIGR01030; rpmH_bact; 1.
PROSITE; PS00784; RIBOSOMAL_L34; 1.
Complete proteome; Ribonucleoprotein; Ribosomal protein.
SEQUENCE 46 AA; 5410 MW; 600916E398938862 CRC64;

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AC Q6CYR2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 508 ribosomal protein L34.
GN OrderedLocustNames=ECA443;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
SEQUENCE FROM N.A.
STRAIN=SCRI 1043 / ATCC BAA-672;
RC PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Almond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors."
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
CC -!- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
DR EMBL; BX950851; CAG77339.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000271; Ribosomal_L34.
DR Pfam; PF00468; Ribosomal_L34; 1.
DR ProDom; PD003101; Ribosomal_L34; 1.
DR TIGRFAMs; TIGR01030; rpmH_bact; 1.
DR PROSITE; PS00784; RIBOSOMAL_L34; 1.
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OM protein - protein search, using sw model

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Perfect score: 23

Sequence: 1 RXRSH 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	23	100.0	5	2	AY34296	Aay34296 Consensus
2	23	100.0	5	2	AY34298	Aay34298 Consensus
3	23	100.0	8	2	AY39453	Aay39453 CD147 bin
4	23	100.0	10	4	AAG96802	Aag96802 Human com
5	23	100.0	10	4	AAG96808	Aag96808 Human com
6	23	100.0	10	8	ADR21474	Adr21474 N-myc dow
7	23	100.0	11	6	AAE14841	Aae14841 LAMP-1 cy
8	23	100.0	12	2	AY39460	Aay39460 CD147 bin
9	23	100.0	15	2	AY39463	Aay39463 CD147 bin
10	23	100.0	15	2	AY01569	Aay01569 Antigenic
11	23	100.0	15	5	AAE27041	Aae27041 Mouse TCR
12	23	100.0	15	5	AAO19143	Aao19143 Truncated
13	23	100.0	15	8	ADOO5885	Adoo5885 Rat MOGI-
14	23	100.0	16	7	ADW47488	Adm47488 Bioactive
15	23	100.0	18	5	AAE19258	Aae19258 Human rec
16	23	100.0	18	7	ADD84768	Add84768 Alpha-gal
17	23	100.0	18	7	ADI28365	Adi28365 Human TTE
18	23	100.0	18	8	ADJ88294	Adj88294 Tobacco m
19	23	100.0	18	8	ADM48698	Adm48698 Human rga
20	23	100.0	19	6	ABP82361	Abp82361 G protein
21	23	100.0	20	2	AAW00869	Aaw00869 T-cell re
22	23	100.0	22	5	AAE19256	Aae19256 Human rec
23	23	100.0	22	7	ADD84766	Add84766 Alpha-gal
24	23	100.0	22	8	ADJ88292	Adj88292 Tobacco m
25	23	100.0	22	8	ADM48696	Adm48696 Human rga

26	23	100.0	23	6	ABO12112	Abol2112 Human zin
27	23	100.0	23	6	ABO13097	Abol3097 Mouse zin
28	23	100.0	24	5	AAE19259	Aae19259 Human rec
29	23	100.0	24	7	ADD84769	Add84769 Alpha-gal
30	23	100.0	24	8	ADJ88295	Adj88295 Tobacco m
31	23	100.0	24	8	ADM48699	Adm48699 Human rga
32	23	100.0	25	4	AAU01685	Aau01685 Gene 28 h
33	23	100.0	25	5	AAE27040	Aae27040 Mouse TCR
34	23	100.0	25	5	AAO19142	Aao19142 Truncated
35	23	100.0	26	5	ABG95061	Abg95061 Human tra
36	23	100.0	26	5	ABG95098	Abg95098 Human tra
37	23	100.0	26	5	AAE19254	Aae19254 Human rec
38	23	100.0	26	7	ADD84764	Add84764 Alpha-gal
39	23	100.0	26	8	ADJ88290	Adj88290 Tobacco m
40	23	100.0	26	8	ADM48694	Adm48694 Human rga
41	23	100.0	27	8	ABO58949	Abo58949 Human gen
42	23	100.0	28	5	AAE19257	Aae19257 Human rec
43	23	100.0	29	2	AAE66180	Aae66180 Portion o
44	23	100.0	29	4	ABE40852	Abbe40852 Peptide #
45	23	100.0	29	4	AAW34620	Aaw34620 Peptide #

ALIGNMENTS

RESULT 1

AAAY34296

ID AAY34296 standard; peptide; 5 AA.

XX

AC AAY34296;

DT 19-NOV-1999 (first entry)

XX

DE Consensus binding site for antibody ABX-CBL.

XX

KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 2

FT /note= "unspecified amino acid"

XX

PN W09945031-A2.

XX

PD 10-SEP-1999.

XX

PF 03-MAR-1999; 99WO-US004583.

XX

PR 03-MAR-1998; 98US-00034607.

XX

PR 03-FEB-1999; 99US-00244253.

XX

(ABGE-) ABGENIX INC.

XX

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX

DR New monoclonal antibody, used for treating e.g. graft versus host

PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX

PS Claim 24; Page 131; 245pp; English.

XX

This sequence represents a consensus binding site for the antibody of the invention. The antibody is a monoclonal antibody (MAB) with an isotype that fixes complement and a variable region that binds to the epitope on CD147 bound by the IgM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB can selectively kill activated T-cells, activated B-cells or resting or activated monocytes. The products and methods can be used

CC for treating diseases involving activated T-cells or B-cells or  
 CC monocytes, e.g. graft versus host disease (GVHD), organ transplant  
 CC rejection diseases (e.g. renal transplant, ocular transplant), cancers  
 CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and  
 CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases  
 CC (e.g. arthritis)  
 XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
 |||||  
 Db 1 RXRSH 5

RESULT 2  
 AAY34298  
 ID AAY34298 standard; peptide; 5 AA.

XX AAY34298;

XX 19-NOV-1999 (first entry)

XX Consensus binding site for antibody ABX-CBL.

KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Synthetic.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX New monoclonal antibody, used for treating e.g. graft versus host  
 PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX Claim 24; Page 131; 245pp; English.

XX This sequence represents a consensus binding site for the antibody of the  
 CC invention. The antibody is a monoclonal antibody (MAb) with an isotype  
 CC that fixes complement and a variable region that binds to the epitope on  
 CC CD147 bound by the IgM MAb ABX-CBL, providing that the antibody is not  
 CC CBL1. The MAb can selectively kill activated T-cells, activated B-cells  
 CC or resting or activated monocytes. The products and methods can be used  
 CC for treating diseases involving activated T-cells or B-cells or  
 CC monocytes, e.g. graft versus host disease (GVHD), organ transplant  
 CC rejection diseases (e.g. renal transplant, ocular transplant), cancers  
 CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and  
 CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases  
 CC (e.g. arthritis)

XX Sequence 5 AA;

Query Match 100.0%; Score 23; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RXRSH 5  
 |||||  
 Db 1 RVRSH 5

RESULT 3

AAY39453

ID AAY39453 standard; peptide; 8 AA.

XX AAY39453;

XX 19-NOV-1999 (first entry)

XX CD147 binding site for antibody ABX-CBL.

KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Synthetic.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX New monoclonal antibody, used for treating e.g. graft versus host  
 PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX Example 12; Page 75; 245pp; English.

XX This sequence represents a binding site for the antibody of the  
 CC invention. The antibody is a monoclonal antibody (MAb) with an isotype  
 CC that fixes complement and a variable region that binds to the epitope on  
 CC CD147 bound by the IgM MAb ABX-CBL, providing that the antibody is not  
 CC CBL1. The MAb can selectively kill activated T-cells, activated B-cells  
 CC or resting or activated monocytes. The products and methods can be used  
 CC for treating diseases involving activated T-cells or B-cells or  
 CC monocytes, e.g. graft versus host disease (GVHD), organ transplant  
 CC rejection diseases (e.g. renal transplant, ocular transplant), cancers  
 CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and  
 CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases  
 CC (e.g. arthritis)

XX Sequence 8 AA;

Query Match 100.0%; Score 23; DB 2; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
 |||||  
 Db 4 RVRSH 8

RESULT 4

AAG96802

ID AAG96802 standard; peptide; 10 AA.

XX

```

AC AAG96802;
XX
XX 18-SEP-2001 (first entry)
XX
DE Human complementary peptide, SEQ ID NO: 2996.
XX
XX Human; complementary peptide; ligand; drug discovery; drug design.
XX
XX OS Homo sapiens.
XX
XX PN WO200142277-A2.
XX
XX PD 14-JUN-2001.
XX
XX PF 13-DEC-2000; 2000WO-GB004776.
XX
XX PR 13-DEC-1999; 99GB-00029464.
XX
XX PA (PROT-) PROTEOM LTD.
XX
XX PI Roberts GW, Heal JR;
XX
XX DR WPI; 2001-408419/43.
XX
XX PT A set of peptide ligands consisting of specific complementary peptides to
XX PT proteins encoded by genes of the human genome, useful in an assay for
XX PT screening and identifying of one or more novel peptides which are drug
XX PT candidates or pro-drugs.
XX
XX PS Example 4; Page 473; 646pp; English.
XX
XX CC The invention relates to a set of complementary peptide ligands generated
XX CC from the human genome. The complementary peptides interact with their
XX CC relevant target proteins encoded in the human genome. They can be used as
XX CC reagents in drug discovery and as lead ligands to facilitate drug design
XX CC and development. The present sequence is a complementary peptide provided
XX CC in the specification
XX
XX SQ Sequence 10 AA;
XX
XX Query Match 100.0%; Score 23; DB 4; Length 10;
XX Best Local Similarity 80.0%; Pred. No. 1.5e+02;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
Db |:|:|
2 RSRSH 6

RESULT 6
ADR21474
ID ADR21474 standard; peptide; 10 AA.
XX
XX AC ADR21474;
XX
XX DT 21-OCT-2004 (first entry)
XX
XX DE N-myc downstream-regulated gene 2 C-terminal repeat sequence.
XX
XX KW anorectic; anabolic; eating disorder; antidiabetic; muscular; cardiant;
XX KW antiinflammatory; immunomodulator; cerebroprotective; antiseborrheic;
XX KW dermatological; antianginal; antiarthritic; respiratory;
XX KW gastrointestinal; endocrine; central nervous system; gene therapy;
XX KW gene expression; hypothalamus tissue; obese animal; lean animal;
XX KW fasted animal; fed animal; myopathy; obesity; anorexia;
XX KW weight maintenance; diabetes; mitochondrial dysfunction disorder;
XX KW genetic disorder; cancer impaired muscle development; heart disease;
XX KW inflammation; immune system disorder; infertility; brain disease;
XX KW metabolic energy level; acne; angina; arthritis; aspiration pneumonia;
XX KW emphysema; gastroenteritis; intestinal flu; Digeorge syndrome;
XX KW Job syndrome; Bruton disease; complement deficiency; Varicocoele;
XX KW Young's syndrome; Myotonic dystrophy; Cystic fibrosis; Kennedy's disease;
XX KW Turner's syndrome; Cushing's syndrome; fat sand rat.
XX
XX OS Homo sapiens.
XX OS Mus sp.
XX
XX PN WO2004063218-A1.
XX
XX PD 29-JUL-2004.
XX
XX PF 13-JAN-2004; 2004WO-AU0000043.
XX
XX PR 13-JAN-2003; 2003US-0439767P.
XX
XX PA (AUTO-) AUTOGEN RES PTY LTD.
XX PA (UYDE-) UNIV DEAKIN.
XX
XX PI Collier G, Walder K, Segal D, Foletta VC;
XX
XX DR WPI; 2004-553717/53.
XX
XX PT New isolated nucleic acid molecule, useful for treating e.g., myopathy,

```

PT obesity, anorexia, weight maintenance, diabetes, disorders associated  
 PT with mitochondrial dysfunction, genetic disorders, heart disease and  
 PT inflammation.

PS Example 4; SEQ ID NO 13; 210pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a sequence of nucleotides encoding or complementary to a sequence  
 CC encoding a molecule or its derivative or homologue where (I) is expressed  
 CC in a larger amount in hypothalamus tissue of obese animals compared to  
 CC lean animals or in fasted animals compared to fed animals. A method  
 CC comprising administering to the mammal an agent for a time and under  
 CC conditions to modulate the expression or activity of AGT-701, AGT-702,  
 CC AGT-704, AGT-705, AGT-706, AGT-707, AGT-708, AGT-709 and/or AGT-710, is  
 CC useful for treating a mammal suffering from a condition characterized by  
 CC one or more symptoms or inter alia a myopathy, obesity, anorexia, weight  
 CC maintenance, diabetes, disorders associated with mitochondrial  
 CC dysfunction, genetic disorders, cancer impaired muscle development, heart  
 CC disease, inflammation, disorders associated with the immune system,  
 CC infertility, disease associated with the brain, and metabolic energy  
 CC levels. Examples of inflammatory diseases include acne, angina,  
 CC arthritis, aspiration pneumonia, emphysema, gastroenteritis and  
 CC intestinal flu. Disorders associated with the immune system include  
 CC DiGeorge syndrome, Job syndrome, Bruton disease, and Complement  
 CC deficiencies. Examples of disorders associated with infertility are  
 CC Varicocele, Young's syndrome, Myotonic dystrophy, Cystic fibrosis,  
 CC Kennedy's disease, Turner's syndrome and Cushing's syndrome. This  
 CC sequence corresponds to a repeat peptide sequence found in the N-myc  
 CC downstream-regulated gene 2 (NRD2G2) protein C-terminal region conserved  
 CC in human and mouse NRD2G2 proteins. The protein encoded by the AGT-701  
 CC nucleic acid sequence of the invention has sequence homology to the NDRG2  
 CC protein sequence.

XX Sequence 10 AA;

Query Match 100.0%; Score 23; DB 8; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
 Db 3 RSRSH 7

RESULT 7

AAE14841  
 ID AAE14841 standard; peptide; 11 AA.

AC AAE14841;

DT 24-MAR-2003 (first entry)

XX LAMP-1 cytoplasmic tail.

XX Chimera; vaccine; trafficking domain; endosome; lysosome; cancer;

KW autoimmune disease; allergic reaction; transplant; graft;

KW hypersensitivity; congenital disease; luminal domain; LAMP-1;

KW lysosomal associated membrane protein; immune response; cytoplasmic tail.

XX Unidentified.

XX Key Location/Qualifiers

FT Domain 8..11

FT /label= Tyr\_motif

FT /note= "Targets molecules to lysosome"

FN WO200280851-A2.

PD 17-OCT-2002.

XX 05-APR-2002; 2002WO-US010757.

XX 05-APR-2001; 2001US-0281607P.

PR 05-APR-2001; 2001US-0281608P.  
 PR 05-APR-2001; 2001US-0281621P.

XX (UYJO ) UNIV JOHNS HOPKINS.

PI August T, Marques B;

XX WPI; 2003-058464/05.

XX Novel chimeric protein for treating cancer, comprises antigen sequence,  
 PT and trafficking domain that directs both membrane and non-membrane  
 PT proteins to endosomal compartment or trafficking domain of endocytic  
 PT receptor.

PS Disclosure; Page 32; 102pp; English.

XX The invention provides chimeric proteins and nucleic acids encoding these  
 CC which can be used to generate vaccines against selected antigens. The  
 CC chimeric protein comprises an antigen domain having at least one epitope,  
 CC and a trafficking domain that directs both membrane and non-membrane  
 CC proteins to an endosomal/lysosomal compartment in a cell and/or to a  
 CC lysosome-related organelle. The antigen used in the chimeric protein is  
 CC taken from a pathogenic organism, e.g. HIV, a cancer-specific polypeptide  
 CC or a molecule associated with an abnormal physiological response (e.g.  
 CC autoimmune disease, an allergic reaction, cancer, reaction to a  
 CC transplant or graft, hypersensitivity reaction, or congenital disease).  
 CC The trafficking domain comprises a luminal domain of a lysosomal  
 CC associated membrane protein (LAMP). Alternatively, or additionally, the  
 CC protein comprises a trafficking domain of an endocytic receptor. The  
 CC vaccine (DNA, RNA, protein) can be used to modulate an immune response  
 CC against any kind of antigen. The invention also provides a method for  
 CC treating a patient with cancer by providing a chimeric protein comprising  
 CC cancer-specific antigen or a nucleic acid encoding the protein. The  
 CC present sequence is lysosomal associated membrane protein (LAMP)-1  
 CC cytoplasmic tail used in the chimeric protein of the invention

XX Sequence 11 AA;

Query Match 100.0%; Score 23; DB 6; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5

Db 1 RKRSRSH 5

RESULT 8

AAV39460

ID AAV39460 standard; peptide; 12 AA.

XX AC AAV39460;

XX 19-NOV-1999 (first entry)

XX CD147 binding site for antibody ABX-CBL.

XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Synthetic.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

```

PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
DR WPI; 1999-540816/45.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Example 12; Page 76; 245pp; English.
XX
CC This sequence represents a binding site for the antibody of the
CC invention. The antibody is a monoclonal antibody (Mab) with an isotype
CC that fixes complement and a variable region that binds to the epitope on
CC CD147 bound by the IgM Mab ABX-CBL, providing that the antibody is not
CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells
CC or resting or activated monocytes. The products and methods can be used
CC for treating diseases involving activated T-cells or B-cells or
CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
XX (e.g. arthritis)
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 23; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
DB |:|
7 RQRSH 11

RESULT 9
AAV39463
ID AAV39463 standard; peptide; 15 AA.
XX
AC AAV39463;
XX
DT 19-NOV-1999 (first entry)
XX
DE CD147 binding site for antibody ABX-CBL.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Synthetic.
XX
PN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
XX
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
DR WPI; 1999-540816/45.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Example 12; Page 77; 245pp; English.
XX

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XX
CC This sequence represents a binding site for the antibody of the
CC invention. The antibody is a monoclonal antibody (Mab) with an isotype
CC that fixes complement and a variable region that binds to the epitope on
CC CD147 bound by the IgM Mab ABX-CBL, providing that the antibody is not
CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells
CC or resting or activated monocytes. The products and methods can be used
CC for treating diseases involving activated T-cells or B-cells or
CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
XX (e.g. arthritis)
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 23; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
DB |:|
11 RVRSH 15

RESULT 10
AAV01569
ID AAV01569 standard; peptide; 15 AA.
XX
AC AAV01569;
XX
DT 17-OCT-2003 (revised)
DT 18-JUN-1999 (first entry)
XX
DE Antigenic peptide of streptokinase.
XX
KW Antigenic peptide; streptokinase; streptokinase-specific antibody;
KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;
KW rheumatic fever.
XX
OS Streptococcus dysgalactiae subsp. equisimilis.
XX
PN WO9908698-A1.
XX
PD 25-FEB-1999.
XX
PF 18-AUG-1998; 98WO-US017114.
XX
PR 18-AUG-1997; 97US-0055911P.
XX
PA (HARD ) HARVARD COLLEGE.
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI Reed GL, Parhami-Seren B;
XX
DR WPI; 1999-190113/16.
XX
PT New polypeptides which bind streptokinase-specific antibodies - useful in
PT thrombolytic therapy.
XX
PS Example 1; Fig 1; 44pp; English.
XX
CC The present sequence represents an antigenic peptide of streptokinase.
CC The specification describes a polypeptide which binds to a streptokinase-
CC specific antibody and prevents the antibody binding to native
CC streptokinase. The specification also describes a synthetic polypeptide
CC (PI) comprising an epitope which binds to an streptokinase-specific
CC antibody and reduces thrombolytic activity of streptokinase. PI is used
CC in thrombolytic therapy, and to prevent or treat glomerulonephritis and
CC rheumatic fever. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 15 AA;

```

```

Query Match      100.0%; Score 23; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RARSH 6

RESULT 11
AAE27041
ID AAE27041 standard; peptide; 15 AA.
AC AAE27041;
XX
XX
DT 13-DEC-2002 (first entry)
DE
DE
KW Mouse TCR intronic JalphaTA39 gene peptide #2.
KW Mouse; T cell receptor; TCR; mesenchymal cell growth; cell therapy;
KW carcinoma; wound healing; intronic J region; joining region; J region;
KW constant domain; C domain; receptor; JalphaTA39.
XX
OS Mus sp.
XX
XX WO200266636-A2.
PN
XX
XX 29-AUG-2002.
PD
XX
XX 20-FEB-2002; 2002WO-IL000130.
PF
XX
XX 20-FEB-2001; 2001IL-00141539.
PR
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
PA
XX
XX Zipori D, Rozenszajn AL, Barda-Saad M, Shav-Tal Y;
PI
XX
XX WPI; 2002-667067/71.
DR
XX
XX New isolated polynucleotide comprising a transcript of a T cell receptor
PT gene, useful for transfecting mesenchymal cells for wound healing or
PT suppression of carcinomas.
XX
PS Claim 20; Page 39; 63pp; English.
CC
CC The invention relates to polynucleotide transcripts of T cell receptor
CC (TCR) gene, as well as protein sequences encoded by these transcripts,
CC and their use in the modulation of mesenchymal cell growth. The invention
CC also concerns cDNA molecules encoded by a TCR gene lacking V region
CC sequences and comprising a constant (C) domain and joining (J) region
CC sequences and a 5' intronic J' sequences upstream to the J region
CC including an in-frame methionine. Polynucleotides of the invention are
CC useful for transfecting mesenchymal cells for wound healing or
CC suppression of carcinomas. Antibodies of the invention are useful as
CC markers of mesenchymal cells. The invention is useful in cell therapy.
CC The present sequence is a peptide encoded by intronic JalphaTA39 gene of
CC mouse TCR
XX
SQ Sequence 15 AA;
Query Match      100.0%; Score 23; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 5 RERSH 9

RESULT 12
AAO19143
ID AAO19143 standard; peptide; 15 AA.
AC AAO19143;
XX
XX
DT 27-NOV-2002 (first entry)
DE
DE
KW Truncated T cell receptor variant peptide from mesenchymal cell #15.
KW Immunoglobulin; Ig; T cell receptor; TCR; variant; mesenchymal cell;
KW haematopoiesis; haematopoietic stem cell; mu heavy chain; mouse;
KW gene therapy; vulnery; cytostatic; wound healing; cancer.
XX
OS Unidentified.
XX
XX WO200266648-A2.
PN
XX
XX 29-AUG-2002.
PD
XX
XX 20-FEB-2002; 2002WO-IL000129.
PF
XX
XX 20-FEB-2001; 2001IL-00141539.
PR
XX
XX 25-SEP-2001; 2001IL-00145658.
PA
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Zipori D, Shav-Tal Y, Barda-Saad M;
PI
XX
XX WPI; 2002-674947/72.
DR
XX
XX New isolated polynucleotide comprising a transcript of an immunoglobulin
PT gene, useful for transfection of mesenchymal cells, for wound healing, or
PT for inducing hemopoiesis after bone marrow transplantation or
PT chemotherapy.
XX
PS Claim 19; Page 16; 48pp; English.
CC
CC The present invention relates to an isolated polynucleotide comprising a
CC transcript of an immunoglobulin (Ig) gene. The polynucleotide lacks
CC variable (V) region sequences and comprises a constant (C) domain and
CC joining (J) region sequences, and a 5' intronic J' sequence upstream to
CC the J region sequence including an in-frame methionine codon. The
CC polynucleotides are useful for the transfection of mesenchymal cells, for
CC wound healing, for inducing haematopoiesis after bone marrow
CC transplantation or chemotherapy, for the suppression of cancer, and for
CC treating disorders involving the proliferation and differentiation of
CC haematopoietic stem cells. The present sequence is a peptide described in
CC the invention
XX
SQ Sequence 15 AA;
Query Match      100.0%; Score 23; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 5 RERSH 9

RESULT 13
ADO05885
ID ADO05885 standard; protein; 15 AA.
AC ADO05885;
XX
XX
DT 15-JUL-2004 (first entry)
DE
DE
KW Rat MOG1-125 C-terminal peptide fragment.
KW MOG; multiple sclerosis; MS; allergic encephalomyelitis; EAE;
KW myelin/oligodendrocyte glycoprotein; rat.
XX
OS Rattus sp.
XX

```





PA (LARG-) LARGE SCALE BIOLOGY CORP.  
XX  
PI Garger SJ, Turpen TH, Kumagai MH;  
XX  
DR WPI; 2002-195873/25.  
XX  
PT New glucocerebrosidase and alpha-galactosidase having a post-  
PT translational modification, useful in enzyme replacement therapy for  
PT treating lysosomal storage diseases, e.g. Gaucher disease, Niemann-Pick  
PT disease, Fabry disease.  
XX  
XX Example 11; Fig 5; 102pp; English.  
PS  
XX The invention relates to production of lysosomal enzymes in plants by  
CC transient expression. The invention particularly relates to  
CC glucocerebrosidase and alpha-galactosidase having a post-translational  
CC modification. The enzymes are useful in enzyme replacement therapy for  
CC treating lysosomal storage diseases (e.g. Gaucher disease, Niemann-Pick  
CC disease, Fabry disease and Tay-Sachs disease), in researches for  
CC developing new approaches to medical treatment of lysosomal storage  
CC diseases and in industrial processes involving enzymatic substrate  
CC hydrolysis. The present sequence is human recombinant alpha-  
CC galactosidase-A C-terminal modified peptide  
XX  
SQ Sequence 18 AA;

Query Match 100.0%; Score 23; DB 5; Length 18;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
|:|  
Db 3 RLRSH 7

Search completed: March 8, 2005, 06:17:01  
Job time : 4.31814 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 2.65337 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-13

Perfect score: 23

Sequence: 1 KXRSH 5

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	7	11	US-09-855-604-23
2	23	100.0	8	17	US-10-808-187-1281
3	23	100.0	10	10	US-09-572-404B-2996
4	23	100.0	10	10	US-09-572-404B-3002
5	23	100.0	15	15	US-10-682-420-61
6	23	100.0	15	15	US-10-682-420-84
7	23	100.0	15	15	US-10-409-613-61
8	23	100.0	15	15	US-10-409-613-84
9	23	100.0	15	15	US-10-442-180-61
10	23	100.0	15	15	US-10-442-180-84
11	23	100.0	15	16	US-10-643-982-22
12	23	100.0	15	17	US-10-683-451-38
13	23	100.0	15	17	US-10-775-337-61

14	23	100.0	15	17	US-10-775-337-84	Sequence 84, Appl
15	23	100.0	16	14	US-10-267-251-25	Sequence 25, Appl
16	23	100.0	18	9	US-09-993-059-29	Sequence 29, Appl
17	23	100.0	18	14	US-10-103-327-29	Sequence 29, Appl
18	23	100.0	18	14	US-10-123-626-29	Sequence 29, Appl
19	23	100.0	18	15	US-10-602-219-29	Sequence 29, Appl
20	23	100.0	18	15	US-10-602-220-29	Sequence 29, Appl
21	23	100.0	18	15	US-10-684-300-9	Sequence 9, Appl
22	23	100.0	18	15	US-10-684-349-9	Sequence 9, Appl
23	23	100.0	19	14	US-10-225-567A-1034	Sequence 1034, Ap
24	23	100.0	22	9	US-09-993-059-27	Sequence 27, Appl
25	23	100.0	22	14	US-10-103-327-27	Sequence 27, Appl
26	23	100.0	22	15	US-10-602-219-27	Sequence 27, Appl
27	23	100.0	22	15	US-10-602-220-27	Sequence 27, Appl
28	23	100.0	22	15	US-10-684-300-7	Sequence 7, Appl
29	23	100.0	22	15	US-10-684-349-7	Sequence 7, Appl
30	23	100.0	24	9	US-09-993-059-30	Sequence 30, Appl
31	23	100.0	24	14	US-10-164-359-13	Sequence 13, Appl
32	23	100.0	24	14	US-10-103-327-30	Sequence 30, Appl
33	23	100.0	24	15	US-10-602-219-30	Sequence 30, Appl
34	23	100.0	24	15	US-10-602-220-30	Sequence 30, Appl
35	23	100.0	24	15	US-10-684-300-10	Sequence 10, Appl
36	23	100.0	24	15	US-10-684-349-10	Sequence 10, Appl
37	23	100.0	25	16	US-10-643-982-21	Sequence 21, Appl
38	23	100.0	26	9	US-09-993-059-25	Sequence 25, Appl
39	23	100.0	26	14	US-10-103-327-25	Sequence 25, Appl
40	23	100.0	26	15	US-10-602-219-25	Sequence 25, Appl
41	23	100.0	26	15	US-10-602-220-25	Sequence 25, Appl
42	23	100.0	26	15	US-10-684-300-5	Sequence 5, Appl
43	23	100.0	26	15	US-10-684-349-5	Sequence 5, Appl
44	23	100.0	27	14	US-10-029-386-32583	Sequence 32583, A
45	23	100.0	28	15	US-10-684-300-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-855-604-23  
; Sequence 23, Application US/09855604  
; Publication No. US20040214165A1  
; GENERAL INFORMATION:  
; APPLICANT: GICQUEL, BRIGITTE  
; APPLICANT: PORTNOI, DENIS  
; APPLICANT: LIM, ENG-MONG  
; APPLICANT: PELICIC, VLADIMIR  
; APPLICANT: GUIGUENO, AGNES  
; APPLICANT: GOGUET DE LA SALMONIERE, YVES  
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,  
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND  
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS  
; FILE REFERENCE: 03715.0062-01000  
; CURRENT APPLICATION NUMBER: US/09/855,604  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/485,536  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/FR98/01813  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: FR 97 10404  
; PRIOR FILING DATE: 1997-08-14  
; PRIOR APPLICATION NUMBER: FR 97 11325  
; PRIOR FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 935  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
US-09-855-604-23

Query Match 100.0%; Score 23; DB 11; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.3e+06; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 0;

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; FEATURE:
; OTHER INFORMATION: sequence located in SFRS3 OR SRP20 OR X16 at 187-196 and may inter
; OTHER INFORMATION: with Sequence 2995 in this patent.
US-09-572-404B-2996

Query Match      100.0%; Score 23; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 1 RSRSH 5

RESULT 4
US-09-572-404B-3002
; Sequence 3002, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3002
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in SFRS3 OR SRP20 OR X16 at 186-195 and may inter
; OTHER INFORMATION: with Sequence 3001 in this patent.
US-09-572-404B-3002

Query Match      100.0%; Score 23; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RSRSH 6

RESULT 5
US-10-682-420-61
; Sequence 61, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PMD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
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; FEATURE:
; OTHER INFORMATION: sequence located in SFRS3 OR SRP20 OR X16 at 187-196 and may inter
; OTHER INFORMATION: with Sequence 2995 in this patent.
US-09-572-404B-2996

Query Match      100.0%; Score 23; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 1 RSRSH 5

RESULT 4
US-09-572-404B-3002
; Sequence 3002, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3002
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in SFRS3 OR SRP20 OR X16 at 186-195 and may inter
; OTHER INFORMATION: with Sequence 3001 in this patent.
US-09-572-404B-3002

Query Match      100.0%; Score 23; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RSRSH 6

RESULT 5
US-10-682-420-61
; Sequence 61, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PMD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
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; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-682-420-61

Query Match      100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RPRSH 6

RESULT 6
US-10-682-420-84
; Sequence 84, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-682-420-84

Query Match      100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RPRSH 6

RESULT 7
US-10-409-613-61
; Sequence 61, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-409-613-84

Query Match      100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RPRSH 6

RESULT 8
US-10-409-613-84
; Sequence 84, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-409-613-84

Query Match      100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RPRSH 6

RESULT 9
US-10-442-180-61
; Sequence 61, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
```

APPLICANT: Le Cann, Pierre  
APPLICANT: BLANCHARD, Phillipe  
APPLICANT: HUTET, Evelyne  
APPLICANT: ARNAULD, Claire  
APPLICANT: TRUONG, Catherine  
APPLICANT: MAHE, Dominique  
APPLICANT: CARIOLET, Roland  
APPLICANT: MADEC, Francois  
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS  
TITLE OF INVENTION: DISEASE (PWD)  
FILE REFERENCE: 065691/0176  
CURRENT APPLICATION NUMBER: US/10/442,180  
CURRENT FILING DATE: 2003-05-21  
PRIOR APPLICATION NUMBER: US/09/514,245  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: FR 97/15396  
PRIOR FILING DATE: 1997-12-05  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 61  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Type B PWD circovirus  
US-10-442-180-61

Query Match 100.0%; Score 23; DB 15; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5  
|:|  
Db 2 RPRSH 6

RESULT 10  
US-10-442-180-84  
; Sequence 84, Application US/10442180  
; Publication No. US20040091502A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le Cann, Pierre  
; APPLICANT: BLANCHARD, Phillipe  
; APPLICANT: HUTET, Evelyne  
; APPLICANT: ARNAULD, Claire  
; APPLICANT: TRUONG, Catherine  
; APPLICANT: MAHE, Dominique  
; APPLICANT: CARIOLET, Roland  
; APPLICANT: MADEC, Francois  
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS  
TITLE OF INVENTION: DISEASE (PWD)  
FILE REFERENCE: 065691/0176  
CURRENT APPLICATION NUMBER: US/10/442,180  
CURRENT FILING DATE: 2003-05-21  
PRIOR APPLICATION NUMBER: US/09/514,245  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: FR 97/15396  
PRIOR FILING DATE: 1997-12-05  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 84  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Type A PWD circovirus  
US-10-442-180-84

Query Match 100.0%; Score 23; DB 15; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5  
|:|  
pb 2 RPRSH 6

RESULT 11  
US-10-643-982-22  
; Sequence 22, Application US/10643982  
; Publication No. US20040101931A1  
; GENERAL INFORMATION:  
; APPLICANT: Zipori, Dov  
; APPLICANT: Shav-Tal, Yaron  
; APPLICANT: Barda-Saad, Mira  
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY VARIANTS EXPRESSED IN MESENCHYMAL CELLS  
FILE REFERENCE: 85189-5000  
CURRENT APPLICATION NUMBER: US/10/643,982  
CURRENT FILING DATE: 2003-08-20  
PRIOR APPLICATION NUMBER: PCT/IL02/00129  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: IL141539  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: IL145658  
PRIOR FILING DATE: 2001-09-25  
NUMBER OF SEQ ID NOS: 42  
SEQ ID NO 22  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-643-982-22

Query Match 100.0%; Score 23; DB 15; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5  
|:|  
Db 5 RERSH 9

RESULT 12  
US-10-683-451-38  
; Sequence 38, Application US/10683451  
; Publication No. US20050009096A1  
; GENERAL INFORMATION:  
; APPLICANT: GENAIN, CLAUDE P.  
; APPLICANT: VON BUDINGEN, HANS-CHRISTIAN  
; APPLICANT: MENGE, TIL P.  
TITLE OF INVENTION: A METHOD FOR DIAGNOSIS AND PROGNOSIS OF MULTIPLE SCLEROSIS  
FILE REFERENCE: 305T-300410US  
CURRENT APPLICATION NUMBER: US/10/683,451  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: US 60/418,001  
PRIOR FILING DATE: 2002-10-11  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 38  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Rattus rattus  
US-10-683-451-38

Query Match 100.0%; Score 23; DB 17; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5  
|:|  
Db 6 RRSRH 10

RESULT 13  
US-10-775-337-61  
; Sequence 61, Application US/10775337  
; Publication No. US20050008651A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre

APPLICANT: ALBINA, Emanuel  
APPLICANT: Le CANN, Pierre  
APPLICANT: BLANCHARD, Philippe  
APPLICANT: HUTET, Evelyne  
APPLICANT: ARNAULD, Claire  
APPLICANT: TRUONG, Catherine  
APPLICANT: MAHE, Dominique  
APPLICANT: CARIOLET, Roland  
APPLICANT: MADEC, Francois  
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS  
TITLE OF INVENTION: DISEASE (PWD)  
FILE REFERENCE: 065691/0176  
CURRENT APPLICATION NUMBER: US/10/775,337  
CURRENT FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: US/09/514,245  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: FR 97/15396  
PRIOR FILING DATE: 1997-12-05  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 61  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Type B PWD circovirus  
US-10-775-337-61

Query Match 100.0%; Score 23; DB 17; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRSH 5  
|:|  
DB 2 RRRSH 6

RESULT 14  
US-10-775-337-84  
Sequence 84, Application US/10775337  
Publication No. US20050008651A1  
GENERAL INFORMATION:  
APPLICANT: JESTIN, Andre  
APPLICANT: ALBINA, Emanuel  
APPLICANT: Le CANN, Pierre  
APPLICANT: BLANCHARD, Philippe  
APPLICANT: HUTET, Evelyne  
APPLICANT: ARNAULD, Claire  
APPLICANT: TRUONG, Catherine  
APPLICANT: MAHE, Dominique  
APPLICANT: CARIOLET, Roland  
APPLICANT: MADEC, Francois  
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS  
TITLE OF INVENTION: DISEASE (PWD)  
FILE REFERENCE: 065691/0176  
CURRENT APPLICATION NUMBER: US/10/775,337  
CURRENT FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: US/09/514,245  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: FR 97/15396  
PRIOR FILING DATE: 1997-12-05  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 84  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Type A PWD circovirus  
US-10-775-337-84

Query Match 100.0%; Score 23; DB 17; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRSH 5  
|:|

Db 2 RRRSH 6  
RESULT 15  
US-10-267-251-25  
Sequence 25, Application US/10267251  
Publication No. US20030134329A1  
GENERAL INFORMATION:  
APPLICANT: No. US20030134329Alman, Thea  
TITLE OF INVENTION: CROSS-SPECIES BIOACTIVE PEPTIDES  
FILE REFERENCE: 14184-011001  
CURRENT APPLICATION NUMBER: US/10/267,251  
CURRENT FILING DATE: 2002-10-09  
PRIOR APPLICATION NUMBER: US 60/328,340  
PRIOR FILING DATE: 2001-10-09  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
US-10-267-251-25

Query Match 100.0%; Score 23; DB 14; Length 16;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRSH 5  
|:|  
DB 4 RRRSH 8

Search completed: March 8, 2005, 07:05:46  
Job time : 2.65337 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 0.549782 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-13

Perfect score: 23

Sequence: 1 RXRSH 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*

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4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	11	1	US-08-006-845-1
2	23	100.0	14	1	US-08-006-845-28
3	23	100.0	15	4	US-09-514-245-61
4	23	100.0	15	4	US-09-514-245-84
5	23	100.0	20	1	US-08-416-336-4
6	23	100.0	21	3	US-09-109-957-9
7	23	100.0	29	5	PCT-US94-05150-37
8	23	100.0	32	4	US-09-270-767-61126
9	23	100.0	33	4	US-09-270-767-40082
10	23	100.0	33	4	US-09-270-767-55298
11	23	100.0	36	3	US-08-789-333F-22
12	23	100.0	36	3	US-09-169-015-32
13	23	100.0	36	3	US-09-133-944-21
14	23	100.0	36	3	US-09-208-827-23
15	23	100.0	36	4	US-08-787-738B-22
16	23	100.0	36	4	US-09-157-748-24
17	23	100.0	36	4	US-09-800-170-75
18	23	100.0	36	4	US-09-626-581D-35
19	23	100.0	36	4	US-09-415-765B-35
20	23	100.0	36	4	US-09-626-580C-35
21	23	100.0	36	4	US-09-749-959-31
22	23	100.0	36	4	US-10-043-074-23
23	23	100.0	36	4	US-09-285-912A-84
24	23	100.0	36	4	US-09-578-030-26
25	23	100.0	36	4	US-09-916-940-22
26	23	100.0	36	4	US-09-419-381-69
27	23	100.0	36	4	US-10-142-662-36

28	23	100.0	36	4	US-10-096-550-22	Sequence 22, Appl
29	23	100.0	39	4	US-09-443-780C-31	Sequence 31, Appl
30	23	100.0	39	4	US-09-079-723-15	Sequence 15, Appl
31	23	100.0	46	4	US-09-732-210-938	Sequence 938, App
32	23	100.0	46	4	US-09-711-164-423	Sequence 423, App
33	23	100.0	47	4	US-09-732-210-936	Sequence 936, App
34	23	100.0	50	4	US-09-270-767-36886	Sequence 36886, A
35	23	100.0	50	4	US-09-270-767-52103	Sequence 52103, A
36	23	100.0	50	4	US-09-270-767-57158	Sequence 57158, A
37	23	100.0	51	4	US-09-732-210-1015	Sequence 1015, Ap
38	23	100.0	62	4	US-09-513-999C-5909	Sequence 5909, Ap
39	23	100.0	63	4	US-09-489-039A-11322	Sequence 11322, A
40	23	100.0	63	4	US-09-489-039A-12618	Sequence 12618, A
41	23	100.0	65	4	US-09-489-039A-11132	Sequence 11132, A
42	23	100.0	65	4	US-09-248-796A-24384	Sequence 24384, A
43	23	100.0	65	4	US-09-640-211A-604	Sequence 604, App
44	23	100.0	67	4	US-09-489-039A-9965	Sequence 9965, Ap
45	23	100.0	68	4	US-09-621-976-6572	Sequence 6572, Ap

#### ALIGNMENTS

##### RESULT 1

US-08-006-845-1  
; Sequence 1, Application US/08006845  
; Patent No. 5633234  
; GENERAL INFORMATION:  
; APPLICANT: August, Thomas J.  
; APPLICANT: Pardoll, Drew M.  
; APPLICANT: Guarneri, Frank G.  
; TITLE OF INVENTION: LYSSOMAL TARGETING OF IMMUNOGENS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner, Birch, McKie and Beckett  
; STREET: 1001 G Street, N.W., Eleventh Floor  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20001-4597  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/006,845  
; FILING DATE: 19930122  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Posorske, Laurence H.  
; REGISTRATION NUMBER: 34,698  
; REFERENCE/DOCKET NUMBER: 1107.041541  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: C-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-08-006-845-1

Query Match 100.0%; Score 23; DB 1; Length 11;  
Best Local Similarity 80.0%; Pred. No. 57;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5

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Db      1 RKRSH 5
; TITLE OF INVENTION:  CIRCOWIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE:      065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE:  2000-02-28
; PRIOR APPLICATION NUMBER:  FR 97/15396
; PRIOR FILING DATE:    1997-12-05
; NUMBER OF SEQ ID NOS:  170
; SOFTWARE:             PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-09-514-245-61
Query Match      100.0%; Score 23; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRSH 5
Db      2 RPRSH 6

RESULT 4
US-09-514-245-84
; Sequence 84, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION:  CIRCOWIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE:      065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE:  2000-02-28
; PRIOR APPLICATION NUMBER:  FR 97/15396
; PRIOR FILING DATE:    1997-12-05
; NUMBER OF SEQ ID NOS:  170
; SOFTWARE:             PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-84
Query Match      100.0%; Score 23; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRSH 5
Db      2 RPRSH 6

RESULT 5
US-08-416-336-4
; Sequence 4, Application US/08416336
; Patent No. 5807714
; GENERAL INFORMATION:
; APPLICANT: Ishizaka, Kimishige
; APPLICANT: Ishii, Yasuyuki
; TITLE OF INVENTION:  METHOD OF PRODUCTION OF ANTIGEN-SPECIFIC
; TITLE OF INVENTION:  GLYCOSYLATION INHIBITING FACTOR
; NUMBER OF SEQUENCES:  8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.

Db      1 RKRSH 5
; TITLE OF INVENTION:  CIRCOWIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE:      065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE:  2000-02-28
; PRIOR APPLICATION NUMBER:  FR 97/15396
; PRIOR FILING DATE:    1997-12-05
; NUMBER OF SEQ ID NOS:  170
; SOFTWARE:             PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-84
Query Match      100.0%; Score 23; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRSH 5
Db      4 RKRSH 8

RESULT 3
US-09-514-245-61
; Sequence 61, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois

Db      1 RKRSH 5
; TITLE OF INVENTION:  CIRCOWIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE:      065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE:  2000-02-28
; PRIOR APPLICATION NUMBER:  FR 97/15396
; PRIOR FILING DATE:    1997-12-05
; NUMBER OF SEQ ID NOS:  170
; SOFTWARE:             PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-84
Query Match      100.0%; Score 23; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRSH 5
Db      4 RKRSH 8

RESULT 3
US-09-514-245-61
; Sequence 61, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
```

STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/416,336  
FILING DATE: 04-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa H.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07246/010001  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-416-336-4

Query Match 100.0%; Score 23; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
|:|  
Db 11 RSRSH 15

RESULT 6  
US-09-109-957-9  
Sequence 9, Application US/09109957  
Patent No. 6136533  
GENERAL INFORMATION:  
APPLICANT: Bekkaoui, Faouzi  
APPLICANT: Modrusan, Zora D.  
APPLICANT: Pische, Isabelle A.  
APPLICANT: Duck, Peter D.  
APPLICANT: Cloney, Lynn P.  
APPLICANT: Wong, Alfred C.K.  
TITLE OF INVENTION: ADDITIVES FOR USE IN CYCLING PROBE REACTIONS  
FILE REFERENCE: 480094.419  
CURRENT APPLICATION NUMBER: US/09/109,957  
CURRENT FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-109-957-9

Query Match 100.0%; Score 23; DB 3; Length 21;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
|:|  
Db 12 RNRSH 16

RESULT 7  
PCT-US94-05150-37  
Sequence 37, Application PC/TUS9405150

GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Purified Mammalian Flt3 Ligands and Agonists and Antagonists T  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.5  
SOFTWARE: Microsoft Word 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05150  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/162,413  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,111  
FILING DATE: 19-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,391  
FILING DATE: 24-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/106,340  
FILING DATE: 13-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/092,549  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/089,263  
FILING DATE: 07-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/065,231  
FILING DATE: 19-MAY-1993  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US94-05150-37

Query Match 100.0%; Score 23; DB 5; Length 29;  
Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
|:|  
Db 12 RCRSH 16

RESULT 8  
US-09-270-767-61126  
Sequence 61126, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7328-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 61126  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-61126

Query Match 100.0%; Score 23; DB 4; Length 32;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 RXRSH 5
    |:|||
Db 2 RXRSH 6

RESULT 9
US-09-270-767-40082
; Sequence 40082, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40082
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-40082

Query Match 100.0%; Score 23; DB 4; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
    |:|||
Db 14 RFRSH 18

RESULT 10
US-09-270-767-55298
; Sequence 55298, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55298
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-55298

Query Match 100.0%; Score 23; DB 4; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
    |:|||
Db 14 RFRSH 18

RESULT 11
US-08-789-333F-22
; Sequence 22, Application US/08789333F
; Patent No. 6153380
; GENERAL INFORMATION:
; APPLICANT: No. 6153380an, Garry P
; APPLICANT: Rothenberg, S. M.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A642601DUBRMSDSS
; CURRENT APPLICATION NUMBER: US/08/789,333F
; CURRENT FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: lysosomal
; OTHER INFORMATION: membrane sequence.
US-08-789-333F-22

Query Match 100.0%; Score 23; DB 3; Length 36;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
    |:|||
Db 26 RKRSH 30

RESULT 12
US-09-169-015-32
; Sequence 32, Application US/09169015
; Patent No. 6180343
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides
; FILE REFERENCE: A66900/DJB/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/169,015
; CURRENT FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; PUBLICATION INFORMATION:
; JOURNAL: Cell. Mol. Biol. Res.
; ISSUE: 41
; PAGES: 405-
; DATE: 1995
US-09-169-015-32

Query Match 100.0%; Score 23; DB 3; Length 36;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
    |:|||
Db 26 RKRSH 30

RESULT 13
US-09-133-944-21
; Sequence 21, Application US/09133944
; Patent No. 6280937
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Pei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHUTTLE VECTORS
; FILE REFERENCE: A66252/DJB/DAV
; CURRENT APPLICATION NUMBER: US/09/133,944
; CURRENT FILING DATE: 1999-08-14
; EARLIER APPLICATION NUMBER: 09/133,949
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 39
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; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: lysosomal  
; OTHER INFORMATION: membrane sequence  
; PUBLICATION INFORMATION:  
; JOURNAL: Cell. Mol. Biol. Res.  
; VOLUME: 41  
; PAGES: 405-405  
; DATE: 1995  
US-09-133-944-21

Query Match 100.0%; Score 23; DB 3; Length 36;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
|:|  
Db 26 RKRSH 30

RESULT 14  
US-09-208-827-23  
; Sequence 23, Application US/09208827  
; Patent No. 6391582  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Ying  
; APPLICANT: Yu, Fei Wen  
; APPLICANT: Lorens, James  
; TITLE OF INVENTION: SHUTTLE VECTORS  
; FILE REFERENCE: A66252-1/DJB/DAV  
; CURRENT APPLICATION NUMBER: US/09/208,827  
; CURRENT FILING DATE: 1998-12-09  
; EARLIER APPLICATION NUMBER: 09/133,949  
; EARLIER FILING DATE: 1998-08-14  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: lysosomal  
; OTHER INFORMATION: membrane sequence  
; PUBLICATION INFORMATION:  
; JOURNAL: Cell. Mol. Biol. Res.  
; VOLUME: 41  
; PAGES: 405-405  
; DATE: 1995  
US-09-208-827-23

Query Match 100.0%; Score 23; DB 3; Length 36;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
|:|  
Db 26 RKRSH 30

RESULT 15  
US-08-787-738B-22  
; Sequence 22, Application US/08787738B  
; Patent No. 6455247  
; GENERAL INFORMATION:  
; APPLICANT: No. 6455247an, Garry P  
; APPLICANT: Rothenburg, Michael S.  
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR  
; TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES  
; FILE REFERENCE: A-64259-1 correction

; CURRENT APPLICATION NUMBER: US/08/787,738B  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: 08/589,108  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: 08/589,911  
; PRIOR FILING DATE: 1996-01-23  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Cricetulus griseus  
US-08-787-738B-22

Query Match 100.0%; Score 23; DB 4; Length 36;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5  
|:|  
Db 26 RKRSH 30

Search completed: March 8, 2005, 05:53:49  
Job time : 1.54978 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 14.5692 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-23

Perfect score: 1083

Sequence: 1 GLLKPSETLSLTCVAVGSGP.....LPKSKVMQGTDEHVVVTSKSE 205

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	948	87.5	231	2 B23746	Ig Fab region IV-J
2	749.5	69.2	627	2 S14683	Ig mu chain precu
3	599.5	55.4	143	2 B49028	Ig heavy chain v-I
4	553.5	51.1	592	2 S25705	Ig mu chain - shee
5	524	48.4	146	1 GH0H2	Ig heavy chain pre
6	521	48.1	140	2 S78052	Ig heavy chain pre
7	518.5	47.9	220	2 A49444	Ig gamma-1 heavy c
8	513	47.4	126	2 S47010	Ig heavy chain v-I
9	512.5	47.3	140	2 A49045	Ig heavy chain v-I
10	495.5	45.8	116	2 S37456	Ig mu chain - huma
11	494.5	45.7	288	2 S29690	Ig heavy chain VDJ
12	488.5	45.1	155	2 S31512	Ig heavy chain - h
13	488.5	45.1	155	2 S31511	Ig heavy chain - h
14	480	44.3	122	2 JL0047	Ig heavy chain v-I
15	478	44.1	137	2 S31676	Ig heavy chain v-I
16	477.5	44.1	114	2 I72667	cold agglutinin FS
17	475.5	43.9	130	2 S31690	Ig heavy chain v-I
18	475.5	43.9	140	2 I37782	Ig variable region
19	469	43.3	97	2 S26898	Ig heavy chain v-I
20	463	42.8	97	2 S26805	Ig heavy chain v-I
21	460	42.5	97	2 S14474	Ig heavy chain v-I
22	459	42.4	97	2 G34964	Ig heavy chain v-I
23	456.5	42.2	146	2 S09711	Ig heavy chain v-I
24	456	42.1	97	2 S31586	Ig heavy chain v-I
25	455	42.0	139	2 S31586	Ig heavy chain v-I
26	453	41.8	130	2 S30534	Ig heavy chain v-I
27	452.5	41.8	135	2 S78051	Ig heavy chain pre
28	452	41.7	145	2 S78055	Ig heavy chain pre
29	450	41.6	106	2 S37454	Ig mu chain - huma

30	450	41.6	452	1 MHU	Ig mu chain C regi
31	450	41.6	453	2 S37769	Ig mu chain C regi
32	450	41.6	473	1 MHU	Ig mu chain C regi
33	450	41.6	474	2 S15590	Ig heavy chain - h
34	446	41.2	470	2 S22080	Ig heavy chain pre
35	444	41.0	568	2 A34891	Ig heavy chain pre
36	443.5	41.0	146	2 S09710	Ig heavy chain v-I
37	442	40.8	231	2 PC4155	Ig gamma-2b chain
38	440.5	40.7	147	2 S31519	Ig heavy chain v-I
39	440	40.6	129	2 S44114	Ig heavy chain v-I
40	435.5	40.2	127	2 S19668	Ig heavy chain v-I
41	434	40.1	97	2 JH0428	Ig gamma chain v-I
42	433.5	40.0	123	2 S30529	Ig heavy chain v-I
43	433	40.0	118	2 S24443	Ig heavy chain v-I
44	431.5	39.8	123	2 S30530	Ig heavy chain v-I
45	431.5	39.8	134	2 S54906	Ig heavy chain v-I

ALIGNMENTS

RESULT 1

B23746

Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000

C:Accession: B23746

R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.

J. Biol. Chem. 266, 2836-2842, 1991

A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin

A:Reference number: A23746; MUID:91131575; PMID:1993660

A:Accession: B23746

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-231 <LEO>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F140-209/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 948; DB 2; Length 231;

Best Local Similarity 87.9%; Pred. No. 1.8e-67;

Matches 188; Conservative 5; Mismatches 7; Indels 14; Gaps 3;

QY	1	GLLKPSETLSLTCVAVGSGFSGYWSWIRQPPGKGLWIGEINHSGSTNYPNLSKSRVTI	60
DB	9	GLLKPSETLSLTGAVYGGFSDYWSWIRQPPGKGLWIGEINHSGSTNYPNLSKSRVTI	68
QY	61	SVDTSKNQFSLKSSVTAAADTAVYCAR---GTTEYYYYYGVMDVWGQGTTVTVSGSGAS	117
DB	69	SVDTSKNQFSLKSSVTAAADTAVYCARPPHDTSGHYWNY-----WGQGTLLTVSGSGAS	123
QY	118	APTLPPLVSCENSPSDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSVLRGKG	177
DB	124	APTLPPLVSCENSPSDTSSVAVGCLAQDFLPDPSITFSWKYKNNSDISSTRGPPSVLRGKG	183
QY	178	YAATSQVLLPKSKVMQGTDEHVV-----TGSKE	205
DB	184	YAATSQVLLPKSKVMQGTDEHVVCKVQHPNGNKE	217

RESULT 2

S14683

Ig mu chain precursor, membrane-bound (clone 201) - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999

C:Accession: S14683; S08047

R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.

Nucleic Acids Res. 18, 4278, 1990

A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.

A:Reference number: S14683; MUID:90332450; PMID:2115996

A:Accession: S14683

A:Molecule type: mRNA

A:Residues: 1-627 <FRI>

A:Cross-References: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451

C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin; membrane protein  
F;1-15/Domain: signal sequence #status predicted <SIG>  
F;16-627/Product: Ig mu chain #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 749.5; DB 2; Length 627;  
Best Local Similarity 68.0%; Pred. No. 2.3e-51;  
Matches 149; Conservative 22; Mismatches 31; Indels 17; Gaps 4;

Qy 4 KPSSETLSLTCVAVGSGFSGYYSWIRQPPGKLEWIGB-INHSGSTNNPSLKSRVTISV 62  
Db 32 KPGSVKVCCKASGTFSSYAISWVRQAPGGGLEWGMGIIPFGTANYAQFQGRVTITA 91  
Qy 63 DTSKNQFSLKSSVTAADTAVVYCARG-----TTEYY-----YYYGMDVMGQGTTVVSS 112  
Db 92 DESTSTAYMEIUSLRSEDATVYCAKTGILGYPGSGWYPNSDYYYGMDVMGQGTTVVSS 151  
Qy 113 SGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFTSWKYKNSDISSTRGPPSV 172  
Db 152 SGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFTSWKYKNSDISSTRGPPSV 211  
Qy 173 LRGGKYAATSOVLLPSKDVMOGTDVHV-----TGSKE 205  
Db 212 LRGGKYAATSOVLLPSKDVMOGTDVHVVKVQHPNGNKE 250

RESULT 3  
B49028  
Ig heavy chain V-IV region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C;Accession: B49028  
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur  
Eur. J. Immunol. 21, 2355-2363, 1991  
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob  
A;Reference number: A49028; MUID:92008140; PMID:1915549  
A;Accession: B49028  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-143 <TIM>  
A;Cross-references: GB:S64473; NID:g236906; PIDN:AAB20012.1; PID:g236907  
A;Experimental source: X-linked agammaglobulinemia patients; B lymphoblastoid cell lines  
A;Note: sequence extracted from NCBI backbone (NCBI:64473, NCBI:64472)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 55.4%; Score 599.5; DB 2; Length 143;  
Best Local Similarity 87.3%; Pred. No. 2.7e-40;  
Matches 117; Conservative 1; Mismatches 9; Indels 7; Gaps 1;

Qy 1 GLLKPSETLSLTCVAVGSGFSGYYSWIRQPPGKLEWIGB-INHSGSTNNPSLKSRVTI 60  
Db 10 GLLKPSETLSLTCVAVGSGFSGYYSWIRQPPGKLEWIGB-INHSGSTNNPSLKSRVTI 69  
Qy 61 SVDTSKNQFSLKSSVTAADTAVVYCARG-----TTEYY-----YYYGMDVMGQGTTVVSS 113  
Db 70 SVDTSKNQFSLKSSVTAADTAVVYCARGPIVVVPAAMRGRGWDVGMVDMGQGTTVVSS 129

Qy 114 GSASAPTLFPLVSC 127  
Db 130 GSRASAPTLFPLVSC 143

RESULT 4  
S25705  
Ig mu chain - sheep  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S25705  
F;Patri, S.; Nau, F.  
Mol. Immunol. 29, 829-836, 1992

A;Title: Isolation and sequence of a cDNA coding for the immunoglobulin mu chain of the  
A;Reference number: S25705; MUID:92342148; PMID:1635560  
A;Accession: S25705  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-592 <PAT>  
A;Cross-references: EMBL:X59994; NID:g1269; PIDN:CAA42611.1; PID:g1270  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;483-554/Domain: immunoglobulin homology <IMM>

Query Match 51.1%; Score 553.5; DB 2; Length 592;  
Best Local Similarity 55.7%; Pred. No. 5.5e-36;  
Matches 112; Conservative 34; Mismatches 50; Indels 5; Gaps 3;

Qy 2 LLKPSETLSLTCVAVGSGFSGYYSWIRQPPGKLEWIGB-INHSGSTNNPSLKSRVTIS 61  
Db 30 LVKPESETLSLTCVSGSSLTVNHSVIRQASGKPEWLGKGGTNTYYPALKSRLSIA 89  
Qy 62 VDTSKNQFSLKSSVTAADTAVVYCARGTTEVYYVYGMVDMGQGTTVVSSGSASAPTL 121  
Db 90 RDTSKSQVLSLSLWADDDTAVVYCARSAGA--YFLADVDIWRGLLTVVSESESHPKV 147  
Qy 122 FPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFTSWKYKNSDISSTR--GFPSVLRGKYA 179  
Db 148 FPLVSCVSPSDENTVALGCLARDVPNSVGSFNKF--NNSTVSSERFWTFPEVLRDGLWS 206  
Qy 180 ATSQVLLPSKDVMOGTDVHV 200  
Db 207 ASSOVALHSSSTFQGTGGLV 227

RESULT 5  
GIHUH2  
Ig heavy chain precursor V-II region (ARH-77) - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
C;Accession: A02101  
R;Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.  
Gene 33, 181-189, 1985  
A;Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequen  
A;Reference number: A02101; MUID:85205332; PMID:3922855  
A;Accession: A02101  
A;Molecule type: mRNA  
A;Residues: 1-146 <KUD>  
A;Cross-references: UNIPROT:P06331  
A;Note: the sequence was determined from the differentiated gene  
C;Genetics:  
A;Gene: GDB:IGHV@  
A;Cross-references: GDB:128528; OMIM:147070  
A;Map position: 14q32.33-14q32.33  
A;Introns: 16/3  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <MAT>  
F;20-117/Region: V segment  
F;35-117/Domain: immunoglobulin homology <IMM>  
F;118-127/Region: D segment  
F;128-146/Region: J segment  
F;42-115/Dsulfide bonds: #status predicted

Query Match 48.4%; Score 524; DB 1; Length 146;  
Best Local Similarity 85.5%; Pred. No. 2.4e-34;  
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

Qy 1 GLLKPSETLSLTCVAVGSGFSGYYSWIRQPPGKLEWIGB-INHSGSTNNPSLKSRVTI 60  
Db 30 GLVFPSETLSLTCVAVGSGFSGYYSWIRQPPGKLEWIGB-INHSGSTNNYKTSLSKRVTI 89  
Qy 61 SVDTSKNQFSLKSSVTAADTAVVYCARGTTEYY-----YYYGMDVMGQGTTVVSS 113



Db 90 SLDT SKNLFSLKLSSVTAADTA VY CARGLLRGWNDVDYYGMDVWGQGT TTVVS9 146

## RESULT 6

S78052`  
Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C;Accession: S78052; S23717  
R;Harindranath, N.  
submitted to the EMBL Data Library, August 1990  
A;Reference number: S78051  
A;Accession: S78052  
A;Molecule type: mRNA  
A;Residues: 1-140 <HAR>  
A;Cross-references: EMBL:X54441; NID:g37815; PIDN:CAA38308.1; PID:g930118  
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockins  
Int. Immunol. 3, 865-875, 1991  
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h  
patient.  
A;Reference number: S23716; MUID:92031262; PMID:1718404  
A;Accession: S23717  
A;Molecule type: mRNA  
A;Residues: 15-111 <HAW>  
A;Cross-references: EMBL:X54441  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>  
F;15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F;29-111/Domain: immunoglobulin homology <IMW>

## RESIST 7

IG gamma-1 heavy chain (New) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 16-Jul-1999  
 C:Accession: A49444  
 R:Saul, F.A.; Poljak, R.J.  
 Proteins 14, 363-371, 1992  
 A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A resolution  
 A:Reference number: A49444; MUID:93066153; PMID:1438175  
 A:Accession: A49444  
 A:Status: Preliminary  
 A:Molecule type: protein  
 A:Residues: 1-220 <SAU>  
 A:Note: sequence modified after extraction from NCBI backbone  
 A:Note: this sequence report includes corrections based on crystal structure refinement  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:137-202/Domain: immunoglobulin homology <IMM>

Db	70	LNTSKNQFSLRLSGVTAADTAVVYCARNIA	-----GGIDVMGQGLSVTVSSASTKGPS	124
QY	121	LPPLVSCENSPDSTSSVAVGCLAQDFLPDXITTSWKYKKNSSSTRGPPSVLR-GGKYA	179	
Db	125	VFLPAPSKSTSG-GTAALGCLVDYPPPTVSW--NSCALTSGVHTFFAVLQSSGLYS	181	
QY	180	ATSOVLPLPSKDMQGTDEHV	199	
Db	182	LSSVVTVFPSSSL--GTOTYI	199	

## RESULT 8

S47010  
Ig heavy chain V4.21-UniqueD-J5 region - human  
C:Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S47010  
R:Mahmoudi, M.; Gasyana, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.  
submitted to the EMBL Data Library, July 1994  
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA an  
A:Reference number: S47009  
A:Accession: S47010  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-126 <MAH>  
A:Cross-references: EMBL:Z35492; NID:g517254; PIDN:CAA84625.1; PID:g517255  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-97/Domain: immunoglobulin homology <IMM>

## RESULT 9

A43045  
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C/Accession: A49045  
R:Grillot-Courvalin, C.; Brouet, J.C.; Pillier, F.; Raessenti, L.Z.; Labaume, S.  
Eur. J. Immunol. 22, 1781-1788, 1992  
A/Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recog  
A/Reference number: A49045; MUID:92324290; PMID:1623923  
A/Accession: A49045  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-140 <GRI>  
A/Cross-references: GB:S39381; NID:G250899; PIDN:AAB2444.1; PID:G250800  
A/Note: sequence extracted from NCBI backbone (NCBI:N108088, NCBI:P108089)  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/34-116/Domain: immunoglobulin homology <IMW>



Search completed: March 8, 2005, 06:39:20  
Job time : 15.6192 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 76.5572 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-23

Perfect score: 1083

Sequence: 1 GLLKPSETLSITCAVYGSF.....LPKDNVQGTDEHVVTGSGS 205

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	965.5	89.2	595	2	Q8WUX4	Q8WUX4 homo sapien
2	965.5	89.2	597	2	Q6GMX5	Q6GMX5 homo sapien
3	965.5	89.2	597	2	Q9BU10	Q9BU10 homo sapien
4	965.5	89.2	625	2	Q9GAA6	Q9GAA6 homo sapien
5	959.5	88.6	597	2	Q9BQ88	Q9BQ88 homo sapien
6	890	82.2	620	2	Q9G5Y0	Q9G5Y0 homo sapien
7	818	75.5	606	2	Q6GMY2	Q6GMY2 homo sapien
8	734	67.8	613	2	Q8WUK1	Q8WUK1 homo sapien
9	732.5	67.6	597	2	Q9G8B9	Q9G8B9 homo sapien
10	595	54.9	465	2	Q6GMX6	Q6GMX6 homo sapien
11	584.5	54.0	576	2	Q6P4I8	Q6P4I8 homo sapien
12	554.5	51.2	613	2	Q8VCX7	Q8VCX7 mus musculus
13	553.5	51.1	476	2	Q6GMX1	Q6GMX1 homo sapien
14	543.5	50.2	477	2	Q6GMX7	Q6GMX7 homo sapien
15	524	48.4	146	1	HV21 HUMAN	P06331 homo sapien
16	512	47.3	614	2	Q7TMT6	Q7TMT6 mus musculus
17	499	46.1	116	2	Q7Z3Y6	Q7Z3Y6 homo sapien
18	498.5	46.0	478	2	Q7Z379	Q7Z379 homo sapien
19	498	46.0	473	2	Q8TC63	Q8TC63 homo sapien
20	498	46.0	492	2	Q7Z374	Q7Z374 homo sapien
21	497	45.9	478	2	Q6NYH3	Q6NYH3 homo sapien
22	496.5	45.8	496	2	Q9GKX8	Q9GKX8 homo sapien
23	479.5	44.3	476	2	Q6MZU7	Q6MZU7 homo sapien
24	473.5	43.7	479	2	Q99M22	Q99M22 mus musculus
25	466	43.0	150	2	Q95973	Q95973 homo sapien
26	451.5	41.7	472	2	Q6N089	Q6N089 homo sapien
27	450	41.6	454	1	MUC HUMAN	P01871 homo sapien
28	446.5	41.2	478	2	Q6P181	Q6P181 homo sapien
29	444.5	41.0	119	2	Q9UL73	Q9UL73 homo sapien
30	439.5	40.6	573	2	Q8WU38	Q8WU38 homo sapien
31	431	39.8	482	2	Q91X92	Q91X92 mus musculus

Query Match

89.2%; Score 965.5; DB 2; Length 595;

32	427.5	39.5	605	2	Q6GN83	Q6GN83 xenopus lae
33	424	39.2	139	2	Q86SX2	Q86SX2 homo sapien
34	423.5	39.1	470	2	Q6PJA4	Q6PJA4 homo sapien
35	418.5	38.6	129	1	HV2F HUMAN	P01824 homo sapien
36	417	38.5	593	2	Q6INM5	Q6INM5 xenopus lae
37	416.5	38.5	464	2	Q6MZU6	Q6MZU6 homo sapien
38	416	38.4	225	2	Q6PAF5	Q6PAF5 xenopus lae
39	415.5	38.4	482	2	Q7Z351	Q7Z351 homo sapien
40	413	38.1	465	2	Q6P6C4	Q6P6C4 homo sapien
41	413	38.1	470	2	Q7TMM1	Q7TMM1 mus musculus
42	405.5	37.4	466	2	Q6IN78	Q6IN78 homo sapien
43	403.5	37.3	480	2	Q91XE1	Q91XE1 mus musculus
44	403	37.2	499	2	Q8N5K4	Q8N5K4 homo sapien
45	402	37.1	475	2	Q6MZQ6	Q6MZQ6 homo sapien

ALIGNMENTS

RESULT 1

Q8WUX4	PRELIMINARY;	PRT;	595 AA.
AC Q8WUX4;			
DT 01-MAR-2002 (Tremblrel. 20, Created)			
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)			
DE Hypothetical protein.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Lymph;			
EX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,			
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA Jones S.J., Marra M.A.;			
RT "Generation and initial analysis of more than 15,000 full-length human			
RT and mouse cDNA sequences."			
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN [2]			
RC SEQUENCE FROM N.A.			
RA TISSUE=Lymph;			
RA Strausberg R.;			
RL Submitted (DSC-2001) to the ENBL/GenBank/DBJ databases.			
DR EMBL; BC019235; AAH19235.2; -			
DR PIR; G34964; G34964.			
DR HSSP; P01861; 1ADQ.			
DR Pfam; PF07654; C1-set; 4.			
DR SMART; SM00409; IG; 2.			
DR SMART; SM00407; IGc1; 4.			
DR SMART; SM00406; IGV; 1.			
DR PROSITE; PS0835; IG LIKE; 5.			
DR PROSITE; PS00290; IG MHC; UNKNOWN_3.			
KW Hypothetical protein.			
SQ SEQUENCE 595 AA; 65290 MW; 0D4B5076545714E CRC64;			

Best Local Similarity 87.6%; Pred. No. 1.3e-77;  
Matches 191; Conservative 2; Mismatches 8; Indels 17; Gaps 3;

QY 1 GLLKPESETLSITCAVYGGSPGYWISWIRQPPGKLEWIGEINHSNSTNNPSLSKSRVTI 60  
Db 36 GLLKPESETLSITCAVYGGSPGYWISWIRQPPGKLEWIGEINHSNSTNNPSLSKSRVTI 95  
QY 61 SVDTSKNQFSLKLSVTAADTAIVYCAR-----GTTEYYYYYGVMDVWGQGTITVTVSS 113  
Db 96 SVDTSKKQLSLKLSVNAADTAIVYCARVITRASPGTDG----RYGMDVWGQGTITVTVSS 151  
QY 114 GSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDXITTFWSKYKNNSDISSTRGFPSVL 173  
Db 152 GSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDXITTFWSKYKNNSDISSTRGFPSVL 211  
QY 174 RGGKYAATSOVLPSKDVMOGTDEHVV-----TGSKE 205  
Db 212 RGGKYAATSOVLPSKDVMOGTDEHVVCKVQHPNGNKE 249

RESULT 2  
Q6GMX5 PRELIMINARY; PRT; 597 AA.

ID Q6GMX5 AC Q6GMX5  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
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RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073767; AAH73767.1; -.  
DR InterPro; IPR003599; Ig-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.cl.  
DR InterPro; IPR003006; Ig.MHC.  
DR InterPro; IPR003596; Ig.V.  
DR Pfam; PF07654; CI-set; 4.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match 89.2%; Score 965.5; DB 2; Length 597;  
Best Local Similarity 87.6%; Pred. No. 1.3e-77;  
Matches 191; Conservative 2; Mismatches 8; Indels 17; Gaps 3;

QY 1 GLLKPESETLSITCAVYGGSPGYWISWIRQPPGKLEWIGEINHSNSTNNPSLSKSRVTI 60  
Db 29 GLLKPESETLSITCAVYGGSPGYWISWIRQPPGKLEWIGEINHSNSTNNPSLSKSRVTI 88  
QY 61 SVDTSKNQFSLKLSVTAADTAIVYCAR-----GTTEYYYYYGVMDVWGQGTITVTVSS 113  
Db 89 SVDTSKKQLSLKLSVNAADTAIVYCARVITRASPGTDG----RYGMDVWGQGTITVTVSS 144  
QY 114 GSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDXITTFWSKYKNNSDISSTRGFPSVL 173  
Db 145 GSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDXITTFWSKYKNNSDISSTRGFPSVL 204  
QY 174 RGGKYAATSOVLPSKDVMOGTDEHVV-----TGSKE 205  
Db 205 RGGKYAATSOVLPSKDVMOGTDEHVVCKVQHPNGNKE 242

RESULT 3  
Q9BU10 PRELIMINARY; PRT; 597 AA.

ID Q9BU10 AC Q9BU10  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE IGHM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
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RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002963; AAH02963.1; -.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.cl.  
DR InterPro; IPR003006; Ig.MHC.  
DR InterPro; IPR003596; Ig.V.  
DR Pfam; PF07654; CI-set; 4.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFAGFB7E055851 CRC64;

Query Match      89.2%; Score 965.5; DB 2; Length 597;
Best Local Similarity 87.6%; Pred. No. 1.3e-77;
Matches 191; Conservative 2; Mismatches 8; Indels 17; Gaps 3;

QY 1 GLLKPESETLSLTCVAVGGSFSGYYSWIRQPPGKLEWIGEHSGSTNYPNPSLSKRVTI 60
DB 1 GLLKPESETLSLTCVAVGGSFSGYYSWIRQPPGKLEWIGEHSGSTNYPNPSLSKRVTI 88
QY 61 SVDTSKNQFSLKLSVTAADTAIVYCAR-----GTTEYYYYYGMVWGQTTVTVSS 113
DB 89 SVDTSKNQFSLKLSVTAADTAIVYCAR-----GTTEYYYYYGMVWGQTTVTVSS 144
QY 114 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDPLPDITFSGWKYKNSDISSTRGPPSVL 173
DB 145 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDPLPDITFSGWKYKNSDISSTRGPPSVL 204
QY 174 RGGKYAATSQVLLPSKQVMDQTHV-----TGSK 205
DB 205 RGGKYAATSQVLLPSKQVMDQTHV-----TGSK 242

RESULT 4
ID Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=24388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.

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DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBFE CRC64;

Query Match      89.2%; Score 965.5; DB 2; Length 625;
Best Local Similarity 87.6%; Pred. No. 1.4e-77;
Matches 191; Conservative 2; Mismatches 8; Indels 17; Gaps 3;

QY 1 GLLKPESETLSLTCVAVGGSFSGYYSWIRQPPGKLEWIGEHSGSTNYPNPSLSKRVTI 60
DB 36 GLLKPESETLSLTCVAVGGSFSGYYSWIRQPPGKLEWIGEHSGSTNYPNPSLSKRVTI 95
QY 61 SVDTSKNQFSLKLSVTAADTAIVYCAR-----GTTEYYYYYGMVWGQTTVTVSS 113
DB 96 SVDTSKNQFSLKLSVTAADTAIVYCAR-----GTTEYYYYYGMVWGQTTVTVSS 151
QY 114 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDPLPDITFSGWKYKNSDISSTRGPPSVL 173
DB 152 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDPLPDITFSGWKYKNSDISSTRGPPSVL 211
QY 174 RGGKYAATSQVLLPSKQVMDQTHV-----TGSK 205
DB 212 RGGKYAATSQVLLPSKQVMDQTHV-----TGSK 249

RESULT 5
ID Q9BOB8 PRELIMINARY; PRT; 597 AA.
AC Q9BOB8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -.

```







RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC015760; AAHL5760.1; -;  
DR PIR; S05271; S05271.  
DR PIR; S24260; S24260.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; CI-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 5.  
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.  
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E263D9 CRC64;

Query Match 67.6%; Score 732.5; DB 2; Length 597;  
Best Local Similarity 69.6%; Pred. No. 8.7e-57;  
Matches 149; Conservative 18; Mismatches 38; Indels 9; Gaps 3;  
QY 1 GLLKPESETLSLTCAVYGGFSGYWSWIRQPPGKLEWIGEHNS-GSTNYPNPSLKSRTV 59  
DB 29 GLLVGGSLRLSCASGFSFSSYANWVRQAPGKLEWISALSGGGTYTADSVGRFT 88  
QY 60 ISVDTSKNQFSLKLSVTAADTAATVYTCARGTTEYYY--YYTGMDVWGQGTITVTVSSGSAS 117  
DB 89 ISRDNRSRDTLYQNNLSRAEDTAATVYCAKDPRGYSASGNVTREDYWGQGTITVTVSSGSAS 148  
QY 118 APTLPPLVSCENSPSDTSSVAVGCLAQDFLDXITFSWKYKXNSDISSTRGFPSPVLRGCK 177  
DB 149 APTLPPLVSCENSPSDTSSVAVGCLAQDFLDXITFSWKYKXNSDISSTRGFPSPVLRGCK 208  
QY 178 YAATSOVLPLPSKDVMOGTDEHV-----TGSKE 205  
DB 209 YAATSOVLPLPSKDVMOGTDEHVCKVQHPNGKE 242

RESULT 10  
Q6GMX6 PRELIMINARY; PRT; 465 AA.  
ID Q6GMX6  
AC Q6GMX6;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073766; AAH73766.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00407; IG; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.  
KW Hypothetical protein.  
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;  
Query Match 54.9%; Score 595; DB 2; Length 465;  
Best Local Similarity 60.5%; Pred. No. 1.2e-44;  
Matches 121; Conservative 22; Mismatches 45; Indels 12; Gaps 5;  
QY 1 GLLKPESETLSLTCAVYGGFSGYWSWIRQPPGKLEWIGEHNSGSTNYPNPSLKSRTV 60  
DB 29 GLVXPESETLSLTCTVSGGSISSYWSWIRQAPGKLEWIGRIYTSNSTNYPNPSLKSRTV 88  
QY 61 SVDTSKNQFSLKLSVTAADTAATVYTCARGTTEYYYGGMDVWGQGTITVTVSSGSASAPT 120  
DB 89 SVDTSKNQFSLKLSVTAADTAATVYTCARGRTYF-----DYWGQGTITVTVSSASTKGPS 142  
QY 121 LPFLVSCENSPSDTSSVAVGCLAQDFLDXITFSWKYKXNSDISSTRGFPSPVLR-GGKYA 179  
DB 143 VFPLAPSSKTSKG-GTAALGCLVDPPEPVTWSN--NSGALTSGVHTFPFVAVLQSSGLYS 199  
QY 180 ATSOVLPLPSKDVMOGTDEHV 199  
DB 200 LSSVTVTPSSSL--GTQTYI 217  
RESULT 11  
Q6P4I8 PRELIMINARY; PRT; 576 AA.  
ID Q6P4I8  
AC Q6P4I8;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE IGHD protein.  
GN Name=IGHD;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]



Db 149 TKGPSVFPPLAPSSKSTSG--GTAALGCLVKDYPPPEVTVSW--NSGALTSGVHTFPFPAVLQS 200  
 Qy 175 GGYAATTSQVLLPSKDVMOQGTDEHV 199  
 Db 206 SGLYSLSSVTVFSSSL--GTQTYI 228  
 RESULT 14  
 Q6GMX7 PRELIMINARY; PRT; 477 AA.  
 AC Q6GMX7; 2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073765; AAH73765.1; -;  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF00674; C1-set; 3.  
 DR SMART; SM00407; IG1; 3.  
 DR SMART; SM00409; IG; 4.  
 DR SMART; SM00406; IG; 1.  
 DR SMART; SM00407; IG1; 3.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;  
 Query Match 50.2%; Score 543.5; DB 2; Length 477;  
 Best Local Similarity 56.3%; Pred. No. 5e-40;  
 Matches 111; Conservative 27; Mismatches 48; Indels 11; Gaps 6;  
 Qy 1 GLKPSFTLSITCAVYGSGFSG--YVWSWIRPQPGKLEWIGEHNSGTSYTNPSLSKRV 58  
 Db 29 GLKPSFTLSITCAVYGSGFSG--YVWSWIRPQPGKLEWIGEHNSGTSYTNPSLSKRV 88  
 Qy 59 TISVDTSKNQSLSKLSVTAADTAVVYCARGTTEYYYY--GMDVWGQGTTVTVSSGS 115  
 Db 89 TISVDTSKNQSLSKLSVTAADTAVVYCARGTTEYYYY--GMDVWGQGTTVTVSSGS 148  
 Qy 116 ASAPTLPPLVSCENSPSDTSVAVGCLAQDFLPDXITFSWKNKNSDIDSTRGFPFSLVR- 174  
 Db 116 ASAPTLPPLVSCENSPSDTSVAVGCLAQDFLPDXITFSWKNKNSDIDSTRGFPFSLVR- 174

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Db      89  SLDTSKNQFSLKSLNSVTADTAIVYCAHGSS-----WDFADYWGQGLTLVTSSASPTSPK 144
Qy      121  LFPLVSCNSPDSSTSVAVGCLAQDFLP-DXITFSWKYKNSDISSTRGFP--SVLRGCK 177
Db      145  VFPL-SLDTSTPD-GNVVACLVQGFPPQEPPLSVTWSESGQN--VTARNFPPSQDASGDL 200
Qy      178  YAATSQVLLPSKDVMOG 194
Db      201  YTTSSQLTLPATQCPDG 217
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RESULT 15

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HV2I_HUMAN
ID HV2I_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
DR F1R; A02101; GIHUH2.
DR HSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.
FT DOMAIN 20 117 V segment.
FT DOMAIN 118 127 D segment.
FT DOMAIN 128 146 J segment.
FT DISULFID 42 115 By similarity.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;
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Query Match 48.4%; Score 524; DB 1; Length 146;
Best Local Similarity 85.5%; Pred. No. 6.5e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

Qy 1 GLLKPESETLSLTCVAVGSGFSGYYSWIRQPPGKLEWIGEINHSNSTYNPSLKSRTVI 60
Db 30 GLVKESETLSLTCVAVGSGFSGYYSWIRQPPGKLEWIGEINHSNSTYNPSLKSRTVI 89
Qy 61 SVDTSKNQFSLKSLNSVTADTAIVYCARCTTEYYY-----YYGMDVWGQGLTLVTSS 113
Db 90 SLDTSKNQFSLKSLNSVTADTAIVYCARGLLRGGWMDVYYGMDVWGQGLTLVTSS 146
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Search completed: March 8, 2005, 06:35:44  
Job time : 78.5572 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 95.0436 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-23

Perfect score: 1083

Sequence: 1 GLLKPSLTSLTCAVGGSP.....LPKDVMOGTDEHVVTVGSKE 205

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1083	100.0	205	2 AAY34299	Aay34299 Igm antib
2	1030	95.1	202	2 AAY34303	Aay34303 Igm antib
3	930	85.9	190	2 AAY34304	Aay34304 Igm antib
4	900.5	83.1	197	2 AAY34300	Aay34300 Igm antib
5	749.5	69.2	627	7 ADP97370	Adp97370 Human imm
6	747	68.0	595	7 ADM05427	Adm05427 Human pro
7	739.5	68.3	203	2 AAY34301	Aay34301 Igm antib
8	738	68.1	596	4 AAM23924	Aam23924 Human EST
9	735	67.9	223	2 AAY08598	Aay08598 Anti-huma
10	729	67.3	223	8 ADL70773	Adl70773 Anti-TNFA
11	727	67.1	588	2 AAW71880	Aaw71880 Anti-huma
12	727	67.1	588	3 AAB12917	Aab12917 Anti-huma
13	726.5	67.1	228	8 ADL70776	Adl70776 Anti-TNFA
14	725.5	67.0	266	8 ADF69305	Adf69305 Human lun
15	718.5	66.3	199	2 AAY34302	Aay34302 Igm antib
16	713	65.8	588	2 AAW71881	Aaw71881 Anti-huma
17	713	65.8	588	3 AAB12918	Aab12918 Anti-huma
18	705	65.1	533	7 ADB65070	Adb65070 Human pro
19	703	64.9	569	8 ADR19330	Adr19330 Chimeric
20	702.5	64.9	570	8 ADR19329	Adr19329 Chimeric
21	690	63.7	571	6 ADP84970	Adp84970 Chimeric
22	680.5	62.8	450	6 ABP96294	Abp96294 4A5-3.1.1
23	667.5	61.6	453	6 ABP96295	Abp96295 4A5-3.1.1
24	652.5	60.2	472	2 AAK93166	Aak93166 Anti-rhes
25	650	60.0	229	7 ADJ32128	Adj32128 Human int

26	643	59.4	223	7 ADJ32112	Adj32112 Human int
27	636.5	58.8	230	7 ADJ32118	Adj32118 Human int
28	635	58.6	537	3 AAY96290	Aay96290 Human IGF
29	623.5	57.6	462	3 AAB26884	Aab26884 Human imm
30	613.5	56.6	464	7 ADE28411	Ade28411 Human ant
31	598	55.2	473	4 AAB36206	Aab36206 Human imm
32	596	55.0	251	5 ABG80712	Abg80712 Amyloid p
33	596	55.0	254	5 ABG80713	Abg80713 Amyloid p
34	596	55.0	263	5 ABG80714	Abg80714 Human IGF
35	595.5	55.0	466	7 ADE28479	Ade28479 Human ant
36	593.5	54.7	580	6 AAO30915	Aao30915 di-NHS76
37	592.5	54.7	466	7 ADE28471	Ade28471 Human ant
38	589	54.4	580	6 AAO30913	Aao30913 di-NHS76
39	586.5	54.2	466	7 ADE28419	Ade28419 Human ant
40	583	53.8	221	7 ADJ32126	Adj32126 Human int
41	579	53.5	229	3 AAB30593	Aab30593 Variable
42	572.5	52.9	154	6 ABP96293	Abp96293 Human ant
43	571.5	52.8	172	3 AAY93713	Aay93713 The heavy
44	571.5	52.8	172	6 AAB35892	Aab35892 Human 2.1
45	571	52.7	241	8 ADS84467	Ad844467 Human ant

## ALIGNMENTS

### RESULT 1

AAY34299

ID AAY34299 standard; protein; 205 AA.

XX AC AAY34299;

XX DT 19-NOV-1999 (first entry)

XX DE Igm antibody CEM 10.1 C3 heavy chain sequence.

XX KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;

XX KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

XX KW organ transplant rejection disease; lymphoma; pancreatic disease;

XX KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 150

FT /label= unknown

FT /note= "encoded by TVC"

XX PN WO9945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX N-PSDB; AAZ20400.

XX PT New monoclonal antibody, used for treating e.g. graft versus host

XX PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 60; Fig 24; 245pp; English.

XX CC This sequence represents the heavy chain of an antibody of the invention.

XX CC The antibody is a monoclonal antibody (mAb) with an isotype that fixes

XX CC complement and a variable region that binds to the epitope on CD147 bound

XX CC by the Igm mAb ABX-CBL, providing that the antibody is not CBL1. The MAb

CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX  
SQ Sequence 205 AA;

Query Match 100.0%; Score 1083; DB 2; Length 205;  
Best Local Similarity 100.0%; Pred. No. 8.5e-67;  
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLLKPSETLSLTCAYVGGSGFYWSWIROPKGLWIGINHSNSTNPNPSLKSRVTI 60  
Db 1 GLLKPSETLSLTCAYVGGSGFYWSWIROPKGLWIGINHSNSTNPNPSLKSRVTI 60  
Qy 61 SVDTSKNQFSLKLSSTVAADTAIVYTCARGTTEYYYYYGMVDVWGQTTVTVSSGSASAPT 120  
Db 61 SVDTSKNQFSLKLSSTVAADTAIVYTCARGTTEYYYYYGMVDVWGQTTVTVSSGSASAPT 120  
Qy 121 LFPLVSCNSPDSPTSSVAVGCLAQDFLPDXITFTFSWKYKNNSDISSTRGFPVSLRGKYAA 180  
Db 121 LFPLVSCNSPDSPTSSVAVGCLAQDFLPDXITFTFSWKYKNNSDISSTRGFPVSLRGKYAA 180  
Qy 181 TSQVLLPSKDVMOGTDHVVVTGSKE 205  
Db 181 TSQVLLPSKDVMOGTDHVVVTGSKE 205

RESULT 2  
RAY34303  
ID AAY34303 standard; protein; 202 AA.

XX AC AAY34303;  
XX DT 19-NOV-1999 (first entry)  
XX DE IgM antibody CEM 13.12 heavy chain sequence.

XX KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
XX KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
XX KW organ transplant rejection disease; lymphoma; pancreatic disease;  
XX KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Misc-difference 147  
FT /label= unknown  
FT /note= "encoded by TYC"  
FT Misc-difference 151  
FT /label= unknown  
FT /note= "encoded by TYC"

XX PN WO9945031-A2.  
XX PD 10-SEP-1999.  
XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.  
XX PR 03-FEB-1999; 99US-00244253.  
XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX DR WPI; 1999-540816/45.  
XX DR N-PSDB; AAZ20404.

PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX  
PS Claim 60; Fig 28; 245pp; English.

XX This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IgM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX

SQ Sequence 202 AA;

Query Match 95.1%; Score 1030; DB 2; Length 202;  
Best Local Similarity 97.5%; Pred. No. 3.7e-63;  
Matches 197; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 KPSETLSLTCAYVGGSGFYWSWIROPKGLWIGINHSNSTNPNPSLKSRVTISVD 63  
Db 1 KLPTLSLTCAYVGGSGFYWSWIROPKGLWIGINHSNSTNPNPSLKSRVTISVD 60  
Qy 64 TSKNQFSLKLSSTVAADTAIVYTCARGTTEYYYYYGMVDVWGQTTVTVSSGSASAPTLP 123  
Db 61 TSKNQFSLKLSSTVAADTAIVYTCARGTTEYYYYYGMVDVWGQTTVTVSSGSASAPTLP 120  
Qy 124 LVSCNSPDSPTSSVAVGCLAQDFLPDXITFTFSWKYKNNSDISSTRGFPVSLRGKYAATSQ 183  
Db 121 LVSCNSPDSPTSSVAVGCLAQDFLPDXITFTFSWKYKNNSDISSTRGFPVSLRGKYAATSQ 180  
Qy 184 VLLPSKDVMOGTDHVVVTGSKE 205  
Db 181 VLLPSKDVMOGTDHVVVTGSKE 202

RESULT 3  
RAY34304  
ID AAY34304 standard; protein; 190 AA.

XX AC AAY34304;  
XX DT 19-NOV-1999 (first entry)  
XX DE IgM antibody CEM 13.5 heavy chain sequence.

XX KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
XX KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
XX KW organ transplant rejection disease; lymphoma; pancreatic disease;  
XX KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.  
XX PN WO9945031-A2.

XX PD 10-SEP-1999.  
XX PF 03-MAR-1999; 99WO-US004583.  
XX PR 03-MAR-1998; 98US-00034607.  
XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX DR WPI; 1999-540816/45.  
XX DR N-PSDB; AAZ20405.





XX New immunoadhesin, useful for treating anthrax and rhinovirus, comprises  
PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and  
PT J chain and secretory component associated with the chimeric toxin  
PT receptor protein.  
XX  
PS Disclosure; SEQ ID NO 47; 288pp; English.  
XX  
CC The invention relates to a novel immunoadhesin comprising a chimeric  
CC toxin receptor protein consisting of a toxin receptor protein linked to  
CC at least a portion of an immunoglobulin heavy chain with a J (joining)  
CC chain and secretory component (SC) associated with the chimeric toxin  
CC receptor protein. The immunoadhesin comprises a chimeric bacterial or  
CC viral toxin receptor protein and the immunoadhesin has plant-specific  
CC glycosylation. The immunoadhesin of the invention demonstrates virucide  
CC and antibacterial activities and may be useful for reducing the binding  
CC of a viral or bacterial antigen to a host cell and thus for treating or  
CC preventing anthrax, as well as human rhinovirus infection which results  
CC in the common cold. The current sequence is that of the human  
CC immunoadhesin-related protein of the invention.  
XX  
SQ Sequence 627 AA;

Query Match 69.2%; Score 749.5; DB 7; Length 627;  
Best Local Similarity 68.0%; Pred. No. 2.3e-43;  
Matches 149; Conservative 22; Mismatches 31; Indels 17; Gaps 4;  
Qy 4 KPSTLSLTCAVYGGSGFYWSWIRQPPGKGLWIGB-INHSGSTYNNPSLKSRVTISV 62  
Db 32 KPGSSVKYCKSKASGDTSSYAISWVRQAPGGGLEWMMGGIIPFGTANYAQKFGQRTVITA 91  
Qy 63 DTSKNQPSLKLSSVTAADTAVYYCARG-----TTEYY----YYYGMDVWGQGTITVTS 112  
Db 92 DESTSTAYMELSSLRSEDTAVYYCAKTIILGPYSGGWTPNSDYIYYGMDVWGQGTITVTS 151  
Qy 113 SGSASAPTLFLPVCSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVS 172  
Db 152 SGSASAPTLFLPVCSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVS 211  
Qy 173 LRGGKYAATSOVLLPSKDVMOGTDEHVV-----TGSKE 205  
Db 212 LRGGKYAATSOVLLPSKDVMOGTDEHVVCKVQHPNGNKE 250

RESULT 6  
ADM05427  
ID ADM05427 standard; protein; 595 AA.

XX ADM05427;  
XX  
XX 20-MAY-2004 (first entry)  
XX  
XX Human protein of the invention SEQ ID NO:4112.  
XX human; gene therapy; diagnostic marker; pharmaceutical.  
XX Homo sapiens.

XX EP1347046-A1.

XX 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX WPI; 2003-723558/69.

DR N-PSDB; ADM02984.  
XX New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.  
XX  
PS Claim 1; SEQ ID NO 4112; 305pp; English.  
XX  
CC The invention relates to a novel human polynucleotide and the encoded  
CC polypeptide. A polynucleotide of the invention may have a use in gene  
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
CC as a primer for synthesizing the polynucleotide or as a probe for  
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines  
CC for regulating their expression and activity, or as a target of gene  
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents a  
XX protein sequence of the invention.  
XX  
SQ Sequence 595 AA;

Query Match 69.0%; Score 747; DB 7; Length 595;  
Best Local Similarity 70.3%; Pred. No. 3.2e-43;  
Matches 149; Conservative 21; Mismatches 34; Indels 8; Gaps 3;  
Qy 1 GLLKPSSTLSLTCAVYGGSGFYWSWIRQPPGKGLWIGB-INHSGSTN-YNPSLKSRVT 59  
Db 30 GLVQPGSLRLSCAASGFTFSNFAHVRQAPGKGLYVSTISSNGRQKYGESVKGRFT 89  
Qy 60 ISVDTSKNQPSLKLSSVTAADTAVYYCARGTTEYYYYYGMVWGQGTITVSSGSASAP 119  
Db 90 ISRDSSKNTLFLQMSLRDEDDTAVYYCARGHS-IDNYHYGVDVWGQGTITVSSGSASAP 148  
Qy 120 TLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVLRGGKYA 179  
Db 149 TLFPLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYA 208  
Qy 180 ATSOVLLPSKDVMOGTDEHVV-----TGSKE 205  
Db 209 ATSOVLLPSKDVMOGTDEHVVCKVQHPNGNKE 240

RESULT 7  
AAY34301  
ID AAY34301 standard; protein; 203 AA.

XX AAY34301;  
XX  
XX 19-NOV-1999 (first entry)  
XX  
XX IgM antibody CEM 10.12 F3 heavy chain sequence.

XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Homo sapiens.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US0004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;

DR WPI; 1999-540816/45.  
 DR N-PSDB; AAZ20402.

PT New monoclonal antibody, used for treating e.g. graft versus host  
 PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX  
 XX Claim 60; Fig 26; 245pp; English.

XX This sequence represents the heavy chain of an antibody of the invention.  
 CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
 CC complement and a variable region that binds to the epitope on CD147 bound  
 CC by the IGM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
 CC can selectively kill activated T-cells, activated B-cells or resting or  
 CC activated monocytes. The products and methods can be used for treating  
 CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
 CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
 CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
 CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)

XX SQ Sequence 203 AA;

Query Match 68.3%; Score 739.5; DB 2; Length 203;  
 Best Local Similarity 71.5%; Pred. No. 3.4e-43;  
 Matches 143; Conservative 24; Mismatches 30; Indels 3; Gaps 2;

Qy 4 KPSETLSITCAVYGGSGFYWIRPPGKLEWIGEBIN-HSGSTNYNPSLKSRVTISV 62  
 Db 2 KPGASVKVCKASGVTFTSYDINVRQATGQGLEWMGMWNPNSGNTGYAQKFGQRTVMNR 61  
 Qy 63 DTSKNQPSLKLSSTVADTAIVYCARG--TTEYIIYYIYGMVMDVWGQGTITVTVSSGSASAPT 120  
 Db 62 NTSISTAYMELSLRSEDATVYICARGGHGGSFYFYIYGMVMDVWGQGTITVTVSSGSASAPT 121  
 Qy 121 LFPLVSCENSPSDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSVLRGGKYAA 180  
 Db 122 LFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAA 181  
 Qy 181 TSQVLLPSKDVMDVWGQGTDEHV 200  
 Db 182 TSQVLLPSKDVMDVWGQGTDEHV 201

RESULT 8  
 AAM23924  
 ID AAM23924 standard; protein; 596 AA.

XX AC AAM23924;

XX 12-OCT-2001 (first entry)

XX Human EST encoded protein SEQ ID NO: 1449.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
 KW gene therapy; nutrition.

OS Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US002697.

XX 25-JAN-2000; 2000US-00491404.

XX 17-JUL-2000; 2000US-00617746.

XX 03-AUG-2000; 2000US-00631451.

XX 15-SEP-2000; 2000US-00663870.

XX (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Aundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX WPI; 2001-476164/51.  
 DR N-PSDB; AAH98583.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use.

XX Claim 20; Page 1011-1012; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a  
 CC protein of the invention

XX SQ Sequence 596 AA;

Query Match 68.1%; Score 738; DB 4; Length 596;  
 Best Local Similarity 69.0%; Pred. No. 1.3e-42;  
 Matches 149; Conservative 19; Mismatches 34; Indels 14; Gaps 4;

Qy 1 GLLKPSLTSITCAVYGGSGFYWIRPPGKLEWIGEBIN-HSGSTNYNPSLKSRVT 59  
 Db 29 GLVQPGSGLRLSCAASGFTFSYWMHVRQAPGKLVWVSRINTDGSSTSYADSVKGRFT 88  
 Qy 60 ISVDTSKNQPSLKLSSTVADTAIVYCAR---GTTEYIIYYIYGMVMDVWGQGTITVTVSSGS 115  
 Db 89 ISRDNAKNTLYLQWNSLRAEDTAVYICARADNCSTSCYKCF---DYWGQGTITVTVSSGS 145  
 Qy 116 ASAPTLPVSCENSPSDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSVLRG 175  
 Db 146 ASAPTLPVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRG 205  
 Qy 176 GKYAATSQVLLPSKDVMDVWGQGTDEHV---TGSK 205  
 Db 206 GKYAATSQVLLPSKDVMDVWGQGTDEHVCKVQHPNGNKE 241

RESULT 9  
 AAY08598  
 ID AAY08598 standard; protein; 223 AA.

XX AC AAY08598;

XX 05-AUG-1999 (first entry)

XX Anti-human TNF-alpha monoclonal antibody H-chain protein.

XX Monoclonal antibody; H chain; heavy chain; anti-human; TNF-alpha;  
 KW tumour necrosis factor; light chain; L chain.

XX Homo sapiens.

XX JP111127855-A.

XX 18-MAY-1999.

XX 27-OCT-1997; 97JP-00293994.

XX 27-OCT-1997; 97JP-00293994.

XX (NIHA) JAPAN ENERGY CORP.

XX WPI; 1999-350318/30.

XX N-PSDB; AAX77407.

XX Recombinant anti-human TNF-alpha human monoclonal antibody - produced

PT stably with a high purity, and in large amounts.

XX Claim 3; Page 12-13; 22pp; Japanese.

XX This invention describes novel recombinant anti-human TNF-alpha human

CC monoclonal antibody consisting of a heavy (H) chain and a light (L)

CC chain. The recombinant anti-human TNF-alpha human monoclonal antibody can

CC be produced stably in a high purity and in a large amount

XX Sequence 223 AA;

Query Match 67.9%; Score 735; DB 2; Length 223;

Best Local Similarity 68.4%; Pred. No. 7.6e-43;

Matches 145; Conservative 22; Mismatches 33; Indels 12; Gaps 3;

Qy 1 GLKPSSTLSITCAVYGSFSGYVWIRPPGKGLWIGIHNHSGSTN-YNPCLKSRVT 59

Db 10 GVQPGRLSLSCAASGFTSSYGMHVRQAPGKGLWVAVISYDGNKYVADSVKGRFT 69

Qy 60 ISVDTSKNQFSLKLSVTAADTAVYVCARGTTEYYYYYGMVWGQGTTVTVSSGSASAP 119

Db 70 ISRDNSKNTLYLQWNSLRAEDTAVYVCARDGLAF-----DIWGQGTMTVTSSGSASAP 124

Qy 120 TLPPLVSCNSPDSSTSSVAVGCLAQDFLPDXITPSWKYKNNSDISSSTRGPPSVLRGGKYA 179

Db 125 TLPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITPSWKYKNNSDISSSTRGPPSVLRGGKYA 184

Qy 180 ATSOVLPLSKDVMQGTDEHVY-----TGSKE 205

Db 185 ATSOVLPLSKDVMQGTDEHVCKVQHENGKNE 216

RESULT 10

ID ADL70773

AC ADL70773;

XX 03-JUN-2004 (first entry)

XX Anti-TNFalpha antibody VH region, SEQ ID 46.

XX Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;

KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;

KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnary;

KW Antiparkinsonian; Nootropic; Cardiant; Antianemic; Antiatherosclerotic;

KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;

KW Tf; transferrin fusion protein; Tf fusion protein; anti-TNFalpha;

XX antibody; VH region.

OS Unidentified.

XX W02004020588-A2.

PN 11-MAR-2004.

XX 28-AUG-2003; 2003WO-US026779.

XX 30-AUG-2002; 2002US-0406977P.

PR 10-MAR-2003; 2003US-00384060.

PR 09-JUL-2003; 2003US-0485404P.

XX (BIOR-) BIOREXIS PHARM CORP.

XX Prior CP, Turner AJ, Sadeghi H;

PI WPI; 2004-239175/22.

DR Novel library containing several fusion proteins each of which comprises

PT first transferrin polypeptide fused to at least one second peptide,

PT useful for screening for transferrin fusion protein having the particular

PT activity.

XX Example 8; SEQ ID NO 46; 243pp; English.

XX The present invention relates to a library (I) of modified fusion

CC proteins of transferrin (Tf) and therapeutic proteins with increased

CC serum half-life or serum stability. Preferred fusion proteins include

CC those modified so that the Tf moiety exhibits no or reduced

CC glycosylation, iron binding and/or Tf receptor binding. The transferrin

CC fusion proteins are useful for treating, preventing or ameliorating

CC disorders or diseases of endocrine system, nervous system, immune system,

CC respiratory system, cardiovascular system, diseases and/or disorders

CC relating to cell proliferation, and/or diseases or disorders relating to

CC blood. The modified fusion proteins are useful in diagnosis, prognosis,

CC prevention and/or treatment of autoimmune disorders; diseases and

CC disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia

CC and thrombocytopenia); allergic reactions such as allergic asthma,

CC anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and

CC eczema; inflammatory conditions e.g., inflammation associated with

CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,

CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders

CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel

CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders

CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative

CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The

CC fusion protein is also useful as an adjuvant to enhance antibacterial or

CC antifungal immune responses, antiparasitic immune responses, etc. The

CC fusion protein is also useful for treating monoclonal gammopathy of

CC undetermined significance (MGUS), Waldenstrom's disease, plasmacytomas,

CC adult respiratory distress syndrome, for stimulating wound repair, for

CC preventing or treating infections of joints, bones, skin, etc. The fusion

CC protein is also useful for treating or preventing thrombosis, myocardial

CC infarction, cancers, thrombocytopenia, sickle cell anaemia,

CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,

CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf

CC and a specific example of a SCA that can be fused to Tf is anti-tumour

CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence

CC from an anti-TNFalpha antibody.

XX Sequence 223 AA;

Query Match 67.3%; Score 729; DB 8; Length 223;

Best Local Similarity 67.9%; Pred. No. 2e-42;

Matches 144; Conservative 22; Mismatches 34; Indels 12; Gaps 3;

Qy 1 GLKPSSTLSITCAVYGSFSGYVWIRPPGKGLWIGIHNHSGSTN-YNPCLKSRVT 59

Db 10 GVQPGRLSLSCAASGFTSSYGMHVRQAPGKGLWVAVISYDGNKYVADSVKGRFT 69

Qy 60 ISVDTSKNQFSLKLSVTAADTAVYVCARGTTEYYYYYGMVWGQGTTVTVSSGSASAP 119

Db 70 ISRDNSKNTLYLQWNSLRAEDTAVYVCARDGLAF-----DIWGQGTMTVTSSGSASAP 124

Qy 120 TLPPLVSCNSPDSSTSSVAVGCLAQDFLPDXITPSWKYKNNSDISSSTRGPPSVLRGGKYA 179

Db 125 TLPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITPSWKYKNNSDISSSTRGPPSVLRGGKYA 184

Qy 180 ATSOVLPLSKDVMQGTDEHVY-----TGSKE 205

Db 185 ATSOVLPLSKDVMQGTDEHVCKVQHENGKNE 216

RESULT 11

AAW71880

ID AAW71880 standard; protein; 588 AA.

XX AAW71880;

AC AAW71880;

XX 18-JAN-1999 (first entry)

XX Anti-human Fas humanised antibody CH11 heavy chain HmuH.

XX Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;

KW autoimmune disease; rheumatoid arthritis; therapy; human;

XX antibody engineering.

OS Homo sapiens.  
XX Synthetic.  
FH Key Location/Qualifiers  
FT 1. .19 /label= Sig\_peptide  
FT 20. .588 /label= Mat\_protein  
FT 50. .54 /label= CDR1  
FT /note= "complementarity determining region 1 from CH11 heavy chain"  
FT 69. .84 /label= CDR2  
FT /note= "complementarity determining region 2 from CH11 heavy chain"  
FT 118. .124 /label= CDR3  
FT /note= "complementarity determining region 3 from CH11 heavy chain"  
XX EP866131-A2.  
XX 23-SEP-1998.  
XX 20-MAR-1998; 98EP-00302113.  
XX 21-MAR-1997; 97JP-00067938.  
XX (SANY ) SANKYO CO LTD.  
XX Serizawa N, Haruyama H, Takahaashi T, Nakahara K, Yonehara S;  
XX WPI; 1998-482965/42.  
XX N-PSDB; AAV61363.  
XX Production of anti-Fas protein humanised antibodies - for use in inducing  
PT apoptosis on Fas expressing cells in the treatment of auto-immune  
PT diseases, especially rheumatoid arthritis.  
XX Claim 21; Page 105-107; 187pp; English.  
XX This is the amino acid sequence of a humanised anti-Fas antibody CH11  
CC heavy chain, designated HmuH. HmuH is based on the heavy chain (see  
CC AAW71888) of murine anti-human Fas monoclonal antibody CH11. The  
CC humanised sequence was designed following selection of donor residues  
CC from CH11 to be grafted onto acceptor molecule 21.28'CL. 2 Heavy chain  
CC sequences (see AAW71880-81) have been designed, and each can be used in  
CC combination with any of 4 light chain sequences (see AAW71876-79) to  
CC provide novel, claimed humanised CH11 IgM antibodies that lack a J chain.  
CC These humanised anti-human Fas antibodies are capable of inducing  
CC apoptosis in cells expressing Fas (e.g. synovialocytes) and are useful in  
CC the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA  
CC sequences encoding the humanised antibodies are claimed, as are vectors  
CC such as pMuH5-1 including the HmuH nucleotide sequence (see AAV61363),  
CC and host cells such as Escherichia coli pMuH5-1 (FERM BP-5863)  
XX Sequence 588 AA;  
SQ  
Query Match 67.1%; Score 727; DB 2; Length 588;  
Best Local Similarity 67.9%; Pred. No. 7.4e-42;  
Matches 142; Conservative 21; Mismatches 32; Indels 14; Gaps 3;  
QY 4 KPSETSLITCAVYGGSGFYWYWIROPKGLWIGEL-NHSGSTNYNPSLKSRTIVS 62  
DB 32 KPGASVKVSCASGYTFTDYNHWVRQAPGGLEWMGYIYPNGTGYNQKFKSKATLV 91  
QY 63 DTSKNQFSLKLSVTAADTAVYVCARGTTEYYYYYGMVDMVQGTITVTVSSGSASPTLF 122  
DB 92 DNSASTAYMELSLRSEDATVYVCARS-----YYANDYWGQGLTVTVSSGSASPTLF 144  
QY 123 PLVSCENSPDTSSTSSVAVGCLAQDFLPDITFESWKYKKNSSDISSTRGPFPSVLRGGKYAATS 182  
|||||

DB 145 PLVSCENSPDTSSTSSVAVGCLAQDFLPDITFESWKYKKNSSDISSTRGPFPSVLRGGKYAATS 204  
QY 183 QVLLPSKDVNMQGTDEHYV-----TGSKE 205  
DB 205 QVLLPSKDVNMQGTDEHYVCKVQHPNGNKE 233  
RESULT 12  
AAB12917  
ID AAB12917 standard; protein; 588 AA.  
XX AC AAB12917;  
XX 16-NOV-2000 (first entry)  
DE Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #86.  
XX Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
KW immunosuppression; autoimmune disease; treatment; rheumatism;  
KW anti-Fas antibody.  
XX OS Synthetic.  
XX JP2000154149-A.  
XX 06-JUN-2000.  
XX 17-SEP-1999; 99JP-00263984.  
XX 18-SEP-1998; 98JP-00264598.  
XX (SANY ) SANKYO CO LTD.  
XX WPI; 2000-454476/40.  
XX N-PSDB; AAA78271.  
XX Anti-human Fas humanizing antibody-containing antirheumatic agents.  
XX Claim 1; Page 75-77; 109pp; Japanese.  
XX The present invention relates to antirheumatic agents which comprise as  
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
CC does not include a J segment, has apoptosis inducing activity, and  
CC consists of a light and heavy chain polypeptide produced synthetically.  
CC The agents of the invention exhibit antirheumatic and immunosuppressive  
CC activity and can be used to treat autoimmune diseases, especially  
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
CC binding properties. Included in the invention are nucleotide sequences of  
CC the IgM light and heavy chains (see AAA78267-A78272) and the  
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also  
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
CC chains used in the invention are represented by sequences AAA78213-  
CC A78266. Primers used for sequencing the human Ig DNA used in the  
CC invention are represented by sequences AAA78277-A78318 and AAA78335-  
CC A78337, while humanised anti-Fas Ig DNA sequencing primers are  
CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer  
CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in  
CC the production of the agent of the invention  
XX Sequence 588 AA;  
SQ  
Query Match 67.1%; Score 727; DB 3; Length 588;  
Best Local Similarity 67.9%; Pred. No. 7.4e-42;  
Matches 142; Conservative 21; Mismatches 32; Indels 14; Gaps 3;  
QY 4 KPSETSLITCAVYGGSGFYWYWIROPKGLWIGEL-NHSGSTNYNPSLKSRTIVS 62  
DB 32 KPGASVKVSCASGYTFTDYNHWVRQAPGGLEWMGYIYPNGTGYNQKFKSKATLV 91  
QY 63 DTSKNQFSLKLSVTAADTAVYVCARGTTEYYYYYGMVDMVQGTITVTVSSGSASPTLF 122  
|||||

Db 92 DNSASTAYMELSLRSBDTAVVYCARS-----YYAMDYWGQGLTVTVSSGSASAPTLF 144  
 QY 123 PLVSCENSPDTSVAVGCLAQDFLPDXITFSWKYKNSDISSTRGPPSVLRGGKYAATS 182  
 Db 145 PLVSCENSPDTSVAVGCLAQDFLPDITFSWKYKNSDISSTRGPPSVLRGGKYAATS 204  
 QY 183 QVLLPSKDVNMQGTDEHV-----TGSKE 205  
 Db 205 QVLLPSKDVNMQGTDEHVCKVQHPNGNKE 233

## RESULT 13

ADL70776

ID ADL70776 standard; protein; 228 AA.

XX

AC ADL70776;

XX

DT 03-JUN-2004 (first entry)

XX

DE Anti-TNFalpha antibody VH region, SEQ ID 49.

XX

KW Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;  
 Dermatology; Antiinfective; Antibacterial; Vasotropic;  
 Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnery;  
 Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antiatherosclerotic;  
 Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;  
 Tf; transferrin fusion protein; Tf fusion protein; anti-TNFalpha;  
 antibody; VH region.

KW

XX

OS Unidentified.

XX

PN W02004020588-A2.

XX

PD 11-MAR-2004.

XX

PF 28-AUG-2003; 2003WO-US026779.

XX

PR 30-AUG-2002; 2002US-0406977P.

XX

PR 10-MAR-2003; 2003US-00384060.

XX

PR 09-JUL-2003; 2003US-0485404P.

XX

XX (BIOR-) BIOREXIS PHARM CORP.

XX

XX Prior CP, Turner AJ, Sadeghi H;

XX

XX WPI; 2004-239175/22.

XX

XX Novel library containing several fusion proteins each of which comprises

XX

XX first transferrin polypeptide fused to at least one second peptide,

XX

XX useful for screening for transferrin fusion protein having the particular

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XX activity.

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CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders  
 CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative  
 CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The  
 CC fusion protein is also useful as an adjuvant to enhance antibacterial or  
 CC antifungal immune responses, antiparasitic immune responses, etc. The  
 CC fusion protein is also useful for treating monoclonal gammopathy of  
 CC undetermined significance (MGUS), Waldenstrom's disease, plasmacytomas,  
 CC adult respiratory distress syndrome, for stimulating wound repair, for  
 CC preventing or treating infections of joints, bones, skin, etc. The fusion  
 CC protein is also useful for treating or preventing thrombosis, myocardial  
 CC infarction, cancers, thrombocytopenia, sickle cell anaemia,  
 CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,  
 CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf  
 CC and a specific example of a SCA that can be fused to Tf is anti-tumour  
 CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence  
 CC from an anti-TNFalpha antibody.

XX

SQ Sequence 228 AA;

XX

Query Match 67.1%; Score 726.5; DB 8; Length 228;

Best Local Similarity 68.9%; Pred. No. 3e-42;

Matches 146; Conservative 19; Mismatches 40; Indels 7; Gaps 2;

QY 1 GLLPKSETSLTCAVYGGSGYVWIRQPPGKLEWIGEIN-HSGSTNYPNLSKSRVT 59

Db 10 GLVQPGGSLRLSCAASGFTSTVYMNWVRQAPGKLEWVSGISGGGGTYYADSVKGRFT 69

QY 60 ISVDTKSNQPSLKLSSVTAADTAVVYCARTGTTYYYYYGMVDVWGQGTTVTVSSGSASAP 119

Db 70 ISRDNSMNTLYLQWNSLRABDTAVVYCAKDLNLSLGGGTDFIWGQGTMTVTVSSGSASAP 129

QY 120 TLPPLVSCENSPDTSVAVGCLAQDFLPDXITFSWKYKNSDISSTRGPPSVLRGGKYA 179

Db 130 TLPPLVSCENSPDTSVAVGCLAQDFLPDITFSWKYKNSDISSTRGPPSVLRGGKYA 189

QY 180 ATSQVLLPSKDVNMQGTDEHV-----TGSKE 205

Db 190 ATSQVLLPSKDVNMQGTDEHVCKVQHPNGNKE 221

RESULT 14

ADL69305

ID ADF69305 standard; protein; 266 AA.

XX

AC ADF69305;

XX

DT 26-FEB-2004 (first entry)

XX

DE Human lung specific protein sequence SEQ ID NO:62.

XX

XX human; lung specific nucleic acid; lung specific protein; lung cancer;

XX

XX cytostatic; gene therapy.

XX

XX Homo sapiens.

XX

XX WO2003102137-A2.

XX

XX PD 11-DEC-2003.

XX

XX PF 30-MAY-2003; 2003WO-US016810.

XX

XX PR 31-MAY-2002; 2002US-0385301P.

XX

XX (DIAD-) DIADEXUS INC.

XX

XX PI Chen S, Macina RA, Sun Y, Liu C, Turner LR;

XX

XX WPI; 2004-053457/05.

XX

XX DR New human lung specific nucleic acid, useful for preparing a composition

XX

XX PT for diagnosing or treating lung cancer.

XX

XX Claim 11; SEQ ID NO 62; 221pp; English.

XX

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XX The present invention describes a human lung specific nucleic acid  
 CC molecule. Also described: (1) a method for determining the presence of a  
 CC lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising  
 CC the nucleic acid molecule; (3) a host cell comprising the vector; (4) a  
 CC method for producing a polypeptide encoded by the nucleic acid molecule;  
 CC (5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody  
 CC or its fragment that specifically binds to the polypeptide; (7) a method  
 CC for determining the presence of a lung specific protein in a sample; (8)  
 CC a method for diagnosing and monitoring the presence and metastases of  
 CC lung cancer in a patient; (9) a kit for detecting a risk of cancer or  
 CC presence of cancer in a patient comprising a means for determining the  
 CC presence the nucleic acid molecule or polypeptide in a sample of a  
 CC patient; (10) a method of treating a patient with lung cancer; and (11) a  
 CC vaccine comprising the polypeptide or the nucleic acid encoding the  
 CC polypeptide. Human LSNA molecules and related proteins have cytostatic  
 CC activity, and can be used in gene therapy. They are useful for preparing  
 CC a composition for diagnosing or treating lung cancer. The present  
 CC sequence represents a human lung specific protein, which is used in the  
 CC exemplification of the present invention.

XX SQ Sequence 266 AA;

Query Match 67.0%; Score 725.5; DB 8; Length 266;  
 Best Local Similarity 69.9%; Pred. No. 4.1e-42;  
 Matches 146; Conservative 19; Mismatches 35; Indels 9; Gaps 3;

QY 4 KPSETLSLTCAVYGGSGFYWSWIRQPPGKLEWIGINSGS-TNYNPSLKSRTVTSV 62  
 DB 24 KFGESLKSCKSGSYFTSYWIGWRQMPGKLEWGIYPCGDSITRYSPFGQVTTISA 83  
 QY 63 DTSKNQFSLKLSVTAADTAVVYCARGTTEYYYYYGMVMDVWGQGTTVTVSSGSASAPTLF 122  
 DB 84 DKSISTAYLQWSSLKASDTAMYCARPIAVAGHYF--DYWGQGTTLTVTVSSGSASAPTLF 141  
 QY 123 PLVSCENSPTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVLRGGKYAATS 182  
 DB 142 PLVSCENSPTSSVAVGCLAQDFLPDITFSWKYKNNSDISSTRGFPVLRGGKYAATS 201  
 QY 183 QVLLPSKDVMOGTDEHVV-----TGSKE 205  
 DB 202 QVLLPSKDVMOGTDEHVVCKVQHPNGKE 230

RESULT 15  
 AAY34302  
 ID AAY34302 standard; protein; 199 AA.  
 XX AAY34302;  
 XX  
 DT 19-NOV-1999 (first entry)  
 XX  
 DE Igm antibody CEM 10.12 G5 heavy chain sequence.  
 XX  
 KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO9945031-A2.  
 XX  
 PD 10-SEP-1999.  
 XX  
 PF 03-MAR-1999; 99WO-US004583.  
 XX  
 PR 03-MAR-1998; 98US-00034607.  
 PR 03-FEB-1999; 99US-00244253.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
 XX WPI; 1999-540816/45.  
 DR N-PSDB; AAZ20403.  
 XX  
 PT New monoclonal antibody, used for treating e.g. graft versus host  
 PT disease, cancers, autoimmune diseases and inflammatory diseases.  
 XX  
 PS Claim 60; Fig 27; 245pp; English.  
 XX  
 CC This sequence represents the heavy chain of an antibody of the invention.  
 CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
 CC complement and a variable region that binds to the epitope on CD147 bound  
 CC by the Igm Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
 CC can selectively kill activated T-cells, activated B-cells or reating or  
 CC activated monocytes. The products and methods can be used for treating  
 CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
 CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
 CC renal transplant, ocular lymphomas) and cancers (e.g. cancers of the blood  
 CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)

XX SQ Sequence 199 AA;

Query Match 66.3%; Score 718.5; DB 2; Length 199;  
 Best Local Similarity 70.7%; Pred. No. 9.1e-42;  
 Matches 140; Conservative 24; Mismatches 31; Indels 3; Gaps 2;

QY 4 KPSETLSLTCAVYGGSGFYWSWIRQPPGKLEWIGIN-HSGSTNYNPSLKSRTVTSV 62  
 DB 4 KPGASVKVSKASGTYFTSYDINWRQATGQGLEWGMWGNPNISGTYAQKFGQRTVMT 63  
 QY 63 DTSKNQFSLKLSVTAADTAVVYCARGTTEYYYYYGMVMDVWGQGTTVTVSSGSASAPTLF 122  
 DB 64 NTSISTAYMELSLRSEDATVYICAR--EEMLVRYYGMDVWGQGTTVTVSSGSASAPTLF 121  
 QY 123 PLVSCENSPTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVLRGGKYAATS 182  
 DB 122 PLVSCENSPTSSVAVGCLAQDFLPDITFSWKYKNNSDISSTRGFPVLRGGKYAATS 181  
 QY 183 QVLLPSKDVMOGTDEHVV 200  
 DB 182 QVLLPSKDVMOGTDEHKV 199

Search completed: March 8, 2005, 06:17:04  
 Job time : 98.0436 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 108.788 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-23

Perfect score: 1083

Sequence: 1 GLLKPSFSLTCAVYGSF.....LPKDVMOGTDEHVVTGSKS 205

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	749.5	69.2	627	13	US-10-047-542-47
2	747	69.0	595	15	US-10-108-260A-4112
3	705	65.1	533	15	US-10-104-047-3224
4	650	60.0	229	10	US-09-972-656-82
5	643	59.4	223	10	US-09-972-656-66
6	639.5	59.0	179	15	US-10-309-762-171
7	636.5	58.8	230	10	US-09-972-656-72
8	613.5	56.6	464	15	US-10-292-088-22
9	595.5	55.0	466	15	US-10-292-088-86
10	593.5	54.8	580	14	US-10-310-719-37
11	592.5	54.7	466	15	US-10-292-088-70
12	589	54.4	580	14	US-10-310-719-35
13	586.5	54.2	466	15	US-10-292-088-30

14	583	53.8	221	10	US-09-972-656-80
15	579	53.5	229	9	US-09-974-449-37
16	571.5	52.8	172	14	US-10-153-382-21
17	571	52.7	241	16	US-10-684-109-106
18	568	52.4	241	16	US-10-684-109-71
19	561	51.8	239	16	US-10-684-109-100
20	560	51.7	241	16	US-10-684-109-88
21	554	51.2	118	15	US-10-371-942-90
22	553	51.1	152	9	US-09-187-693-68
23	552	51.0	253	10	US-09-880-748-954
24	552	51.0	253	15	US-10-293-418-954
25	545	50.3	250	14	US-10-194-975-110
26	543.5	50.2	193	15	US-10-264-049-4331
27	543.5	50.2	254	10	US-09-880-748-1659
28	543.5	50.2	254	15	US-10-293-418-1659
29	542	50.0	429	14	US-10-194-801C-6
30	541	50.0	255	10	US-09-880-748-1642
31	541	50.0	255	15	US-10-293-418-1642
32	535.5	49.4	252	10	US-09-880-748-1326
33	535.5	49.4	252	15	US-10-293-418-1326
34	535	49.4	173	15	US-10-309-762-173
35	534.5	49.4	250	10	US-09-880-748-993
36	534.5	49.4	250	10	US-09-880-748-1413
37	534.5	49.4	250	15	US-10-293-418-993
38	534.5	49.4	250	15	US-10-293-418-1413
39	534	49.3	249	10	US-09-880-748-957
40	534	49.3	249	15	US-10-293-418-957
41	534	49.3	447	14	US-10-194-801C-2
42	533.5	49.3	467	14	US-10-211-357-8
43	533.5	49.3	467	14	US-10-211-357-10
44	533.5	49.3	467	14	US-10-211-357-12
45	533	49.2	249	10	US-09-880-748-1321

#### ALIGNMENTS

#### RESULT 1

US-10-047-542-47  
; Sequence 47, Application US/10047542  
; Publication No. US20020168367A1  
; GENERAL INFORMATION:  
; APPLICANT: LARRICK, JAMES W.  
; APPLICANT: WYCOFF, KEITH L.  
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
; TITLE OF INVENTION: AND BACTERIAL DISEASES  
; FILE REFERENCE: 030905.0004.CIP1  
; CURRENT APPLICATION NUMBER: US/10/047,542  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: PCT/US01/13932  
; PRIOR FILING DATE: 2001-04-28  
; PRIOR APPLICATION NUMBER: 60/200,298  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 627  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-047-542-47

Query Match 69.2%; Score 749.5; DB 13; Length 627;  
Best Local Similarity 68.0%; Pred. No. 5e+46;  
Matches 149; Conservative 22; Mismatches 31; Indels 17; Gaps 4;  
QY 4 KPSETLSLTCVYGSFSGYVSWTRQPPGKLEWIGR-INHSGTNTNPSLKSRTISV 62  
Db 32 KFGSSVKVYSCKASGCTFSSYAISWVRQAPGQGLEWGGIPIFGTANYAQKFGQRTVTA 91  
QY 63 DTSKNQPSLKLSSTTAADTAVYVCARG-----TTEYV----YYYGMDVWGQGTIVTVS 112  
Db 92 DESTSTAYMELSSLSRSDTAVYVCARTGILPYSSGWPNSDYIYYGMDVWGQGTIVTVS 151

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QY 113 SGSASAPTLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSV 172
Db 152 SGSASAPTLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSV 211
QY 173 LRGGKYAATSOVLPLSKDVMOGTDHVV-----TGSKE 205
Db 212 LRGGKYAATSOVLPLSKDVMOGTDHVVCKVQHPNGNKE 250

RESULT 2
US-10-108-260A-4112
; Sequence 4112, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4112
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4112

Query Match 69.0%; Score 747; DB 15; Length 595;
Best Local Similarity 70.3%; Pred. No. 7.1e-46;
Matches 149; Conservative 21; Mismatches 34; Indels 8; Gaps 3;

QY 1 GLLKPSETLSLTCAVYGGSFSGYWSWIRQPPGKGLEWIGINHSNSTN-YNPSLKSRTI 59
Db 30 GLVQPGGSLRLSCAASGTFNFAHWIRQAPGKLEIVSTISSNGRQKYGESVKGRFT 89
QY 60 ISVDTSKNQFSLKLSSTAAADTAVYVCARGTTEYYYYYGMVMOGQTTVTVSSGSASAP 119
Db 90 ISRDSSKNTLFLMGSLREDDTAVYVCARGHS-IDNYHYGVDVMOGQTTVTVSSGSASAP 148
QY 120 TLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSVLRGGKYA 179
Db 149 TLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSVLRGGKYA 208
QY 180 ATSOVLPLSKDVMOGTDHVV-----TGSKE 205
Db 209 ATSOVLPLSKDVMOGTDHVVCKVQHPNGNKE 240

RESULT 3
US-10-104-047-3224
; Sequence 3224, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3224
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3224

Query Match 65.1%; Score 705; DB 15; Length 533;
Best Local Similarity 67.9%; Pred. No. 6.8e-43;
Matches 144; Conservative 16; Mismatches 44; Indels 8; Gaps 3;

QY 1 GLLKPSETLSLTCAVYGGSFSGYWSWIRQPPGKGLEWIGINHSNSTNYPNPSLKSRTI 60
```

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Db 29 GLVQPGGSLRLSCAASGTFNFAHWIRQAPGKLEIVSTISSNGRQKYGESVKGRFTV 88
QY 61 SVDTSKNQFSLKLSSTAAADTAVYVCARGTTEYY-YYYYYGMVMOGQTTVTVSSGSASAP 119
Db 89 SRDGSQNTLYLESSLRPDDTAVYVCVRDHRNYADTSPYGRK-WGQGTTLVTVSSGSASAP 147
QY 120 TLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSVLRGGKYA 179
Db 148 TLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSVLRGGKYA 207
QY 180 ATSOVLPLSKDVMOGTDHVV-----TGSKE 205
Db 208 ATSOVLPLSKDVMOGTDHVVCKVQHPNGNKE 239

RESULT 4
US-09-972-656-82
; Sequence 82, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-82

Query Match 60.0%; Score 650; DB 10; Length 229;
Best Local Similarity 64.2%; Pred. No. 2.7e-39;
Matches 131; Conservative 20; Mismatches 43; Indels 10; Gaps 5;

QY 1 GLLKPSETLSLTCAVYGGSFSGYWSWIRQPPGKLEWIGINHSNSTNYPNPSLKSRTI 60
Db 10 GLLKPSETLSLTCAVYGGSFSGYWSWIRQPPGKLEWIGINHSNSTNYPNPSLKSRTI 69
QY 61 SVDTSKNQFSLKLSSTAAADTAVYVCARGTTEYYYYYGMVMOGQTTVTVSSGSASAP 116
Db 70 SVDTSKNQFSLKLSSTAAADTAVYVCARGTTEYYYYYGMVMOGQTTVTVSSAST 129
QY 117 SAPTLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSVLR-G 175
Db 130 KGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSS 186
QY 176 KYAATSOVLPLSKDVMOGTDHVV 199
Db 187 GLYSLSSVTVTPSSSL--GTQTYI 208

RESULT 5
US-09-972-656-66
; Sequence 66, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 223
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```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-66

Query Match      59.4%; Score 643; DB 10; Length 223;
Best Local Similarity 64.5%; Pred. No. 8.4e-39;
Matches 129; Conservative 21; Mismatches 42; Indels 8; Gaps 5;

QY 1 GLLKPSETLSLTCVAVGSGFSGYYSWIRQPPGKGLEWIGEHSGSTNPNPGLKSRVTI 60
Db 10 GLLKPSETLSLTCVAVGSGFSGYYSWIRQPPGKGLEWIGEHSGSTNPNPGLKSRVTI 69

QY 61 SVDTSKNQFSLKLSSTVTAADTAIVYTCARGTTTEYYYYYGMVDMVGQGTTVTVSSGSASAPT 120
Db 70 SVDTSKNQFSLKLSSTVTAADTAIVYTCARGTARNRSP--DYWGQGTTLTVTVSSASTKGPS 127

QY 121 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSPVL 179
Db 128 VPPLAPSSKSTSG-GTAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPVAVLQSSGLYS 184

QY 180 ATSOVLLPSKVMQGTDEHV 199
Db 185 LSSVTVTPSSSL--GTQTYI 202

RESULT 6
US-10-309-762-171
; Sequence 171, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY CARBOXIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 171
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-171

Query Match      59.0%; Score 639.5; DB 15; Length 179;
Best Local Similarity 69.3%; Pred. No. 1.2e-38;
Matches 122; Conservative 19; Mismatches 30; Indels 5; Gaps 3;

QY 1 GLLKPSETLSLTCVAVGSGFSGYYSWIRQPPGKGLEWIGEHSGSTNPNPGLKSRVTI 60
Db 4 GLVKPSETLSLTCTVSGGSISSYIWIWIRQPPGKGLEWIGIYIYSGSTNPNPGLKSRVTI 63

QY 61 SVDTSKNQFSLKLSSTVTAADTAIVYTCARG--TTEYYYYYGMVDMVGQGTTVTVSSGSASA 118
Db 64 SVDTSKNQFSLKLSSTVTAADTAIVYTCARDQHSVVYIYGMVDMVGQGTTVTVSSASTKG 123

QY 119 PTLPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSPVL 174
Db 124 PSVFPAPCSRSTSE--STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPVAVLIQ 176

RESULT 7
US-09-972-656-72
; Sequence 72, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
```

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; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-72
```

```
Query Match      58.8%; Score 636.5; DB 10; Length 230;
Best Local Similarity 62.9%; Pred. No. 2.6e-38;
Matches 129; Conservative 20; Mismatches 45; Indels 11; Gaps 5;

QY 1 GLLKPSETLSLTCVAVGSGFSGYYSWIRQPPGKGLEWIGEHSGSTNPNPGLKSRVTI 60
Db 10 GLLKPSETLSLTCVAVGSGFSGYYSWIRQPPGKGLEWIGEHSGSTNPNPGLKSRVTI 69

QY 61 SVDTSKNQFSLKLSSTVTAADTAIVYTCARGTTTEYYYYY----YGMVDMVGQGTTVTVSSGS 115
Db 70 SVDTSKNQFSLKLSSTVTAADTAIVYTCARDKGSRIITFGVVGSGAGFDYMGQGTTLTVTVSSAS 129

QY 116 ASPTLPPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSPVL 174
Db 130 TKGPSVFPPLAPSSKSTSG-GTAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPVAVLOS 186

QY 175 GKVAATSOVLLPSKVMQGTDEHV 199
Db 187 SGLYSLSSVTVTPSSSL--GTQTYI 209
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```
RESULT 8
US-10-292-088-22
; Sequence 22, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-22
```

```
Query Match      56.6%; Score 613.5; DB 15; Length 464;
Best Local Similarity 63.9%; Pred. No. 2.3e-36;
Matches 122; Conservative 22; Mismatches 40; Indels 7; Gaps 4;

QY 1 GLLKPSETLSLTCVAVGSGFSGYYSWIRQPPGKGLEWIGEHSGSTNPNPGLKSRVTI 60
Db 29 GLVKPSETLSLTCTVSGGSISSYIWIWIRQPPGKGLEWIGRVTYTSSTNPNPGLKSRVTM 88

QY 61 SVDTSKNQFSLKLSSTVTAADTAIVYTCARGTTTEYYYYYGMVDMVGQGTTVTVSSGSASAPT 120
Db 89 SVDTSKNQFSLKLSSTVTAADTAIVYTCAR--DGLYRGYGMVDMVGQGTTVTVSSASTKGPS 145

QY 121 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSPVL 179
Db 146 VFPLAPCSRSTSE--STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPVAVLQSSGLYS 202
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```
; OTHER INFORMATION: IL-2 variant
US-10-310-719-37

Query Match      54.8%; Score 593.5; DB 14; Length 580;
Best Local Similarity 62.7%; Pred. No. 8.1e-35;
Matches 121; Conservative 20; Mismatches 41; Indels 11; Gaps 5;

Qy 1 GLLKPSETLSLTCAYVGGSP-SGYVSWIRQPPGKGLEWIGEINHSGSTNPNPSLKSRVT 59
Db 10 GLVAPSETLSLTCAYVGGSYSSGYVWIRQPPGKGLEWIGSIYHSGSTNPNPSLKSRVT 69
Qy 60 ISVDTSKNQFSLKLSVTAADTAVVYCARGTEYYYYYGMVWGQGTVTTVSSGSASAP 119
Db 70 ISVDTSKNQFSLKLSVTAADTAVVYCARGKWSKF-----DYWGQGTTLTVSSASTKGP 123
Qy 120 TLFPLVSCNSPDTSSVAVGCLAQDFLPDXITFSWKYKNSDLSSTRGFPVLR-GGKY 178
Db 124 SVFPLAPCSRSTSE-STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLY 180
Qy 179 AATSOVLLPSKD 191
Db 181 LSSVTVTPSSN 193

RESULT 11
US-10-292-088-70
; Sequence 70, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-86

Query Match      55.0%; Score 595.5; DB 15; Length 466;
Best Local Similarity 63.4%; Pred. No. 4.7e-35;
Matches 121; Conservative 21; Mismatches 44; Indels 5; Gaps 4;

Qy 1 GLLKPSETLSLTCAYVGGSPGYVSWIRQPPGKGLEWIGEINHSGSTNPNPSLKSRVTI 60
Db 29 GLVAPSETLSLTCVSGSIRGYVSWIRQPPGKGLEWIGIYIYSGSTNPNPSLKSRVTI 88
Qy 61 SVDTSKNQFSLKLSVTAADTAVVYCARGTEYYYYYGMVWGQGTVTTVSSGSASAPT 120
Db 89 SVDTSKNQFSLKLSVTAADTAVVYCARRGGLYGDYGW-FAPWGQGTTLTVSSASTKGPS 147
Qy 121 LFPVLVSCNSPDTSSVAVGCLAQDFLPDXITFSWKYKNSDLSSTRGFPVLR-GGKYA 179
Db 148 VFPLAPCSRSTSE-STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLYS 204
Qy 180 ATSOVLLPSKD 190
Db 205 LSSVTVTPSSN 215

RESULT 10
US-10-310-719-37
; Sequence 37, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-NHS76 (gamma4h) (FN>AQ) -ala-IL2 (D20T) heavy chain fused to
```

```
; OTHER INFORMATION: IL-2 variant
US-10-310-719-37

Query Match      54.8%; Score 593.5; DB 14; Length 580;
Best Local Similarity 62.7%; Pred. No. 8.1e-35;
Matches 121; Conservative 20; Mismatches 41; Indels 11; Gaps 5;

Qy 1 GLLKPSETLSLTCAYVGGSP-SGYVSWIRQPPGKGLEWIGEINHSGSTNPNPSLKSRVT 59
Db 10 GLVAPSETLSLTCAYVGGSYSSGYVWIRQPPGKGLEWIGSIYHSGSTNPNPSLKSRVT 69
Qy 60 ISVDTSKNQFSLKLSVTAADTAVVYCARGTEYYYYYGMVWGQGTVTTVSSGSASAP 119
Db 70 ISVDTSKNQFSLKLSVTAADTAVVYCARGKWSKF-----DYWGQGTTLTVSSASTKGP 123
Qy 120 TLFPLVSCNSPDTSSVAVGCLAQDFLPDXITFSWKYKNSDLSSTRGFPVLR-GGKY 178
Db 124 SVFPLAPCSRSTSE-STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLY 180
Qy 179 AATSOVLLPSKD 191
Db 181 LSSVTVTPSSN 193

RESULT 11
US-10-292-088-70
; Sequence 70, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-70

Query Match      54.7%; Score 592.5; DB 15; Length 466;
Best Local Similarity 62.8%; Pred. No. 7.7e-35;
Matches 120; Conservative 22; Mismatches 44; Indels 5; Gaps 4;

Qy 1 GLLKPSETLSLTCAYVGGSPGYVSWIRQPPGKGLEWIGEINHSGSTNPNPSLKSRVTI 60
Db 29 GLVAPSETLSLTCVSGSIRGYVSWIRQPPGKGLEWIGIYIYSGSTNPNPSLKSRVTI 88
Qy 61 SVDTSKNQFSLKLSVTAADTAVVYCARGTEYYYYYGMVWGQGTVTTVSSGSASAPT 120
Db 89 SVDTSKNQFSLKLSVTAADTAVVYCARGKGLYGDYGW-FAPWGQGTTLTVSSASTKGPS 147
Qy 121 LFPVLVSCNSPDTSSVAVGCLAQDFLPDXITFSWKYKNSDLSSTRGFPVLR-GGKYA 179
Db 148 VFPLAPCSRSTSE-STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLYS 204
Qy 180 ATSOVLLPSKD 190
Db 205 LSSVTVTPSSN 215

RESULT 12
US-10-310-719-35
; Sequence 35, Application US/10310719
; Publication No. US20030166163A1
```



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; SEQ ID NO 37
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-449-37

Query Match      53.5%; Score 579; DB 9; Length 229;
Best Local Similarity 59.3%; Pred. No. 3.6e-34;
Matches 121; Conservative 26; Mismatches 47; Indels 10; Gaps 6;

Qy 1 GLLKPSETLSLTCAVYGGSF--GYVSWIRQPPGKGLEWIGETINHSNSTYNPSPSKSRV 58
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 10 GLVKPSETLSLTCTVSGGSISSGGYTWIRQPPGKGLEWIGYIYSGSTSYNPSPSKSRV 69
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 59 TISVDTSKNQPSLKLSSVTAADTAVYCA--RGTEVYVYVYVYVYVYVYVYVYVYVYV 116
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 70 TMSVDTSKNQPSLRLTSVTAADTAVYCARERGETGLYPYVYIDVWGTGTVTVSSAST 129
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 117 SAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDXITFWSKYKNNSDISSTRGFPSVLR-G 175
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KGPSVFFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTFPAVLQSS 186
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 176 GKAAATSOVLLPSKDVNQGTDEHV 199
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 187 GLYSLSSVVTVPSSSL--GTQTYI 208
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Search completed: March 8, 2005, 07:05:47  
Job time : 109.788 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 22.5411 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-23

Perfect score: 1083

Sequence: 1 GLLRPSELTSLTCAVGGSF.....LPKDVMOGTDEHVTGSK 205

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	652.5	60.2	472	3	US-08-793-450-8
2	598	55.2	473	3	US-09-049-672A-4
3	571.5	52.8	172	4	US-09-472-087-7
4	571.5	52.8	172	4	US-09-472-087-86
5	556	51.3	832	3	US-08-630-820-7
6	556	51.3	832	4	US-09-273-453-7
7	542	50.0	429	4	US-09-372-425A-6
8	534	49.3	447	4	US-09-372-425A-2
9	533.5	49.3	467	3	US-08-523-894-8
10	533.5	49.3	467	3	US-08-523-894-10
11	533.5	49.3	467	3	US-08-523-894-12
12	527.5	48.7	123	3	US-08-793-450-4
13	526.5	48.6	487	4	US-09-800-729-145
14	525.5	48.5	476	3	US-08-487-550-12
15	525.5	48.5	476	4	US-09-526-098-12
16	525.5	48.5	476	4	US-09-383-916-12
17	517.5	47.8	476	3	US-08-487-550-4
18	517.5	47.8	476	4	US-09-526-098-4
19	517.5	47.8	476	4	US-09-383-916-4
20	517	47.7	139	4	US-09-203-768A-2
21	512.5	47.3	219	3	US-09-460-384-37
22	497	45.9	122	1	US-08-360-125-11
23	497	45.9	122	2	US-08-450-578-11
24	497	45.9	122	2	US-09-017-628-11
25	497	45.9	122	2	US-09-014-880-11
26	497	45.9	122	2	US-08-450-363-11
27	497	45.9	122	4	US-09-467-903-11

28	491	45.3	467	4	US-08-030-175-42	Sequence 42, Appl
29	488	45.1	467	4	US-08-030-175-41	Sequence 41, Appl
30	486.5	44.9	229	2	US-08-887-352B-20	Sequence 20, Appl
31	486.5	44.9	229	3	US-09-109-207C-20	Sequence 20, Appl
32	486.5	44.9	229	3	US-09-296-005-20	Sequence 20, Appl
33	486.5	44.9	229	4	US-09-920-171-20	Sequence 20, Appl
34	486.5	44.9	229	4	US-09-716-028-20	Sequence 20, Appl
35	486.5	44.9	229	4	US-10-113-996-20	Sequence 20, Appl
36	486.5	44.9	233	2	US-08-887-352B-25	Sequence 25, Appl
37	486.5	44.9	233	3	US-09-109-207C-25	Sequence 25, Appl
38	486.5	44.9	233	3	US-09-296-005-25	Sequence 25, Appl
39	486.5	44.9	233	4	US-09-920-171-25	Sequence 25, Appl
40	486.5	44.9	233	4	US-09-716-028-25	Sequence 25, Appl
41	486.5	44.9	233	4	US-10-113-996-25	Sequence 25, Appl
42	486.5	44.9	451	2	US-08-887-352B-14	Sequence 14, Appl
43	486.5	44.9	451	2	US-08-887-352B-16	Sequence 16, Appl
44	486.5	44.9	451	3	US-08-466-151-65	Sequence 65, Appl
45	486.5	44.9	451	3	US-09-109-207C-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-08-793-450-8  
; Sequence 8, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHABRIHI, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/793,450  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 472 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-793-450-8

Query Match 60.2%; Score 652.5; DB 3; Length 472;  
Best Local Similarity 64.9%; Pred. No. 1.9e-51;  
Matches 131; Conservative 22; Mismatches 40; Indels 9; Gaps 6;

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QY 1 GLLKPSETLSLTCVAVYGGFSGYWWSWIRQPPKGLEWIGEHSGSTNYPNPSLKSRVTI 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 29 GLLKPSETLSLTCVYGGFSGYWWSWIRQPPKGLEWIGEHSGSTNYPNPSLKSRVTI 88
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SVDTSKNQFSLKLSSVTAADTAVVYCARGTTEYYYYY--MDVMGQGTTVTVSSGSASA 118
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 SVDTSKNQFSLKLSSVTAADTAVVYCAR-APEYKWKYHGDWFDPMGQGTTVTVSSASTKG 147
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 PTLFPLVSCENSPSDTSSVAVGCLAQDFLPDXITFWSWKYKNNSDISSTRGPPSVLR-CGK 177
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 148 PSVFPPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGL 204
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 178 YAATSOVLLPSKDVMOGTDEHV 199
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 YLSVSVTVTPSSSL--GTQTYI 224
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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## RESULT 2

```
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
```

## GENERAL INFORMATION:

```
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
```

```
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
```

```
; NUMBER OF SEQUENCES: 28
```

```
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESS: Incyte Pharmaceuticals, Inc.
```

```
; STREET: 3174 Porter Drive
```

```
; CITY: Palo Alto
```

```
; STATE: CA
```

```
; COUNTRY: USA
```

```
; ZIP: 94304
```

```
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
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; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
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```
; SOFTWARE: FastSeq for Windows Version 2.0
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```
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/09/049,672A
```

```
; FILING DATE: HEREWITH
```

```
; CLASSIFICATION: 536
```

```
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
```

```
; FILING DATE:
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Cerrone, Michael C
```

```
; REGISTRATION NUMBER: 39,132
```

```
; REFERENCE/DOCKET NUMBER: PF-0497 US
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: 650-855-0555
```

```
; TELEFAX: 650-845-4166
```

```
; TELEX:
```

```
; INFORMATION FOR SEQ ID NO: 4:
```

```
; SEQUENCE CHARACTERISTICS:
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```
; LENGTH: 473 amino acids
```

```
; TYPE: amino acid
```

```
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
```

```
; IMMEDIATE SOURCE:
```

```
; LIBRARY: PANCUT01
```

```
; CLONE: 1513264
```

```
US-09-049-672A-4
```

```
Query Match
```

```
Best Local Similarity 55.2%; Score 598; DB 3; Length 473;
```

```
Pred. No. 1.8e-46;
```

```
Matches 124; Conservative 22; Mismatches 48; Indels 8; Gaps 5;
QY 1 GLLKPSETLSLTCVAVYGGFS--GYWWSWIRQPPKGLEWIGEHSGSTNYPNPSLKSRV 58
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 29 GLVPRSETLSLTCVAVYGGFSITSGGYWWSWIRQPPKGLEWIGIYYISGSTLYNPSLKSRV 88
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 TISVDTSKNQFSLKLSSVTAADTAVVYCARGTTEYYYYY--MDVMGQGTTVTVSSGSASA 118
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 TISVDTSKNQFSLKLSSVTAADTAVVYCARDDVGLRGNGYGMVDMGQGTLLTVSSASTKG 148
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 PTLFPLVSCENSPSDTSSVAVGCLAQDFLPDXITFWSWKYKNNSDISSTRGPPSVLR-CGK 177
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 149 PSVFPPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGL 205
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 178 YAATSOVLLPSKDVMOGTDEHV 199
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 206 YLSVSVTVTPSSSL--GTQTYI 225
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

## RESULT 3

```
US-09-472-087-7
```

```
; Sequence 7, Application US/09472087
```

```
; Patent No. 6682736
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: HANSON, DOUGLAS C.
```

```
; APPLICANT: NEVEU, MARK J.
```

```
; APPLICANT: MUELLER, EILLEN E.
```

```
; APPLICANT: HANKE, JEFFREY H.
```

```
; APPLICANT: GILMAN, STEVEN C.
```

```
; APPLICANT: DAVIS, C. GEOFFREY
```

```
; APPLICANT: CORVALAN, JOSE R.
```

```
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
```

```
; FILE REFERENCE: AEX-PF1
```

```
; CURRENT APPLICATION NUMBER: US/09/472,087
```

```
; CURRENT FILING DATE: 1999-12-23
```

```
; PRIOR APPLICATION NUMBER: 60/113,647
```

```
; PRIOR FILING DATE: 1998-12-23
```

```
; NUMBER OF SEQ ID NOS: 147
```

```
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 7
```

```
; LENGTH: 172
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
```

```
US-09-472-087-7
```

```
Query Match 52.8%; Score 571.5; DB 4; Length 172;
```

```
Best Local Similarity 64.2%; Pred. No. 1.2e-44;
```

```
Matches 113; Conservative 22; Mismatches 32; Indels 9; Gaps 4;
```

```
QY 1 GLLKPSETLSLTCVAVYGGFS--GYWWSWIRQPPKGLEWIGEHSGSTNYPNPSLKSRV 58
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 GLVPRQILSLTCTVSGSISGGHYWWSWIRQHPKGLEWIGIYYIGNTYINPSLKSRV 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 TISVDTSKNQFSLKLSSVTAADTAVVYCARGTTEYYYYY--MDVMGQGTTVTVSSGSASA 118
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 TISVDTSKNQFSLKLSSVTAADTAVVYCARDSG----YYGIDVMGQGTTVTVSSASTKG 119
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 PTLFPLVSCENSPSDTSSVAVGCLAQDFLPDXITFWSWKYKNNSDISSTRGPPSVLR 174
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 PSVFPPLAPCSRSTSE-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLIQ 172
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

## RESULT 4

```
US-09-472-087-86
```

```
; Sequence 86, Application US/09472087
```

```
; Patent No. 6682736
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: HANSON, DOUGLAS C.
```

```
; APPLICANT: NEVEU, MARK J.
```

```
; APPLICANT: MUELLER, EILLEN E.
```

```
; APPLICANT: HANKE, JEFFREY H.
```

```
; APPLICANT: GILMAN, STEVEN C.
```

```
; APPLICANT: DAVIS, C. GEOFFREY
```



APPLICANT: CORVALAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PF1  
CURRENT APPLICATION NUMBER: US/09/472,087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 86  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-472-087-86

Query Match 52.8%; Score 571.5; DB 4; Length 172;  
Best Local Similarity 64.2%; Pred. No. 1.2e-44;  
Matches 113; Conservative 22; Mismatches 32; Indels 9; Gaps 4;  
QY 1 GLLKPSETLSLTCAVYGGFS--GYVWSWIRPPGKLEWIGEIHNHSGSTNPNLSKSRV 58  
DB 4 GLVKPSQLSLCTVSGSGSISSGHHWSWIRHPKGLEWIGYIYIGNTYNPNLSKSRV 63  
QY 59 TISVDTSKNQFSLKSSVTAADTAVVYCARGTEYYYYYGMVWGQGTTVTVSSGSASA 118  
DB 64 TISVDTSKNQFSLKSSVTAADTAVVYCARGSD----YYGIDVWGQGTTVTVSSASTKG 119  
QY 119 PTLFPLVCENSPDTSVAVGCLAQDFLPDXITFSWKYKKNNSDISSTRGPPSVLR 174  
DB 120 PSVFFPLAPCSRSTSE--STNALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPVAVLQ 172

RESULT 5  
US-08-630-820-7  
Sequence 7, Application US/08630820  
Patent No. 6008023  
GENERAL INFORMATION:  
APPLICANT: OPPER, Martin  
APPLICANT: BOSSLET, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 7;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 832 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-820-7  
Query Match 51.3%; Score 556; DB 3; Length 832;  
Best Local Similarity 55.9%; Pred. No. 2.6e-42;  
Matches 113; Conservative 32; Mismatches 45; Indels 12; Gaps 7;  
QY 1 GLLKPSETLSLTCAVYGGSF--SGYYWSWIRPPGKLEWIGEIHNHSGSTNPNLSKSRV 59  
DB 11 GLVRSQTLSTCTVSGFTISSGYSHWVRPPGKLEWIGYIOYSGITNPNLSKSRV 70  
QY 60 ISVDTSKNQFSLKSSVTAADTAVVYCARGTEYYYYYGMVWGQGT--TVTVSSGSAS 117  
DB 71 MLVDTSKNQFSLKSSVTAADTAVVYCAREDDYVHWYF---DVMQGSILTVTVSSASTK 127  
QY 118 APTLFPLVCENSPDTSVAVGCLAQDFLPDXITFSWKYKKNNSDISSTRGPPSVLR-GG 176  
DB 128 GPSVFFPLAPCSRSTSG--GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPVAVLQSSG 184  
QY 177 KYAATSOVLLPSKDVMOGTDEH 198  
DB 185 LYSLSVTVTFSSSL--GTQTY 204  
RESULT 6  
US-09-273-453-7  
Sequence 7, Application US/09273453  
Patent No. 6602688  
GENERAL INFORMATION:  
APPLICANT: OPPER, Martin  
APPLICANT: BOSSLET, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/273,453  
FILING DATE: 22-Mar-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,820  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 7;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 832 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7;  
US-09-273-453-7

Query Match	51.3%;	Score	556;	DB	4;	Length	932;
Best Local Similarity	55.9%;	Pred. No.	2.6e-42;				
Matches	113;	Conservative	32;	Mismatches	45;	Indels	12;
Gaps	7;						

  

QY	1	GLLKPSFTLSLTCATVYGGSF--SGYYMSWIROPCKGLEWIGEINHSGSTNNPSLKSRVT	59
DB	11	GLVRPSQTLSLTCVTSGFTISSGYSMSHWVRQPPCKGLEWIGYIQYSGITNNPSLKSRVT	70
QY	60	ISVDTSKNQPSLKLSSVTAADTAIVYCARGTTEYYYYGMDVWGQGT--TVTVSSSGAS	117
DB	71	MLVDTSKNQPSLRLSSVTAADTAIVYCAREDYDHYTF--DVRGQGSVLTVTVSSASTK	127
QY	118	APTLFPLVLCENSPSDTSSVAVGCLAODFLPDXITTFSKYKKNSDISSTRGFPSVLR--GG	176
DB	128	GPSVFPLAPCSRSTSG--GTAALGCLVKDYFPEPVTWSW--NSGALTSGVHTFPAVLQSSG	184
QY	177	KYAATSQVLLPFSKDVWGQTDDEH	198
DB	185	LYSLSSVTVFPSSSL--GTOTY	204

## RESULT 7

```

US-09-372-425A-6
; Sequence 6, Application US/09372425A
; Patent No. 6475749
; GENERAL INFORMATION:
; APPLICANT: Sherie L. Morrison
; APPLICANT: Ramon Montano
; TITLE OF INVENTION: Improved Rh Antibody
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,425A
; FILING DATE: August 11, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenakmp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 510015-223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Heavy chain without Tailpiece - AA
US-09-372-425A-6

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Query Match 50.0%; Score 542; DB 4; Length 429;  
Best Local Similarity 57.1%; Pred. No. 2.1e-41;  
Matches 120; Conservative 11; Mismatches 35; Indels 44; Gaps 6;

Qy	61	SVDTSKNQP	SVLKLSSVTAADTA	NYCYCAR	-----GTEYV	--YYVGMVDWGCGT	TTTV	111
Db	89	SVDTSKNQP	SVKLTSTVTAADTA	NYCYCAR	SHRCHTSISCF	YLYGLGYIYIMD	WGKGT	148
Qy	112	SS	-----	GSASATLP	PLV	---SCENSP	-----	STSSVA 138
Db	149	SSELKTL	PGDTHTTC	PCBP	KSCDTPPC	PCRP	EPKSCDTPPC	208
Qy	139	VGCLAQD	FL--	PKXIT	PSWKYK	NSDISST	166	
Db	209	PRCPAP	ELLGGPSV	FLFP	PKPKD	TLMI	SRT 238	

## RESULT 8

US-09-372-425A-2  
 ; Sequence 2, Application US/09372425A  
 ; Patent No. 6475749  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sherie L. Morrison  
 ; APPLICANT: Ramon Montano  
 ; TITLE OF INVENTION: Improved Rh Antibody  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSES: Oppenheimer Wolff & Donnelly LLP  
 ; STREET: 2029 Century Park East, Suite 3800  
 ; CITY: Los Angeles  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 90067  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: Windows 98  
 ; SOFTWARE: MS Word  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/372,425A  
 ; FILING DATE: August 11, 1999  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Oldenakmp, David J.  
 ; REGISTRATION NUMBER: 29,421  
 ; REFERENCE/DOCKET NUMBER: 510015-223  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (310) 788-5000  
 ; TELEFAX: (310) 788-5100  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 447 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Heavy chain with Tailpiece - A  
 ; US-09-372-425A-2

	Query Match	49.3%;	Score 534;	DB 4;	Length 447;	
	Best Local Similarity	56.7%;	Pred. No. 1.2e-40;			
	Matches 119;	Conservative 11;	Mismatches 36;	Indels 44;	Gaps 6	
<hr/>						
Qy	1	GLLKPSSTLSITCAVYGGSPGYWMSWIROPKGGLEIWGEINHSNSTYNPPLSKSRVTI	60			
Db	29	GLLKPSSTLSITCAVYGGSPGSHWSWIROPKGGLEIWGEIDHSESNSTYNPPLSKSRVTI	88			
Qy	61	SVDTSKNQFSILKLSSVTAADTAVYYCAR-----GTTEYY--YYYYGMVDWGQGTTTVT	111			
		:				
Db	89	SVDTSKNQFSPVKLTSVTAADTAVYYCARSRHCTSI SCFYLYGIYYYYMDVGKGTTTVT	148			
		:				
Qy	112	SS-----GSASAPTLFPLV-----SCENSP-----SDTSSVA	138			
		:				
Db	149	SSELKPLGDTHTCRCPPBPKS CDTPPCPRCPPEPKSCDTPPCPRCPPEKSCDTPPC	208			



```
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22314-3187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/523,894
/ FILING DATE: 06-SEP-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Teskin, Robin L.
/ REGISTRATION NUMBER: 35,030
/ REFERENCE/DOCKET NUMBER: 012712-165
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-836-6620
/ TELEFAX: 703-836-2021
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 467 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-523-894-12

Query Match 49.3%; Score 533.5; DB 3; Length 467;
Best Local Similarity 56.7%; Pred. No. 1.4e-40;
Matches 110; Conservative 27; Mismatches 48; Indels 9; Gaps 6;

Qy 1 GLLKPSETLSLTCVAVGSGFSQ-YVWSWIRPPGKLEWIGIINHS-GSTNPNPSLKSRV 58
Db 29 GLVKPSETLSLTCVSGSGISGDYWFWRQSPGKLEWIGIYVSGGGTNYNPSLNRRV 88

Qy 59 TISVDTSKNQPSLKLSSVTAADTAVYVCARGTTEYYYYYGVMDVWGQGTTVTVSSGASA 118
Db 89 SISIDTSKNFLSLKLSRVTAADTAVYVCASNILKYLHW---LLYWGQGLVTVSSASTKG 145

Qy 119 PTLPLVSCNSPDTSSVAVGCLAQDFLPXITPFSWKYKNNSDISSTRGPPSVLR-CGK 177
Db 146 PSVFFLPACSRSTSS-STAALGCLVKDYFPPEVTVVSW--NSGALTSGVHTTFAVLQSSGL 202

Qy 178 YAATSOVLPLSKDV 191
Db 203 YLSLSSVTVTPSSSL 216

RESULT 12
US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: P.C.
; ADDRESSSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/793,450
/ FILING DATE: 03-MAR-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 94/10566
/ FILING DATE: 02-SEP-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OBLON, NORMAN F.
/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 660-118-0 PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-413-3000
/ TELEFAX: 703-413-2220
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 123 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-793-450-4

Query Match 48.7%; Score 527.5; DB 3; Length 123;
Best Local Similarity 88.7%; Pred. No. 8.2e-41;
Matches 102; Conservative 3; Mismatches 7; Indels 3; Gaps 2;

Qy 1 GLLKPSETLSLTCVAVGSGFSGYWMIROPPGKLEWIGIINHSNSTNPNPSLKSRVTI 60
Db 10 GLLKPSETLSLTCVYGGSGFYWMIROPPGKLEWIGIINHSNSTNPNPSLKSRVTI 69

Qy 61 SVDTSKNQPSLKLSSVTAADTAVYVCARGTTEYYYYYGVMDVWGQGTTVTVSS 113
Db 70 SVDTSKNQPSLKLSSVTAADTAVYVCAR-APEYKWKYHGDWDFPWGQGTTVTVSS 123

RESULT 13
US-09-800-729-145
; Sequence 145, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-145

Query Match 48.6%; Score 526.5; DB 4; Length 487;
Best Local Similarity 56.2%; Pred. No. 6.4e-40;
Matches 114; Conservative 25; Mismatches 51; Indels 13; Gaps 8;

Qy 1 GLLKPSETLSLTCVAVGSGFS--GYWWSWIRPPGKLEWIGIINHSNSTNPNPSLKSRV 58
Db 29 GLVKPSETLSLTCVYGGSGISGGHGYWWSWIRPPGKLEWIGIYVSGGYVYVNPSPKSRV 88

Qy 59 TISVDTSKNQPSLKLSSVTAADTAVYCA---RGTE-YYYYYGVMDVWGQGTTVTVSSG 114
Db 89 TISVDTSONQPSLRLSSVTAADTAVYCAKDHRATRDGYQLEYRGDFYWGQGIILTVSSA 148

Qy 115 SASAPTLFPLVSCNSPDTSSVAVGCLAQDFLP-DXITFESWKYKNNSDISSTRGFP--S 171
Db 149 SPTSPKVPFL--SLDSTPOD--GNVVVAVCLVQGFPPQEPUSVTVWSESGQN--VTARNFPFSQ 204
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QY 172 VLGGKYAATSOVLPLPSKDVMOG 194  
DB 205 DASGLYTTSQLTUPATQCPDG 227

## RESULT 14

US-08-487-550-12

; Sequence 12, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER &amp; MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-487-550-12

Query Match

Best Local Similarity 48.5%; Score 525.5; DB 3; Length 476;

Matches 113; Conservative 27; Mismatches 51; Indels 17; Gaps 8;

QY 1 GLKPSETLSLTCAVYGGSFS-GYVWSWIRQPPGKLEWIGEI-NHSGSTNYPNLSKSRV 58

DB 29 GLVKESETLSLTCAVVGSGISGGYWGWIQPPGKLEWIGSFYSSGNTNYPNLSKSOV 88

QY 59 TISVDTSKNQFSLKLSVTAADTAVYVCARGTTEYYYYYGM-----DVMGGGTTVTVS 112

DB 89 TISTDTSKNQFSLKLSNMTAADTAVYVCV---DRLFSVVGWVYNNWFDVWPGVLVTVS 145

QY 113 SGSASAPTLFPLVSCNPSDTSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVS 172

DB 146 SASTKGPSVFPLAPSSKSTSG-GTAAAGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAV 202

QY 173 LR-GGKYAATSOVLPLPSKDVMOGTDH 199

DB 203 LOSSGLYSLSSVTVVPSSSL--GTQTYI 228

## RESULT 15

US-09-526-098-12

; Sequence 12, Application US/09526098

; Patent No. 6492134

; GENERAL INFORMATION:

;

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER &amp; MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/526,098

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-526-098-12

Query Match

Best Local Similarity 48.5%; Score 525.5; DB 4; Length 476;

Matches 113; Conservative 27; Mismatches 51; Indels 17; Gaps 8;

QY 1 GLKPSETLSLTCAVYGGSFS-GYVWSWIRQPPGKLEWIGEI-NHSGSTNYPNLSKSRV 58

DB 29 GLVKESETLSLTCAVVGSGISGGYWGWIQPPGKLEWIGSFYSSGNTNYPNLSKSOV 88

QY 59 TISVDTSKNQFSLKLSVTAADTAVYVCARGTTEYYYYYGM-----DVMGGGTTVTVS 112

DB 89 TISTDTSKNQFSLKLSNMTAADTAVYVCV---DRLFSVVGWVYNNWFDVWPGVLVTVS 145

QY 113 SGSASAPTLFPLVSCNPSDTSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVS 172

DB 146 SASTKGPSVFPLAPSSKSTSG-GTAAAGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAV 202

QY 173 LR-GGKYAATSOVLPLPSKDVMOGTDH 199

DB 203 LOSSGLYSLSSVTVVPSSSL--GTQTYI 228

Search completed: March 8, 2005, 05:53:51

Job time : 24.5411 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.5183 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-24

Perfect score: 776

Sequence: 1 LSLPVTGEPASISCRSSQS.....VVCLLNFFYPREAKEHQSP 148

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: Piri:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567	73.1	135	2 S40342	Ig kappa chain - h
2	562	72.4	219	2 PC4203	Ig kappa chain (mo
3	561	72.3	121	2 S40371	Ig kappa chain - h
4	553	71.3	219	2 S52028	Ig kappa chain - m
5	551	71.0	197	2 S29593	Ig kappa chain (WM
6	544	70.1	136	2 S40357	Ig kappa chain V-J
7	541	69.7	219	2 S16112	Ig kappa chain V r
8	539	69.5	217	2 S42772	Ig kappa chain - m
9	539	69.5	219	2 S38865	Ig kappa chain - m
10	533	68.7	215	2 JE0242	Ig kappa chain NIG
11	530	68.3	132	2 S26882	Ig kappa chain V r
12	529	68.2	125	2 S40356	Ig kappa chain - h
13	529	68.2	225	2 JL0029	Ig kappa chain pre
14	528	68.0	124	2 S03876	Ig kappa chain V-I
15	526	67.8	112	2 S58207	Ig light chain V r
16	525	67.7	112	1 K2HUGM	Ig kappa chain pre
17	516	66.5	112	2 S58206	Ig light chain V r
18	507	65.3	215	2 JE0241	Ig kappa chain NIG
19	501.5	64.6	126	2 S40339	Ig kappa chain - h
20	497	64.0	215	2 A23746	Ig kappa chain V-I
21	490.5	63.2	240	2 S06084	Ig kappa chain pre
22	489	63.0	131	2 S40372	Ig kappa chain V-J
23	488	62.9	215	2 JE0243	Ig kappa chain NIG
24	484.5	62.4	216	2 JE0241	Ig kappa chain An3
25	482	62.1	113	1 K2HUTW	Ig kappa chain V-I
26	472.5	60.9	214	2 S68212	Ig kappa chain (Ma
27	469	60.4	123	2 S40319	Ig kappa chain V r
28	468.5	60.4	112	1 K2HUMU	Ig kappa chain V-I
29	465.5	60.0	220	2 A31790	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S40342  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C:Accession: S40342  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40342  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-135 <KL>  
A:Cross-references: UNIPROT:Q8NEKO; EMBL:X72452; NID:G441372; PID:G441373  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 567; DB 2; Length 135;  
Best Local Similarity 97.3%; Pred.No. 1.7e-42;  
Matches 108; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHNSGYNVLDWYLDKPGQSPQLLYLGSNRRASGVDPDRFS 60  
|||||  
Db 22 LSLPVTGEPASISCRSSQSLHNSGYNVLDWYLDKPGQSPQLLYLGSNRRASGVDPDRFS 81  
|||||  
QY 61 GSGSGTDTFLKISRVEADVGVIYCMQTRPTPTFGQGTKEIKRTVAAPS 111  
|||||  
Db 82 GSGSGTDTFLKISRVEADVGVIYCMQALQTPRTPTFGQGTKEIKRTVAAPS 132  
|||||

RESULT 2

PC4203  
Ig kappa chain (monoclonal antibody MABA34) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 11-Jan-2000  
C:Accession: PC4203  
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Han, M.H.  
Gene 173, 257-259, 1996  
A>Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mor  
A:Reference number: PC4202; MUID:97082978; PMID:8964510  
A:Accession: PC4203  
A:Molecule type: mRNA  
A:Residues: 1-219 <KWA>  
A:Cross-references: GB:U99147; NID:G1594225; PIDN:AA52821.1; PID:G1594226  
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:1-112/Domain: V region #status predicted <VRG>  
F:113-219/Domain: C region #status predicted <CRG>

Query Match 72.4%; Score 562; DB 2; Length 219;





Db 89 GSGSGTDFTLKISRVEADGVVYCNQALQTPWTFGGTKVEIKRTVA 136

```

RESULT 7
SI6112
I9 kappa chain V region (G2a) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: SI6112
R:Vaesen, M.; Froesch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.;
Biol. Chem. Hoppe-Seyler 372, 451-453, 1991
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha
A:Reference number: SI6112; MUID: 92000313; PMID:1910583
A:Accession: SI6112
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-219 <BIT>
A:Cross-references: UNIPROT:Q8VC16; UNIPROT:Q99M37
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

```

Query Match	69.7%;	Score 541;	DB 2;	Length 219;
Best Local Similarity	75.0%;	Pred. No. 5.3e-40;		
Matches 105;	Conservative 12;	Mismatches 23;	Indels 0;	Gaps 0;
Qy	1	LSPVTPCEPASISICRSGQSILHNGYNYLDWYLQKPGQSPOLLILYLSNRRASGVPRFS	60	
		: :        :	: :        :	
Db	9	LSPVSLGDQASISICRSGQSILHNGYNYLYWYLQKPGQSPKPLIYRVSNRFSGVPRFS	68	
		: :        :	: :        :	
Qy	61	GSGSGTDFTLLKISRVEADGVYICYCMQTPRTTFGGQTKVEIKRTVAAPSVFIFPPPSDE	120	
		: :        :	: :        :	
Db	69	GSGSGTDFTLLKISRVEADGLGVYFCQGTHTVPYTFGGGTRLEIKRADAAPTSLIFPPPSSE	128	
		: :        :	: :        :	
Qy	121	QLKSGTASVWCLNNFYPRE	140	
		: :        :	: :        :	
Db	129	OLTSGGASVWCFLNFFPKD	148	
		: :        :	: :        :	

```

RESULT 8
S42772
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:G414143; PIDN:CAAS3226.1; PID:G414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

```

Query Match	69.5%;	Score 539;	DB 2;	Length 217;
Best Local Similarity	73.6%;	Pred. No. 7.8e-40;		
Matches 103; Conservative	14;	Mismatches 23;	Indels 0;	Gaps 0;
Qy	1	LSPVTPCEPASISICRSSQSILHNSGYNVLDWYLKQPGQSPQLLIYLGSNRSASGVGPDRFS	60	
Db	7	LSPVSLGDQASISICRSSQSLVHTNGTLYLHWYLKQPGSPKVLIVKYSTFGSGVGPDRFS	66	
Qy	61	GSGSGTDTFLKISRVEAEDVGIVYCMQTRQTRPFTFGQTKVEIKRTVAAPSGVFIFFPDSDE	120	
Db	67	GSGSGTDTFTKISRVEAEDLVGYFSCQSYVPFFTFGSGTKLEIKRDAAPTSVIFPPSSE	126	
Qy	121	QKSGTASVVCLLNNFYPRE	140	
Db	127	QLTSGASVVCFLNNFYPKD	146	

RESULT 9  
S38865  
Ig kappa chain - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 15-Jun-2001  
C/Accession: S38865  
R/Kipp, B.; Becker, W.; Schlaak, M.  
submitted to the EMBL Data Library, November 1993  
A/Description: Combination of a defined specificity and desired isotype by  
A/Reference number: S38864  
A/Accession: S38865  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-219 <IP>  
A/Cross-references: EMBL:227396; NID:G416538; PIDN:CAAB1787.1; PID:G416539  
C/Superfamily: immunoglobulin v region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

	Query Match	69.58;	Score 539;	DB 2;	Length 219;
	Best Local Similarity	74.3;	Pred. No. 7.9e-40;		
	Matches 104;	Conservative 13;	Mismatches 23;	Indels 0;	Gaps 0;
Qy	1	LSLPVTPEPASISCRSSQSILHSNGYNVLDWYLQKPGSQSPOLLIIYLGNSRASGVPPDRFS	60		
Db	9	LSUSVIGDQASISCRSSQSLVHTNGNTYLHWYLQKPGELSPKLIIYVSNRFGVPPDRFS	68		
Qy	61	GSQSGTDFTLKI SRVEAEDGVIIYCMOTRQTPRTFGQGTKEIKRTVAAPSVFIFPPSDE	120		
Db	69	GSQSGTDFTLKI SRVEAEDLGVIYFCSQVTHVPWTFGGGTLEIKRAADAAPTVISIFPPSSE	128		
Qy	121	QLKSGTASVCLLNFPYRE	140		
Db	129	QLTSGGASVVCFLNFPYRKD	148		

```

RESULT 10
JE0242
Ig kappa chain NIG26 precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JE0242
R/Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.
submitted to JIPID, November 1998
A/Description: Structure relationship of kappatype light chains with AL amy
A:Reference number: JE0241
A/Accession: JE0242
A:Molecule type: protein
A/Residues: 1-215 <ALI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F: 16-91/Domain: immunoglobulin homology <TM>

```

	Query Match	68.7%	Score 533;	DB 2;	Length 215;
	Best Local Similarity	73.1%	Pred. No. 2.6e-39;		
	Matches 106;	Conservative 14;	Mismatches 21;	Indels 4;	Gaps 2
Qy	2	SLPVTGPASISCRSSQSLLHNGNYLDWYLOKPGOSPOLLIYLGASNRASGVDPDRFSG	61		
Db	10	TLSSUSGERATLSCRASQSV--SN--NLYAWYQQPGQAPSLLIYDASSRATGIPDRFSG	65		
Qy	62	SGSGTDDFTLKISRVAEDDVGIYYCMQTRQTPRTFGQGTKEVIEKRTVAAPSFIIPPPSDEQ	121		
Db	66	SGSGTDDILTISGLEPDAFYVYQQYDPRPWTFGQGTKEVIEKRTVAAPSFIIPPPSDEQ	125		
Qy	122	LKSGTASVCLLNNFYPREAKEHOK	146		
Db	126	LKSGTASVCLLNNFYPREAKVOWK	150		

RESULT 11  
S26882  
Ig kappa chain V region (V607) - human

C:Species: Homo sapiens (man)  
C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
C:Accession: S26882  
R:Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combrinato, G.; Zachau, H.G.  
Nature 347, 90-92, 1990  
A:Title: Megabase inversions in the human genome as physiological events.  
A:Reference number: S26882; MUID:90370099; PMID:2118596  
A:Accession: S26882  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-132 <WEI>  
A:Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367  
C:Genetics:  
A:Introns: 17/1  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:136-115/Domain: immunoglobulin homology <IMM>  
  
Query Match 68.3%; Score 530; DB 2; Length 132;  
Best Local Similarity 96.2%; Pred. No. 2.8e-39;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFS 60  
Db 29 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFS 88  
Qy 61 GSGSGTDTLTKISRVEADVGIYCMQTRPTRTFGQGTKEIK 104  
Db 89 GSGSGTDTLTKISRVEADVGIYCMQALQTPQTFTGQGTKEIK 132  
  
RESULT 12  
S40356  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40356  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40356  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-125 <KLE>  
A:Cross-references: EMBL:X72466; NID:g441400; PIDN:CAA51134.1; PID:g441401  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:125-104/Domain: immunoglobulin homology <IMM>  
  
Query Match 68.2%; Score 529; DB 2; Length 125;  
Best Local Similarity 93.5%; Pred. No. 3.2e-39;  
Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFS 60  
Db 18 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFS 77  
Qy 61 GSGSGTDTLTKISRVEADVGIYCMQTRPTRTFGQGTKEIKRTVA 108  
Db 78 GSGSGTDTLTKISRVEADVGIYCMQVLIQPLTFGGGTKEIKRTVA 125  
  
RESULT 13  
JL0029  
Ig kappa chain precursor (RP93) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C:Accession: JL0029  
R:Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.  
J. Exp. Med. 167, 954-973, 1988  
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphospho  
A:Reference number: JL0029; MUID:86171315; PMID:3127529

A:Accession: JL0029  
A:Molecule type: mRNA  
A:Residues: 1-225 <CHI>  
A:Cross-references: UNIPROT:Q99W37  
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell  
A:Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132  
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because  
ect except for four positions shown above  
C:Comment: The protein is an anti-phosphorylcholine antibody.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:7-225/Product: Ig kappa chain #status predicted <ILC>  
F:7-106/Domain: V region #status predicted <VAR>  
F:107-119/Domain: J region #status predicted <JLR>  
F:120-225/Domain: C region #status predicted <COR>  
  
Query Match 68.2%; Score 529; DB 2; Length 225;  
Best Local Similarity 72.1%; Pred. No. 6e-39;  
Matches 101; Conservative 16; Mismatches 23; Indels 0; Gaps 0;  
  
Qy 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFS 60  
Db 15 LSLPVSGLGQASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFS 74  
Qy 61 GSGSGTDTLTKISRVEADVGIYCMQTRPTRTFGQGTKEIKRTVAAPSVFIFPP 120  
Db 75 GSGSGTDTLTKISRVEADVGIYCFQSSSHVWTFGGGTKEIKRAADAAPTVISFPPTSE 134  
Qy 121 QKSGTASVCLLNFPYRE 140  
Db 135 QLTSGGASVVCFLNFPYRK 154  
  
RESULT 14  
S03876  
Ig kappa chain V-II region (Inc) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C:Accession: S03876  
R:Perri, G.; Stoppini, M.; Iadarola, P.; Bellotti, V.; Merlini, G.  
Biochim. Biophys. Acta 995, 103-108, 1989  
A:Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.  
A:Reference number: S03876; MUID:89194238; PMID:2495028  
A:Accession: S03876  
A:Molecule type: protein  
A:Residues: 1-124 <PER>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>  
  
Query Match 68.0%; Score 528; DB 2; Length 124;  
Best Local Similarity 87.1%; Pred. No. 3.9e-39;  
Matches 101; Conservative 6; Mismatches 9; Indels 0; Gaps 0;  
  
Qy 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFS 60  
Db 9 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFS 68  
Qy 61 GSGSGTDTLTKISRVEADVGIYCMQTRPTRTFGQGTKEIKRTVAAPSVFIFPP 116  
Db 69 GSGSGTDTLTKISRVEADVGIYCMQALQTPWTFGGGTKEIKRTVAAPSVFIFPP 124  
  
RESULT 15  
S58207  
Ig light chain V region anti-F(ab')2 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 13-Jan-1996 #sequence\_revision 19-Apr-1996 #text\_change 21-Jan-2000  
C:Accession: S58207  
R:Weischof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebe, S.; Breitling, I.  
submitted to the EMBL Data Library, July 1995  
A:Description: Characterization of heavy and light chain immunoglobulin variable region  
A:Reference number: S58206

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A:Accession: S58207
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEL>
A:Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F16-95/Domain: immunoglobulin homology <IMM>

Query Match      67.8%; Score 526; DB 2; Length 112;
Best Local Similarity 96.2%; Pred. No. 5.3e-39;
Matches 100; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSLPTPGEPASISCRSSQSLHNSGNYLDWYLOKPGOSPOLLIIYLGSNRASGVDRFS 60
   |||||||
Db 9 LSLPTPGEPASISCRSSQSLHNSGNYLDWYLOKPGOSPOLLIIYLGSNRASGVDRFS 68
   |||||||

QY 61 GSGSGTDFTLKISRVEAEDVGIIYCMQTQTPRTFGQTKVEIK 104
   |||||||
Db 69 GSGSGTDFTLKISRVEAEDVGIIYCMQALQTPWTFGQTKVEIK 112
   |||||||

Search completed: March 8, 2005, 06:39:21
Job time : 11.5683 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 55.2705 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-24

Perfect score: 776

Sequence: 1 LSLPTPEPASISCRSSQS.....VVCLLNFPYREAKHQKSP 148

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	717	92.4	Q8NEK0	Q8nek0 homo sapien
2	691.5	89.1	Q6PIH6	Q6pih6 homo sapien
3	621	80.0	Q6P491	Q6p491 homo sapien
4	607	78.2	Q8TCD0	Q8tcd0 homo sapien
5	541	69.7	Q65ZC0	Q65zc0 mus musculus
6	526	67.8	Q6GMV9	Q6gmv9 homo sapien
7	525	67.7	Q6GMV9	Q6gmv9 homo sapien
8	522.5	67.3	Q6PII8	Q6pii8 homo sapien
9	511	65.9	Q6PJF2	Q6pjf2 homo sapien
10	505.5	65.1	Q6P5S8	Q6p5s8 homo sapien
11	490.5	63.2	Q6GMW1	Q6gmw1 homo sapien
12	490	63.1	Q6GMW0	Q6gmw0 homo sapien
13	488.5	63.0	Q72473	Q72473 homo sapien
14	482	62.1	Q72473	Q72473 homo sapien
15	481.5	62.0	Q6PIH7	Q6pih7 homo sapien
16	480.5	61.9	Q6GMX0	Q6gmx0 homo sapien
17	478.5	61.7	Q6GMX8	Q6gmx8 homo sapien
18	474.5	61.1	Q723Y4	Q723y4 homo sapien
19	473.5	61.0	Q6PIT5	Q6pit5 homo sapien
20	468.5	60.4	Q723Y4	Q723y4 homo sapien
21	459.5	59.2	Q6GMX9	Q6gmx9 homo sapien
22	449.5	57.9	Q6PIH4	Q6pih4 homo sapien
23	437.5	56.4	Q723Y4	Q723y4 homo sapien
24	435.5	56.1	Q6PIT5	Q6pit5 homo sapien
25	432	55.7	Q6PIT5	Q6pit5 homo sapien
26	432	55.7	Q6PIT5	Q6pit5 homo sapien
27	426.5	55.0	Q723Y4	Q723y4 homo sapien
28	425	54.8	Q723Y4	Q723y4 homo sapien
29	419	54.0	Q723Y4	Q723y4 homo sapien
30	419	54.0	Q723Y4	Q723y4 homo sapien
31	416.5	53.7	Q723Y4	Q723y4 homo sapien

32	414	53.4	113	1	KV2F_MOUSE	P01630 mus musculus
33	408.5	52.6	114	2	Q9UL80	Q9ul80 homo sapien
34	408.5	52.6	241	2	Q63ZX4	Q63zx4 mus musculus
35	407	52.4	113	1	KV2E_MOUSE	P03976 mus musculus
36	388	50.0	112	1	KV2D_MOUSE	P01629 mus musculus
37	386	49.7	112	2	Q6LEM8	Q6lem8 mus musculus
38	385	49.6	113	1	KV2C_MOUSE	P01628 mus musculus
39	378	48.7	112	1	KV2A_MOUSE	P01626 mus musculus
40	377.5	48.6	108	1	KV1_CANFA	P01618 canis faml
41	364.5	47.0	114	1	KV4A_HUMAN	P01625 homo sapien
42	360.5	46.5	134	1	KV4C_HUMAN	P06314 homo sapien
43	359	46.3	129	1	KV3L_HUMAN	P01835 homo sapien
44	355	45.7	109	1	KV3D_HUMAN	P01622 homo sapien
45	352	45.4	120	1	KV2B_MOUSE	P01627 mus musculus

#### ALIGNMENTS

#### RESULT 1

ID	Q8NEK0	PRELIMINARY;	PRT;	239 AA.
AC	Q8NEK0;			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RX	MEDLINE=2338857; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Huiyok S.W., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.			
DR	EMBL; BC030814; AAH30814.1; -.			
DR	PIR; S23638; S23638.			
DR	PIR; S34091; S34091.			
DR	PIR; S40342; S40342.			
DR	PIR; S40357; S40357.			
DR	HSSP; P01834; I17Z.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig.cl.			
DR	InterPro; IPR003006; Ig.MHC.			
DR	InterPro; IPR003596; Ig.v.			
DR	Pfam; PF07654; C1-set; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			

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DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein_
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match          92.4%; Score 717; DB 2; Length 239;
Best Local Similarity 94.5%; Pred. No. 1.7e-64;
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPOLLIYLGSNRASGVDPDRFS 60
Db 29 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPOLLIYLGSNRASGVDPDRFS 88
QY 61 GSGSGTDFTLKISRVEADVGIYCMOTRQTPRTFGQGTKEIKRTVAAPSVFIFFPSDE 120
Db 89 GSGSGTDFTLKISRVEADVGIYCMQGLQTPQIFGQGTKEIKRTVAAPSVFIFFPSDE 148
QY 121 QLKSGTASVCLNNFYPREAKEHQK 146
Db 149 QLKSGTASVCLNNFYPREAKVQWK 174

RESULT 2
Q6PIH6 PRELIMINARY; PRT; 240 AA.
ID Q6PIH6
AC Q6PIH6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034142; AAH34142.1; -.
DR HSSP; P01837; IKB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS0835; IG LIKE; 2.
KW PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein_
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8B8B781EC4 CRC64;

Query Match          89.1%; Score 691.5; DB 2; Length 240;
Best Local Similarity 91.8%; Pred. No. 6.7e-62;
Matches 135; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPOLLIYLGSNRASGVDPDRFS 60
Db 29 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPOLLIYLGSNRASGVDPDRFS 88
QY 61 GSGSGTDFTLKISRVEADVGIYCMOTRQTPRTFGQGTKEIKRTVAAPSVFIFFPSD 119
Db 89 GSGSGTDFTLKISRVEADVGIYCMQALQTPPTFGQGTKEIKRTVAAPSVFIFFPSD 148
QY 120 EQLKSGTASVCLNNFYPREAKEHQK 146
Db 149 EQLKSGTASVCLNNFYPREAKVQWK 175

RESULT 3
Q6P491 PRELIMINARY; PRT; 239 AA.
ID Q6P491
AC Q6P491;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063599; AAH63599.1; -.
DR HSSP; P01837; ILCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
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DR SMART: SM00406; IGV: 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match
Best Local Similarity 80.0%; Score 621; DB 2; Length 239;
Matches 121; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYKPGQSPOLLIYLGNSRASGVDPDRFS 60
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DQ 29 LSSPTVLGPASISCRSSQSLHNSGNYLDWYKPGQSPOLLIYKISNRFSGVDPDRFS 88
QY 61 GSGSGTDFTLKISRVEAEDVGIYCMQTRQTRPTFGQGTKEIKRTVAAPSFIIPPSPDE 120
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DQ 89 GSGAGTDFTLKISRVEAEDVGIYCMQTRQTRPTFGQGTKEIKRTVAAPSFIIPPSPDE 148
QY 121 OLKSGTASVCLNNFYPREAKEHOK 146
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DQ 149 QLKSGTASVCLNNFYPREAKEHOK 174

RESULT 4
Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; 1172.
DR InterPro; IPR007110; Ig-like.
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DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV: 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match
Best Local Similarity 78.2%; Score 607; DB 2; Length 239;
Matches 117; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYKPGQSPOLLIYLGNSRASGVDPDRFS 60
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DQ 29 LSLPVTLPASISCRSSQSLHNSGNYLDWYKPGQSPOLLIYKISNRFSGVDPDRFS 88
QY 61 GSGSGTDFTLKISRVEAEDVGIYCMQTRQTRPTFGQGTKEIKRTVAAPSFIIPPSPDE 120
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DQ 89 GSGSGTDFTLKISRVEAEDVGIYCMQTRQTRPTFGQGTKEIKRTVAAPSFIIPPSPDE 148
QY 121 OLKSGTASVCLNNFYPREAKEHOK 146
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DQ 149 QLKSGTASVCLNNFYPREAKEHOK 174

RESULT 5
Q65ZC0 PRELIMINARY; PRT; 219 AA.
ID Q65ZC0
AC Q65ZC0;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
RT allergen Chi t 1."
EL Int. Arch. Allergy Immunol. 110:348-353(1996).
DR EMBL; Z37499; CA85724.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV: 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON TER 1
FT NON TER 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match
Best Local Similarity 69.7%; Score 541; DB 2; Length 219;
Matches 104; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYKPGQSPOLLIYLGNSRASGVDPDRFS 60
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DQ 9 LSLSVSLGDAQSISCRSSQSLVHTNGTYLHWYKPGQSPOLLIYVSNRFSGVDPDRFS 68
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Db 87 SSGGDTFTLTKISRVAEADVGIIYCHQTRQ-TPTFTGQGTKEIKRTVAAPSVFIIPPSDE 146
122 LKSGTASVVCLLNNFYPREAKEHQK 146
147 LKSGTASVVCLLNNFYPREAKVQWK 171

RESULT 12
Q6GMW0 PRELIMINARY; PRT; 235 AA.
ID Q6GMW0
AC Q6GMW0
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 63.1%; Score 490; DB 2; Length 235;
Best Local Similarity 66.4%; Pred. No. 1.9e-41;
Matches 97; Conservative 19; Mismatches 24; Indels 6; Gaps 2;

QY 2 SLVPTGPBPASISCRSSQSLHNSNGYNYLDWYLOKPGQSPQLLIYLGNSRAGVDPFRSG 61
Db 30 TUSVSPGERATLSCRASQSI-----SNLAWYQQRPGQAPRLIYICASRVITGIPFRSG 84

QY 62 SSGGDTFTLTKISRVAEADVGIIYCHQTRQ-TPTFTGQGTKEIKRTVAAPSVFIIPPSDEQ 121

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QY 62 SSGGDTFTLTKISRVAEADVGIIYCHQTRQ-TPTFTGQGTKEIKRTVAAPSVFIIPPSDE 120
Db 85 SSGGTEFTLSISLQSDFAVYFCQYNDWLLYTFQGTGKLEIKRTVAAPSVFIIPPSDE 144
121 QKSGTASVVCLLNNFYPREAKEHQK 146
145 QKSGTASVVCLLNNFYPREAKVQWK 170

RESULT 13
Q7Z473 PRELIMINARY; PRT; 234 AA.
ID Q7Z473
AC Q7Z473
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 63.0%; Score 488.5; DB 2; Length 234;
Best Local Similarity 67.6%; Pred. No. 2.7e-41;
Matches 98; Conservative 12; Mismatches 30; Indels 5; Gaps 1;

QY 2 SLVPTGPBPASISCRSSQSLHNSNGYNYLDWYLOKPGQSPQLLIYLGNSRAGVDPFRSG 61
Db 30 SFSASTGDRVTITCRASQSI-----GSLAWYQQRPGKAPQLLIYAAASTLQSGVSPFRSG 84

QY 62 SSGGDTFTLTKISRVAEADVGIIYCHQTRQ-TPTFTGQGTKEIKRTVAAPSVFIIPPSDEQ 121

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85 SASGTDFTLISCLQSEDFATYYCQYYTPTWTFQGGTKVBIKRTVAAPSVFIFPPSDEQ 144

122 LKSGTASVVCLLNFFYPREAKEHOK 146  
145 LKSGTASVVCLLNFFYPREAKVQWK 169

RESULT 14  
KV2D\_HUMAN STANDARD; PRT; 113 AA.

AC P01617;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig kappa chain V-II region TEW.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE (BENCE-JONES PROTEIN TEW).  
RX MEDLINE=74148480; PubMed=4596149;  
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;  
RT "Amino acid sequence of a kappa Bence Jones protein from a case of  
RT primary amyloidosis.";  
RL Biochemistry 12:3763-3780(1973).  
RN [2]  
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).  
RX MEDLINE=73166638; PubMed=4700495;  
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,  
RA Glenner G.G.;  
RT "Structural identity of Bence Jones and amyloid fibril proteins in a  
RT patient with plasma cell dyscrasia and amyloidosis.";  
RL J. Clin. Invest. 52:1276-1281(1973).  
CC -I- MISCELLANEOUS: The major amyloid protein appears to be identical  
CC with the Bence Jones protein isolated from the same patient.  
CC -I- MISCELLANEOUS: This protein was isolated from the urine of a  
CC patient with plasma cell dyscrasia and amyloidosis.  
CC -I- MISCELLANEOUS: The C region of this chain has the INV (1,2)  
CC marker.

DR PIR; A90370; K2HUTW.  
DR HSP; Q99W37; I191.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
KW Amyloid; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON TER 113 113  
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 62.1%; Score 482; DB 1; Length 113;  
Best Local Similarity 85.7%; Pred. No. 4.9e-41;  
Matches 90; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHNSGVNYLDWYLPKQGSPLLIIYLGNSRASGVDPDRFS 60  
DB 9 LSLPVTGEPASISCRSSQSLHNSGVNYLDWYLPKQGSPLLIIYLGNSRASGVDPDRFS 68  
QY 61 GSGGTDFTLKISRVEADVGIYCMQTRPTPTFGGQTKVEIKR 105

69 GSGGTDFTLKISRVEADVGVVYCMZALQALPITFGGQTRLEIKR 113

RESULT 15  
Q6PIH7 PRELIMINARY; PRT; 236 AA.

AC Q6PIH7;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalutz J., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC034141; AAH34141.1; --  
DR HSP; P01607; IAR2.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; CI-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 2.  
DR PROSITE; PS0835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 62.0%; Score 481.5; DB 2; Length 236;  
Best Local Similarity 66.0%; Pred. No. 1.4e-40;  
Matches 95; Conservative 13; Mismatches 31; Indels 5; Gaps 1;

QY 3 LPVTGEPASISCRSSQSLHNSGVNYLDWYLPKQGSPLLIIYLGNSRASGVDPDRFS 62  
DB 33 LSASVGDRTVITCRASQGI-----SSYLAWYQKPKGAPNLLIIAASLTQSGVPSRFS 87  
QY 63 GSGGTDFTLKISRVEADVGIYCMQTRPTPTFGGQTKVEIKRTVAAPSVFIFPPSDEQL 122  
DB 88 GSGGTDFTLKISRVEADVGIYCMQTRPTPTFGGQTKVEIKRTVAAPSVFIFPPSDEQL 147  
QY 123 KSGTASVVCLLNFFYPREAKEHOK 146

Db 148 KSGTASVVCLLNNEYBREAKVQWK 171

Search completed: March 8, 2005, 06:35:45  
Job time : 56.2705 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 68.6168 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-24

Perfect score: 776

Sequence: 1 LSLPVTGCEPASISCRSSQS.....VCLLNFFYPREAKEHOKSP 148

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2002s.\*

6: Geneseq2003as.\*

7: Geneseq2003bs.\*

8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	776	100.0	148	2 AAY34309	Aay34309 IgM antib
2	723	93.2	238	8 ADL93653	Adl93653 Human CD4
3	722	93.0	238	8 ADL93654	Adl93654 Human CD4
4	720	92.8	239	7 ADE28405	Ade28405 Human ant
5	719	92.7	238	8 ADL93650	Adl93650 Human CD4
6	719	92.7	239	7 ADE28465	Ade28465 Human ant
7	717	92.4	239	7 ADE28521	Ade28521 Human ant
8	717	92.4	239	7 ADE28397	Ade28397 Human ant
9	716	92.3	238	8 ADL93649	Adl93649 Human CD4
10	716	92.3	239	7 ADE28477	Ade28477 Human ant
11	713	91.9	219	8 ADR16817	Adr16817 Human bre
12	709	91.4	239	3 AAY82616	Aay82616 Human PTH
13	709	91.4	239	7 ADE28421	Ade28421 Human ant
14	707.5	91.2	237	8 ADL93657	Adl93657 Human CD4
15	707	91.1	219	8 ADH34590	Adh34590 021 light
16	707	91.1	239	3 AAY82618	Aay82618 Human PTH
17	705	90.9	219	7 ADJ32150	Adj32150 Human int
18	704	90.7	238	8 ADL93652	Adl93652 Human CD4
19	704	90.7	239	7 ADE28461	Ade28461 Human ant
20	702	90.5	239	7 ADE28469	Ade28469 Human ant
21	697.5	89.9	237	8 ADL93658	Adl93658 Human CD4
22	697.5	89.9	237	8 ADL93651	Adl93651 Human CD4
23	695	89.6	143	2 AAY34313	Aay34313 IgM antib
24	692	89.2	239	3 AAY82617	Aay82617 Human PTH
25	691	89.0	239	3 AAY82615	Aay82615 Human PTH

## ALIGNMENTS

### RESULT 1

AAY34309

ID: AAY34309 standard; protein; 148 AA.

AC AAY34309;

DT 19-NOV-1999 (first entry)

DE IGM antibody CEM 10.1 C3 kappa chain sequence.

KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

(ABGE-) ABGENIX INC.

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX N-PSDB; AAZ20410.

PT New monoclonal antibody, used for treating e.g. graft versus host

PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX Claim 61; Fig 24; 245pp; English.

CC This sequence represents the kappa chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAb) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IGM MAb ABX-CBL, providing that the antibody is not CBL1. The MAb  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood





CC and may have a use in antibody therapy. The protein is useful for  
CC preparing a composition for treating inflammatory disorders, e.g.,  
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
CC multiple sclerosis or neoplastic disorder, which is a malignant or  
CC metastatic cancer. The present sequence represents a human CD44-binding  
CC antibody light chain.

XX  
SQ Sequence 238 AA;  
Query Match 93.0%; Score 722; DB 8; Length 238;  
Best Local Similarity 95.2%; Pred. No. 5.8e-49;  
Matches 139; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 LSLPVTGEPASISCRSSQSLHSGYNYLDWYLOKPGSPQLLIYLGSNRAGVDPDRFS 60  
DQ 28 LSLPVTGEPASISCRSSQSLHSGYNYLDWYLOKPGSPQLLIYLGSNRAGVDPDRFS 87  
QY 61 GSGSGTDTFLKISRVEADVGIYCMQOTRPTRTGQGTKEIKRTVAAPSFIIPPSDE 120  
DQ 88 GSGSGTDTFLKISRVEADVGIYCMQALQTPMTFGQGTKEIKRTVAAPSFIIPPSDE 147  
QY 121 QLKSGTASVCLNNFYPREAKEHOK 146  
DQ 148 QLKSGTASVCLNNFYPREAKVQWK 173

RESULT 4  
ADE28405  
ID ADE28405 standard; protein; 239 AA.  
AC ADE28405;  
XX  
XX  
DT 29-JAN-2004 (first entry)  
DE Human anti-CD40 antibody 7-1-2 variable region light chain protein.  
XX  
XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
XX human; variable region light chain; 7-1-2.

XX Homo sapiens.  
XX WO2003040170-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 08-NOV-2002; 2002WO-US036107.  
XX  
XX 09-NOV-2001; 2001US-0348980P.  
XX (PFIZ ) PFIZER PROD INC.  
XX (ABGE-) ABGENIX INC.  
XX  
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
XX  
XX WPI; 2003-441521/41.  
XX N-PSDB; ADE28404.

XX New chimeric or human monoclonal antibody or its antigen-binding portion  
PT that specifically binds to and activates human CD40, useful for enhancing  
PT an immune response in a human, or treating cancer, HIV, neutropenia or  
PT viral infections.

XX Claim 1; SEQ ID NO 12; 177pp; English.  
XX  
XX The invention relates to a novel chimeric or human monoclonal antibody or  
CC its antigen-binding portion that specifically binds to and activates  
CC human CD40. The anti-CD40 antibody of the invention demonstrates  
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
CC activities and may be useful for treating a hyperproliferative disorder  
CC such as cancer, viral and bacterial infection or genetic, primary or  
CC combined immunodeficiency conditions including neutropenia or HIV

CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
CC in a biological sample in vitro or in vivo, as well as during gene  
CC therapy procedures. The current sequence is that of the human anti-CD40  
CC antibody variable region light chain protein of the invention.

XX  
SQ Sequence 239 AA;  
Query Match 92.8%; Score 720; DB 7; Length 239;  
Best Local Similarity 94.5%; Pred. No. 8.3e-49;  
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 LSLPVTGEPASISCRSSQSLHSGYNYLDWYLOKPGSPQLLIYLGSNRAGVDPDRFS 60  
DQ 29 LSLPVTGEPASISCRSSQSLHSGYNYLDWYLOKPGSPQLLIYLGSNRAGVDPDRFS 88  
QY 61 GSGSGTDTFLKISRVEADVGIYCMQOTRPTRTGQGTKEIKRTVAAPSFIIPPSDE 120  
DQ 89 GSGSGTDTFLKISRVEADVGIYCMQALQTPMTFGQGTKEIKRTVAAPSFIIPPSDE 148  
QY 121 QLKSGTASVCLNNFYPREAKEHOK 146  
DQ 149 QLKSGTASVCLNNFYPREAKVQWK 174

RESULT 5  
ADL93650  
ID ADL93650 standard; protein; 238 AA.  
XX  
XX AC ADL93650;  
XX  
XX DT 17-JUN-2004 (first entry)

XX Human CD44-binding antibody light chain HAE-G2-kappa-light SEQ ID NO:145.  
XX  
XX human; CD44; light chain immunoglobulin variable domain;  
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;  
KW antinflammatory; immunosuppressive; antiarthritic; antineumatic;  
KW dermatological; vasotropic; neuroprotective; antibody therapy;  
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
KW graft versus host response; multiple sclerosis; neoplastic disorder;  
KW cancer; antibody.

XX Homo sapiens.  
XX WO2004024750-A2.  
XX  
XX 25-MAR-2004.  
XX  
XX 15-SEP-2003; 2003WO-US029318.  
XX  
XX 13-SEP-2002; 2002US-0410758P.  
XX 09-MAY-2003; 2003US-0469123P.  
XX (DYAX-) DYAX CORP.  
XX  
XX Rondon IJ, Edge A, Baribault Kent R;  
XX  
XX WPI; 2004-270003/25.

XX New protein comprising a light chain (LC) immunoglobulin variable domain  
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
PT useful for preparing a composition for treating inflammatory or  
PT neoplastic disorders.

XX Disclosure; SEQ ID NO 145; 128pp; English.  
XX  
XX The invention relates to a novel isolated protein comprising a light  
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
CC immunoglobulin variable domain sequence that form an antigen binding site  
CC with binding affinity for the human CD44 extracellular domain and where  
CC CDR3 of the LC variable domain sequence. A protein of the invention has  
CC cytostatic, antinflammatory, immunosuppressive, antiarthritic,  
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,

CC and may have a use in antibody therapy. The protein is useful for  
CC preparing a composition for treating inflammatory disorders, e.g.,  
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
CC multiple sclerosis or neoplastic disorder, which is a malignant or  
CC metastatic cancer. The present sequence represents a human CD44-binding  
CC antibody light chain.  
XX  
SQ

Query Match 92.7%; Score 719; DB 8; Length 238;  
Best Local Similarity 94.5%; Pred. NO. 9.9e-49;  
Matches 138; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
QY 1 LSLPVTGPEPASISCRSSQSLHSGNYLDWYLQKPGQSPQLLIYLGSRASGVDPDRFS 60  
DB 28 LSLPVTGPEPASISCRSSQSLHSGNYLDWYLQKPGQSPQLLIYLGSRASGVDPDRFS 87  
QY 61 GSGSGTDTFLKISRVEADVGIYCMQTRPTFGQGTKEIKRTVAAPSVFIAPPSPDE 120  
DB 88 GSGSGTDTFLKISRVEADVGIYCMQALQIPWTFGGQTKLEIKRTVAAPSVFIAPPSPDE 147  
QY 121 QKSGTASVWCLNNFYPREAKEHOK 146  
DB 148 QKSGTASVWCLNNFYPREAKVQWK 173

RESULT 6  
ADE28465  
ID ADE28465 standard; protein; 239 AA.  
XX  
AC ADE28465;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human anti-CD40 antibody 23-28-1 full length light chain protein.  
XX  
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; light chain; 23-28-1.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040170-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 08-NOV-2002; 2002WO-US036107.  
XX  
PR 09-NOV-2001; 2001US-0348980P.  
XX  
PA (PFIZ ) PFIZER PROD INC.  
PA (ABGE-) ABGENIX INC.  
XX  
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
XX  
DR WPI; 2003-441521/41.  
DR N-PSDB; ADE28464.  
XX

PT New chimeric or human monoclonal antibody or its antigen-binding portion  
PT that specifically binds to and activates human CD40, useful for enhancing  
PT an immune response in a human, or treating cancer, HIV, neutropenia or  
PT viral infections.  
XX  
PS Claim 7; SEQ ID NO 72; 177pp; English.  
XX  
CC The invention relates to a novel chimeric or human monoclonal antibody or  
CC its antigen-binding portion that specifically binds to and activates  
CC human CD40. The anti-CD40 antibody of the invention demonstrates  
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
CC activities and may be useful for treating a hyperproliferative disorder  
CC such as cancer, viral and bacterial infection or genetic, primary or  
CC combined immunodeficiency conditions including neutropenia or HIV  
CC infection. The anti-CD40 antibodies may also be useful for detecting  
CC in a biological sample in vitro or in vivo, as well as during gene  
CC therapy procedures.

CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
CC in a biological sample in vitro or in vivo, as well as during gene  
CC therapy procedures. The current sequence is that of the human anti-CD40  
CC antibody full length light chain protein of the invention.  
XX  
SQ Sequence 239 AA;

Query Match 92.7%; Score 719; DB 7; Length 239;  
Best Local Similarity 94.5%; Pred. No. 1e-48;  
Matches 138; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
QY 1 LSLPVTGPEPASISCRSSQSLHSGNYLDWYLQKPGQSPQLLIYLGSRASGVDPDRFS 60  
DB 29 LSLPVTGPEPASISCRSSQSLHSGNYLDWYLQKPGQSPQLLIYLGSRASGVDPDRFS 88  
QY 61 GSGSGTDTFLKISRVEADVGIYCMQTRPTFGQGTKEIKRTVAAPSVFIAPPSPDE 120  
DB 89 GSGSGTDTFLKISRVEADVGIYCMQALQIPWTFGGQTKVEIKRTVAAPSVFIAPPSPDE 148  
QY 121 QKSGTASVWCLNNFYPREAKEHOK 146  
DB 149 QKSGTASVWCLNNFYPREAKVQWK 174

RESULT 7  
ADE28521  
ID ADE28521 standard; protein; 239 AA.  
XX  
AC ADE28521;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human anti-CD40 antibody 23-29-1L-R174K mutant VL light chain protein.  
XX  
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; light chain; mutein; mutant; 23-29-1L-R174K.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040170-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 08-NOV-2002; 2002WO-US036107.  
XX  
PR 09-NOV-2001; 2001US-0348980P.  
XX  
PA (PFIZ ) PFIZER PROD INC.  
PA (ABGE-) ABGENIX INC.  
XX  
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
XX  
DR WPI; 2003-441521/41.  
XX

PT New chimeric or human monoclonal antibody or its antigen-binding portion  
PT that specifically binds to and activates human CD40, useful for enhancing  
PT an immune response in a human, or treating cancer, HIV, neutropenia or  
PT viral infections.  
XX  
PS Claim 7; SEQ ID NO 101; 177pp; English.  
XX  
CC The invention relates to a novel chimeric or human monoclonal antibody or  
CC its antigen-binding portion that specifically binds to and activates  
CC human CD40. The anti-CD40 antibody of the invention demonstrates  
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
CC activities and may be useful for treating a hyperproliferative disorder  
CC such as cancer, viral and bacterial infection or genetic, primary or  
CC combined immunodeficiency conditions including neutropenia or HIV  
CC infection. The anti-CD40 antibodies may also be useful for detecting  
CC in a biological sample in vitro or in vivo, as well as during gene  
CC therapy procedures. The current sequence is that of the human anti-CD40

CC antibody mutant variable region light chain protein of the invention.  
XX NOTE: this sequence appears to have an incorrect SEQ ID NO.  
SQ Sequence 239 AA;

Query Match 92.4%; Score 717; DB 7; Length 239;  
Best Local Similarity 95.2%; Pred. No. 1.4e-48;  
Matches 139; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHNSGYNLDWYLPKPGQSPQLLYLGSNRASGVDPDRFS 60  
DB 29 LSLPVTGEPASISCRSSQSLPGNGYNLDWYLPKPGQSPQLLYLGSNRASGVDPDRFS 88  
QY 61 GSGSGTDFTLKISRVEAEDVGYYCMQTRPTRTFGQGTKEIKRTVAAPSFIIPPDSDE 120  
DB 89 GSGSGTDFTLKISRVEAEDVGYYCMQALQTPRTFGQGTKEIKRTVAAPSFIIPPDSDE 148  
QY 121 QLKSGTASVVCLLNNFYPREAKEHOK 146  
DB 149 QLKSGTASVVCLLNNFYPREAKVQWK 174

RESULT 8  
ADE28397  
ID ADE28397 standard; protein; 239 AA.  
XX  
AC ADE28397;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human anti-CD40 antibody 3-1-1 variable region light chain protein.  
XX  
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; variable region light chain; 3-1-1.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040170-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 08-NOV-2002; 2002WO-US036107.  
XX  
PR 09-NOV-2001; 2001US-0348980P.  
XX  
PA (PRIZ ) PRIZER PROD INC.  
PA (ABGE-) ABGENIX INC.  
XX  
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
DR WPI; 2003-441521/41.  
DR N-PSDB; ADE28396.  
XX  
PT New chimeric or human monoclonal antibody or its antigen-binding portion  
PT that specifically binds to and activates human CD40, useful for enhancing  
PT an immune response in a human, or treating cancer, HIV, neutropenia or  
PT viral infections.  
XX  
PS Claim 1; SEQ ID NO 4; 177pp; English.  
XX  
CC The invention relates to a novel chimeric or human monoclonal antibody or  
CC its antigen-binding portion that specifically binds to and activates  
CC human CD40. The anti-CD40 antibody of the invention demonstrates  
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
CC activities and may be useful for treating a hyperproliferative disorder  
CC such as cancer, viral and bacterial infection or genetic, primary or  
CC combined immunodeficiency conditions including neutropenia or HIV  
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
CC in a biological sample in vitro or in vivo, as well as during gene  
CC therapy procedures. The current sequence is that of the human anti-CD40  
CC antibody variable region light chain protein of the invention.

XX SQ Sequence 239 AA;

Query Match 92.4%; Score 717; DB 7; Length 239;  
Best Local Similarity 93.8%; Pred. No. 1.4e-48;  
Matches 137; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHNSGYNLDWYLPKPGQSPQLLYLGSNRASGVDPDRFS 60  
DB 29 LSLPVTGEPASISCRSSQSLLYSNGYNFLDWYLPKPGQSPQLLYLGSNRASGVDPDRFS 88  
QY 61 GSGSGTDFTLKISRVEAEDVGYYCMQTRPTRTFGQGTKEIKRTVAAPSFIIPPDSDE 120  
DB 89 GSGSGTDFTLKISRLEAEDVGYYCMQALQTPRTFGQGTKEIKRTVAAPSFIIPPDSDE 148  
QY 121 QLKSGTASVVCLLNNFYPREAKEHOK 146  
DB 149 QLKSGTASVVCLLNNFYPREAKVQWK 174

RESULT 9  
ADL93649  
ID ADL93649 standard; protein; 238 AA.  
XX  
AC ADL93649;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human CD44-binding antibody light chain HAB-A3-kappa-light SEQ ID NO:144.  
XX  
KW human; CD44; light chain immunoglobulin variable domain;  
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;  
KW antinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
KW dermatological; vasotropic; neuroprotective; antibody therapy;  
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
KW graft versus host response; multiple sclerosis; neoplastic disorder;  
KW cancer; antibody.  
XX  
OS Homo sapiens.  
XX  
PN WO2004024750-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 15-SEP-2003; 2003WO-US029318.  
XX  
PR 13-SEP-2002; 2002US-0410758P.  
PR 09-MAY-2003; 2003US-0469123P.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Rondon IJ, Edge A, Baribault Kent R;  
DR WPI; 2004-270003/25.  
XX  
PT New protein comprising a light chain (LC) immunoglobulin variable domain  
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
PT useful for preparing a composition for treating inflammatory or  
PT neoplastic disorders.  
XX  
PS Disclosure; SEQ ID NO 144; 128pp; English.  
XX  
CC The invention relates to a novel isolated protein comprising a light  
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
CC immunoglobulin variable domain sequence that form an antigen binding site  
CC with binding affinity for the human CD44 extracellular domain and where  
CC CDR3 of the LC variable domain sequence. A protein of the invention has  
CC cytostatic, antinflammatory, immunosuppressive, antiarthritic,  
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,  
CC and may have a use in antibody therapy. The protein is useful for  
CC preparing a composition for treating inflammatory disorders, e.g.,  
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
CC multiple sclerosis or neoplastic disorder, which is a malignant or



Db 69 GSGSGTDYTLKISRVEAEDGVVYCMQGLQTPRTFGQGRLEIKRTVAAPSVFIIPPSPDE 128  
QY 121 QLKSGTASVCLNNFYPREAKEHOK 146  
Db 129 QLKSGTASVCLNNFYPREAKVQWK 154  
RESULT 12  
ID AAY82616  
XX AAY82616 standard; protein; 239 AA.  
AC AAY82616;  
XX 02-AUG-2000 (first entry)  
XX Human PTHrP monoclonal antibody clone 2G4-12-20 protein SEQ ID NO:16.  
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
KW fracture; cachexia; tooth disease; periodontal disease; gingivitis; sepsis;  
KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
KW antiarthritic; cytostatic; antiinflammatory.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 5 /label= Val, Ala, Asp, Gly  
FT Misc-difference 13 /label= Val, Ala, Asp, Gly  
FT Misc-difference 25 /note= "possibly Leu"  
FT Misc-difference 27 /label= Ile, Thr, Asn, Ser  
FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys  
FT Misc-difference 216 /note= "possible Val"  
XX  
PN JP2000080100-A.  
XX 21-MAR-2000.  
XX 12-OCT-1998; 98JP-00304793.  
XX 17-JUN-1998; 98JP-00188196.  
PR 26-JUN-1998; 98JP-00196729.  
XX (NIBS ) JAPAN TOBACCO INC.  
PA  
XX WPI; 2000-286723/25.  
DR N-PSDB; AAA13926.  
XX  
PT A human monoclonal antibody to parathyroid hormone related protein. -  
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
PT including metastasis, and pain.  
XX  
PS Claim 31; Page 48-49; 88pp; Japanese.  
XX  
CC The present invention describes a human monoclonal antibody to  
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
CC its fragments, following the stimulation of PTHrP has the following  
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
CC the release of calcium from bone; or (c) inhibits elevation of blood  
CC calcium content. The monoclonal antibody can be used in the treatment of  
CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome  
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
CC antiinflammatory activities. The present sequence represents a human  
CC PTHrP monoclonal antibody clone protein sequence from the present  
CC invention  
XX  
SQ Sequence 239 AA;

Query Match 91.4%; Score 709; DB 3; Length 239;  
Best Local Similarity 93.2%; Pred. No. 6.1e-48;  
Matches 136; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 1 LSLPVTGPEPASISCRSSQSLHNSGNYLDWLYLQKPGSQPOLLIYLGNSRASGVDPDRFS 60  
Db 29 LSLPVTGPEPASISCRSSQSLHNSGNYLDWLYLQKPGSQPOLLIYLGNSRASGVDPDRFS 88  
QY 61 GSGSGTDFTLKISRVEAEDGVVYCMQGLQTPRTFGQGRLEIKRTVAAPSVFIIPPSPDE 120  
Db 89 GSGSGTDFTLKISRVEAEDGVVYCMQGLQTPRTFGQGRLEIKRTVAAPSVFIIPPSPDE 148  
QY 121 QLKSGTASVCLNNFYPREAKEHOK 146  
Db 149 QLKSGTASVCLNNFYPREAKVQWK 174  
RESULT 13  
ID ADE28421 standard; protein; 239 AA.  
XX ADE28421;  
XX 29-JAN-2004 (first entry)  
XX Human anti-CD40 antibody 15-1-1 variable region light chain protein.  
DE anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; variable region light chain; 15-1-1.  
XX Homo sapiens.  
OS  
XX WO2003040170-A2.  
XX 15-MAY-2003.  
XX 08-NOV-2002; 2002WO-US036107.  
XX 09-NOV-2001; 2001US-0348980P.  
PR (PFIZ ) PFIZER PROD INC.  
PA (ABGE-) AGENIX INC.  
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
XX WPI; 2003-441521/41.  
DR N-PSDB; ADE28420.  
XX  
PT New chimeric or human monoclonal antibody or its antigen-binding portion  
PT that specifically binds to and activates human CD40, useful for enhancing  
PT an immune response in a human, or treating cancer, HIV, neutropenia or  
PT viral infections.  
XX  
PS Claim 1; SEQ ID NO 28; 177pp; English.  
XX  
CC The invention relates to a novel chimeric or human monoclonal antibody or  
CC its antigen-binding portion that specifically binds to and activates  
CC human CD40. The anti-CD40 antibody of the invention demonstrates  
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
CC activities and may be useful for treating a hyperproliferative disorder  
CC such as cancer, viral and bacterial infection or genetic, primary or  
CC combined immunodeficiency conditions including neutropenia or HIV  
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
CC in a biological sample in vitro or in vivo, as well as during gene  
CC therapy procedures. The current sequence is that of the human anti-CD40  
CC antibody variable region light chain protein of the invention.  
XX  
SQ Sequence 239 AA;

Query Match 91.4%; Score 709; DB 7; Length 239;  
Best Local Similarity 92.5%; Pred. No. 6.1e-48;



CC disorder or disease such as leukaemias, neoplasm, bile duct carcinoma,  
CC bladder carcinoma, viral disorder or disease associated with severe acute  
CC respiratory syndrome (SARS), herpes simplex virus (HSV), hepatitis B  
CC virus (HBV), HIV and bacterial disorder or disease associated with  
CC Mycobacterium tuberculosis, Pseudomonas aeruginosa and Vibrio cholerae.  
XX  
SQ Sequence 219 AA;

Query Match 91.1%; Score 707; DB 8; Length 219;  
Best Local Similarity 92.5%; Pred. No. 8e-48;  
Matches 135; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPOLLIYLGSRASGVDPDRFS 60  
Db :|||||  
Qy 9 VSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPOLLIYLGSRASGVDPDRFS 68  
Db :|||||  
Qy 61 GSGSGTDTLTKISRVEADVGIYCMQTRQTPRTFGQTKVEIKRTVAAPSVFIPPPSDE 120  
Db :|||||  
Qy 69 GSGSGTDTLTKISRVEADVGIYCMQTRQTPRTFGQTKVEIKRTVAAPSVFIPPPSDE 128  
Db :|||||  
Qy 121 QLKSGTASVVCLLNNFYPREAKEHOK 146  
Db :|||||  
Qy 129 QLKSGTASVVCLLNNFYPREAKEVQWK 154  
Db :|||||

Search completed: March 8, 2005, 06:17:05  
Job time : 69.6168 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 78.5397 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-24

Perfect score: 776

Sequence: 1 LSLPVTGPSPASISCRSSQS.....VVCLLNFPYPRAKHQKSP 148

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA.\*
- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	723	93.2	238	16	US-10-663-244-148
2	722	93.0	238	16	US-10-663-244-148
3	720	92.8	239	15	US-10-292-088-16
4	719	92.7	238	16	US-10-663-244-145
5	719	92.7	239	15	US-10-292-088-56
6	717	92.4	239	15	US-10-292-088-8
7	717	92.4	239	15	US-10-292-088-102
8	716	92.3	238	16	US-10-663-244-144
9	716	92.3	239	15	US-10-292-088-80
10	713	91.9	219	16	US-10-698-041-4
11	709	91.4	239	15	US-10-292-088-32
12	707.5	91.2	237	16	US-10-663-244-152
13	705	90.9	239	16	US-09-972-656-104

14	704	90.7	238	16	US-10-663-244-147
15	704	90.7	239	15	US-10-292-088-40
16	702	90.5	239	15	US-10-292-088-64
17	697.5	89.9	237	16	US-10-663-244-146
18	697.5	89.9	237	16	US-10-663-244-153
19	686	88.4	239	15	US-10-108-260A-4028
20	676	87.1	239	10	US-09-992-600A-8
21	676	87.1	239	10	US-09-924-340-8
22	676	87.1	239	10	US-09-992-095B-8
23	676	87.1	239	10	US-09-999-570-8
24	676	87.1	239	14	US-10-000-489-8
25	676	87.1	239	14	US-10-000-986-8
26	676	87.1	239	14	US-10-154-678-8
27	676	87.1	239	17	US-10-838-854-8
28	675	87.0	247	15	US-10-466-164-69
29	671	86.5	133	14	US-10-153-382-39
30	667.5	86.0	220	9	US-09-822-698A-24
31	666	85.8	219	10	US-09-972-656-106
32	660	85.1	219	10	US-09-972-656-94
33	657	84.7	239	15	US-10-404-724-12
34	657	84.7	239	17	US-10-816-276-8
35	650	83.8	239	15	US-10-404-724-49
36	650	83.8	239	17	US-10-816-276-45
37	642	82.7	239	15	US-10-404-724-41
38	642	82.7	239	15	US-10-404-724-45
39	642	82.7	239	17	US-10-816-276-37
40	642	82.7	239	17	US-10-816-276-41
41	640	82.5	239	15	US-10-404-724-43
42	640	82.5	239	15	US-10-404-724-47
43	640	82.5	239	17	US-10-816-276-39
44	640	82.5	239	17	US-10-816-276-43
45	632	81.4	239	15	US-10-404-724-10

ALIGNMENTS

RESULT 1

US-10-663-244-148  
; Sequence 148, Application US/10663244  
; Publication No. US20040110933A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac J.  
; APPLICANT: Edge, Albert  
; APPLICANT: Kent, Rachel Baribault  
; TITLE OF INVENTION: CD44 LIGANDS  
; FILE REFERENCE: 10280-063001  
; CURRENT APPLICATION NUMBER: US/10/663,244  
; CURRENT FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US 60/410,758  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: US 60/469,123  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 148  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
US-10-663-244-148

Query Match	93.2%	Score 723;	DB 16;	Length 238;
Best Local Similarity	95.2%	Pred. No. 1.1e-49;		
Matches 139;	Conservative 1;	Mismatches 6;	Indels 0;	Gaps 0;
Qy	1	LSLPVTGPSPASISCRSSQSLHSGNYLDWLKPGQSPOLLIYLGNSRAGVDPDRFS	60	
Db	28	LSLPVTGPSPASISCRSSQSLHSGNYLDWLKPGQSPOLLIYLGNSRAGVDPDRFS	87	
Qy	61	GGSGTDFTLKLSRVEADVGIIYCMQRTQTRTTCQGTKEIKRTVAAPSFIIPPSDE	120	

Db 88 GSGSGTDTFLKISRVEADVGVYCMQALQTPRTFTGGTKVEIKRTVAAPSVFIPPPSDE 147  
QY 121 QLKSGTASVWCLNNFYPREAKEHOK 146  
Db 148 QLKSGTASVWCLNNFYPREAKVQWK 173

## RESULT 2

US-10-663-244-149  
; Sequence 149, Application US/10663244  
; Publication No. US20040110933A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac J.  
; APPLICANT: Edge, Albert  
; APPLICANT: Kent, Rachel Baribault  
; TITLE OF INVENTION: CD44 LIGANDS  
; FILE REFERENCE: 10280-063001  
; CURRENT APPLICATION NUMBER: US/10/663,244  
; PRIOR FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US 60/410,758  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: US 60/469,123  
; PRIOR FILING DATE: 2003-05-09  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 149  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
US-10-663-244-149

Query Match 93.0%; Score 722; DB 16; Length 238;  
Best Local Similarity 95.2%; Pred. No. 1.4e-49;  
Matches 139; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPOLLIYLGSNRAGVDPDRFS 60  
Db 28 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPOLLIYLGSNRAGVDPDRFS 87  
QY 61 GSGSGTDTFLKISRVEADVGVYCMQALQTPRTFTGGTKVEIKRTVAAPSVFIPPPSDE 120  
Db 88 GSGSGTDTFLKISRVEADVGVYCMQALQTPWTFTGGTKVEIKRTVAAPSVFIPPPSDE 147  
QY 121 QLKSGTASVWCLNNFYPREAKEHOK 146  
Db 148 QLKSGTASVWCLNNFYPREAKVQWK 173

## RESULT 3

US-10-292-088-16  
; Sequence 16, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-088-16

Query Match 92.8%; Score 720; DB 15; Length 239;  
Best Local Similarity 94.5%; Pred. No. 2e-49;  
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPOLLIYLGSNRAGVDPDRFS 60  
Db 29 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPOLLIYLGSNRAGVDPDRFS 88  
QY 61 GSGSGTDTFLKISRVEADVGVYCMQALQTPRTFTGGTKVEIKRTVAAPSVFIPPPSDE 120  
Db 89 GSGSGTDTFLKISRVEADVGVYCMQALQTPRTFTGGTKVEIKRTVAAPSVFIPPPSDE 148  
QY 121 QLKSGTASVWCLNNFYPREAKEHOK 146  
Db 149 QLKSGTASVWCLNNFYPREAKVQWK 174

## RESULT 4

US-10-663-244-145  
; Sequence 145, Application US/10663244  
; Publication No. US20040110933A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac J.  
; APPLICANT: Edge, Albert  
; APPLICANT: Kent, Rachel Baribault  
; TITLE OF INVENTION: CD44 LIGANDS  
; FILE REFERENCE: 10280-063001  
; CURRENT APPLICATION NUMBER: US/10/663,244  
; CURRENT FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US 60/410,758  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: US 60/469,123  
; PRIOR FILING DATE: 2003-05-09  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 145  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
US-10-663-244-145

Query Match 92.7%; Score 719; DB 16; Length 238;  
Best Local Similarity 94.5%; Pred. No. 2.4e-49;  
Matches 138; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPOLLIYLGSNRAGVDPDRFS 60  
Db 28 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPOLLIYLGSNRAGVDPDRFS 87  
QY 61 GSGSGTDTFLKISRVEADVGVYCMQALQTPRTFTGGTKVEIKRTVAAPSVFIPPPSDE 120  
Db 88 GSGSGTDTFLKISRVEADVGVYCMQALQTPWTFTGGTKVEIKRTVAAPSVFIPPPSDE 147  
QY 121 QLKSGTASVWCLNNFYPREAKEHOK 146  
Db 148 QLKSGTASVWCLNNFYPREAKVQWK 173

## RESULT 5

US-10-292-088-56  
; Sequence 56, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US

```

: CURRENT APPLICATION NUMBER: US-10/292,088
: CURRENT FILING DATE: 2003-03-14
: PRIOR APPLICATION NUMBER: 60/348,980
: PRIOR FILING DATE: 2001-11-09
: NUMBER OF SEQ ID NOS: 147
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 56
: LENGTH: 239
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-292-088-56

```

Query Match	92.7%	Score 719;	DB 15;	Length 239;
Best Local Similarity	94.5%;	Pred. No. 2.4e-49;		
Matches 138; Conservative 2;	Mismatches 6;	Indels 0;	Gaps 0;	
Qy	1	LSLPVTGPEPASISCRSSOSLLHSGNYNYLDWYLQKPGSQPOLIYLGSNRCASGVPPRFS	60	
Db	29	LSLPVTGPEPASISCRSSQSLLYSGNYNYLDWYLQKPGQPHLLIYLGSNNRCSGVPPRFS	88	
Qy	61	GSQSGTDFTLLKISRVEAEDVGIIYVCMQTRPTPRFGQGTKEIKRTVAAPSVFIFPPSDE	120	
Db	89	GSQSGTDFTLLKISRVEAEDVGIIYVCMQALQTPRFGQGTKEIKRTVAAPSVFIFPPSDE	148	
Qy	121	QLKSGTASVVCLLNNFYPREAKEHQK	146	
Db	149	OLKSGTASVVCLLNNFYPREAKVQWK	174	

```

RESULT 6
US-10-232-088-8
; Sequence 8, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn ver. 2.1
;
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-8

```

	Query Match	92.4%;	Score 717;	DB 15;	Length 239;
	Best Local Similarity	93.8%;	Pred. 0.34e-49;		
	Matches 137; Conservative	4;	Mismatches 5;	Indels 0;	Gaps 0;
Qy	1 LSLPVTGEPASISCRSSQLLHSGNYNLDWYLKQPGSQPLLIIYLGSNRASGVPPRFS	60			
Dd	29 LSLPVTGEPASISCRSSQLLYNGYNFLDWYLKQPGSQPLLIIYLGSNRASGVPPRFS	88			
Qy	61 GSGSGDTFTLKISRVEADVGVIYCMTOPRTFGGTKEIKRTVAAPSVPFPPSPDE	120			
Dd	89 GSGSGDTFTLKISRLEADVGVVCMALQTPTFRFGGTKEIKRTVAAPSVPFPPSPDE	148			
Qy	121 QLSGTSASVCLLNFPYPREAKEHQK	146			
Dd	149 OLKSGETASVCLLNFPYPREAKVOWK	174			

RESULT 7  
US-10-292-088-102  
; Sequence 102, Application US/10292088

```

Publication No. US20030211000A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: ABX-PR/3 US
CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2003-03-
PRIOR APPLICATION NUMBER: 60/3
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 102
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-088-102

```

	Query Match	92.4%;	Score 717;	DB 15;	Length 239;
	Best Local Similarity	95.2%;	Pred. No. 3.4e-49;		
	Matches 139;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
Qy	1	LSLPVTGEPASISCRSSQSILHSHNGYNYLDWYLKPGQSPQLLIYLGNSRASGVDPFRFS	60		
Db	29	LSLPVTGEPASISCRSSQSLLPGNGYNYLDWYLKPGQSPQLLIYLGNSRASGVDPFRFS	88		
Qy	61	GSQSGDTFTLKISRVEAEDVGIIYCYMOTRPTPTFGQGTKEIKRTVAAPSVFIPPSPDE	120		
Db	89	GSQSGDTFTLKISRVEAEDVGIIYCYMAQLQTPRTPTFGQGTKEIKRTVAAPSVFIPPSPDE	148		
Qy	121	QLKSGTASVCLNNFYPREAKEHQK	146		
Db	149	OLKSGTASVCLNNFYPREAKVOWK	174		

```

RESULT 8
US-10-663-244-144
; Sequence 144, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated
US-10-663-244-144

```

```

Query Match      32.3%; Score 716; DB 16; Length 238;
Best Local Similarity 94.5%; Pred. No. 4.1e-49;
Matches 138; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LSPVTTGEPASISCRSSQSLHNSGNYNYLDWYLQKQPQLIYLGSNRASGVPRFS 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 28 LSLPVTGEPASISCRSSQSLHNSGNYNYLDWYLQKQPQLIYLGSNRASGVPRFS 87
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Ov 61 GSGSGTDTLLKISRVEABDVGIIYCYMOTRPTRTFGCTKVEIKRTVAAPSVFIPPSPDE 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```



```

; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-152

Query Match          91.2%; Score 707.5; DB 16; Length 237;
Best Local Similarity 94.5%; Pred. No. 1.9e-48;
Matches 137; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 2 SLPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRASGVDPDRFS 61
Db 29 SLPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRASGVDPDRFS 88

QY 62 GSGGTDFTLKISRVEAEDVGIYCMQTRPTFTGQGTKEIKRTVAAPSVFIIPPDSDEQ 121
Db 89 GSGGTDFTLKISRVEAEDVGIYCMQALQTP-TFGQGTKEIKRTVAAPSVFIIPPDSDEQ 147

QY 122 LKSGTASVCLLNPNFYPREAKEHOK 146
Db 148 LKSGTASVCLLNPNFYPREAKVQWK 172

RESULT 13
US-09-972-656-104
; Sequence 104, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deehpande, Rajendra
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE OF INVENTION: Neutralizing Activity
; CURRENT APPLICATION NUMBER: US/09/972,656
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 104
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-104

Query Match          90.9%; Score 705; DB 10; Length 219;
Best Local Similarity 91.8%; Pred. No. 2.8e-48;
Matches 134; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRASGVDPDRFS 60
Db 9 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRASGVDPDRFS 68

QY 61 GSGGTDFTLKISRVEAEDVGIYCMQTRPTFTGQGTKEIKRTVAAPSVFIIPPDSDE 120
Db 69 GSGGTDFTLKISRVEAEDVGIYCMQALQTP-TFTGQGTKEIKRTVAAPSVFIIPPDSDE 128

QY 121 QKSGTASVCLLNPNFYPREAKEHOK 146
Db 129 QKSGTASVCLLNPNFYPREAKVQWK 154

RESULT 14
US-10-663-244-147
; Sequence 147, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
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; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-147

Query Match          90.7%; Score 704; DB 16; Length 238;
Best Local Similarity 93.2%; Pred. No. 3.6e-48;
Matches 136; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRASGVDPDRFS 60
Db 28 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRASGVDPDRFS 87

QY 61 GSGGTDFTLKISRVEAEDVGIYCMQTRPTFTGQGTKEIKRTVAAPSVFIIPPDSDE 120
Db 88 GSGGTDFTLKISRVEAEDVGIYCMQALQTP-TFGQGTKEIKRTVAAPSVFIIPPDSDE 147

QY 121 QKSGTASVCLLNPNFYPREAKEHOK 146
Db 148 QKSGTASVCLLNPNFYPREAKVQWK 173

RESULT 15
US-10-292-088-40
; Sequence 40, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 40
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-40

Query Match          90.7%; Score 704; DB 15; Length 239;
Best Local Similarity 92.5%; Pred. No. 3.7e-48;
Matches 135; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRASGVDPDRFS 60
Db 29 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRASGVDPDRFS 88

QY 61 GSGGTDFTLKISRVEAEDVGIYCMQTRPTFTGQGTKEIKRTVAAPSVFIIPPDSDE 120
Db 89 GSGGTDFTLKISRVEAEDVGIYCMQVLTQPTFTGPTGKVDIKRTVAAPSVFIIPPDSDE 148

QY 121 QKSGTASVCLLNPNFYPREAKEHOK 146
Db 149 QKSGTASVCLLNPNFYPREAKVQWK 174

Search completed: March 8, 2005, 07:05:48
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Job time : 79.5397 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.2736 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-24

Perfect score: 776

Sequence: 1 LSLPVTGPGEASISCRSSQS.....VVCLLNFPYFAKEHQKSP 148

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A-COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B-COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS-COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	676	87.1	239	US-10-000-489-8	Sequence 8, Appli
2	671	86.5	133	US-09-472-087-26	Sequence 26, Appl
3	671	86.5	133	US-09-472-087-116	Sequence 116, App
4	621	80.0	239	US-08-487-550-6	Sequence 6, Appli
5	621	80.0	239	US-09-526-098-6	Sequence 6, Appli
6	621	80.0	239	US-09-383-916-6	Sequence 6, Appli
7	609	78.5	238	US-09-698-705-10	Sequence 10, Appl
8	591	76.2	139	US-09-472-087-25	Sequence 25, Appl
9	591	76.2	139	US-09-472-087-114	Sequence 114, App
10	585	75.4	218	US-09-698-705-12	Sequence 12, Appl
11	585	75.4	242	US-08-398-613A-56	Sequence 56, Appl
12	585	75.4	242	US-08-398-612A-56	Sequence 56, Appl
13	585	75.4	242	US-08-398-611A-56	Sequence 56, Appl
14	585	75.4	242	US-08-491-334A-56	Sequence 56, Appl
15	585	75.4	242	US-09-027-449-42	Sequence 42, Appl
16	585	75.4	242	US-08-804-444A-42	Sequence 42, Appl
17	585	75.4	242	US-09-026-985-42	Sequence 42, Appl
18	585	75.4	242	US-09-121-952A-42	Sequence 42, Appl
19	585	75.4	242	US-09-234-340A-42	Sequence 42, Appl
20	557	71.8	238	US-09-192-545-4	Sequence 4, Appli
21	550	70.9	173	PCR-US91-02942-3	Sequence 3, Appli
22	550	70.9	173	PCR-US91-02946-3	Sequence 3, Appli
23	548	70.6	222	US-09-479-614-26	Sequence 26, Appl
24	548	70.6	242	US-09-479-614-20	Sequence 20, Appl
25	547	70.5	216	US-09-254-180C-182	Sequence 182, App
26	546	70.4	216	US-09-254-180C-132	Sequence 132, App
27	546	70.4	216	US-09-254-180C-183	Sequence 183, App

28	545.5	70.3	240	4	US-09-301-593-36	Sequence 36, Appl
29	538.5	69.4	224	4	US-09-456-090A-82	Sequence 82, Appl
30	538.5	69.4	224	4	US-09-456-090A-88	Sequence 88, Appl
31	538.5	69.4	224	4	US-09-456-090A-90	Sequence 90, Appl
32	538.5	69.4	224	4	US-09-453-234-82	Sequence 82, Appl
33	538.5	69.4	224	4	US-09-453-234-88	Sequence 88, Appl
34	538.5	69.4	224	4	US-09-453-234-90	Sequence 90, Appl
35	538	69.3	219	3	US-09-027-449-72	Sequence 72, Appl
36	538	69.3	219	3	US-09-026-985-72	Sequence 72, Appl
37	538	69.3	219	4	US-09-121-952A-72	Sequence 72, Appl
38	538	69.3	219	4	US-09-234-340A-72	Sequence 72, Appl
39	538	69.3	239	4	US-09-627-896B-22	Sequence 22, Appl
40	538	69.3	242	3	US-09-027-449-51	Sequence 51, Appl
41	538	69.3	242	3	US-09-027-449-56	Sequence 56, Appl
42	538	69.3	242	3	US-09-027-449-62	Sequence 62, Appl
43	538	69.3	242	3	US-08-804-444A-51	Sequence 51, Appl
44	538	69.3	242	3	US-08-804-444A-56	Sequence 56, Appl
45	538	69.3	242	3	US-09-026-985-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1  
US-10-000-489-8  
; Sequence 8, Application US/10000489  
; Patent No. 6794363  
; GENERAL INFORMATION:  
; APPLICANT: Benjanin, Stephanie  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.US6.DIV  
; CURRENT APPLICATION NUMBER: US/10/000,489  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: US 09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: JPatent  
; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
US-10-000-489-8

Query Match 87.1%; Score 676; DB 4; Length 239;  
Best Local Similarity 89.7%; Pred. No. 1.1e-58;  
Matches 131; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy	1	LSLPVTGPGEASISCRSSQSLLHNSGNYLDWYLOKPGSQPOLLYLGSNRASGVDRFS	60
Db	29	LFLPVTGPGEASISCRSSQSLLHVQGSYLDWYHVKPGSQPOLLYLGSNRASGVDRFS	88
Qy	61	GGSGTDTFLKISRVEADVGIYCKMOTRQTPRTFGQGTKEIKRTVAAPSVFIIPPSDE	120
Db	89	GGSGTDTFLKISRVEADVGVYCMQALQTFPTFGTGRVTDIKRTVAAPSVFIIPPSDE	148
Qy	121	QLKSGTASVVCLLNNFPYFAKEHOK	146
Db	149	QLKSGTASVVCLLNNFPYFAKEVQWK	174

RESULT 2  
US-09-472-087-26  
; Sequence 26, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-26

Query Match 86.5%; Score 671; DB 4; Length 133;  
Best Local Similarity 95.5%; Pred. No. 1.7e-58;  
Matches 127; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 7 PGPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFSGSGGT 66  
DB 1 PGPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFSGSGGT 60  
  
QY 67 DFTLKISRVEADVGIYYCMQTRPTFTFGGKTKVEIKRTVAAPSVFIIPPSDEQLKSGT 126  
DB 61 DFTLKISRVEADVGIYYCMQALQTLTFTFGGKTKVEIKRTVAAPSVFIIPPSDEQLKSGT 120  
  
QY 127 ASVVCLLNNFYPR 139  
DB 121 ASVVCLLNNFYPR 133

RESULT 3  
US-09-472-087-116  
; Sequence 116, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 116  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-116

Query Match 86.5%; Score 671; DB 4; Length 133;  
Best Local Similarity 95.5%; Pred. No. 1.7e-58;  
Matches 127; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 PGPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFSGSGGT 66  
DB 1 PGPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFSGSGGT 60  
  
QY 67 DFTLKISRVEADVGIYYCMQTRPTFTFGGKTKVEIKRTVAAPSVFIIPPSDEQLKSGT 126  
DB 61 DFTLKISRVEADVGIYYCMQALQTLTFTFGGKTKVEIKRTVAAPSVFIIPPSDEQLKSGT 120  
  
QY 127 ASVVCLLNNFYPR 139  
DB 121 ASVVCLLNNFYPR 133  
  
RESULT 4  
US-08-487-550-6  
; Sequence 6, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,550  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-487-550-6

Query Match 80.0%; Score 621; DB 3; Length 239;  
Best Local Similarity 82.9%; Pred. No. 2.8e-53;  
Matches 121; Conservative 7; Mismatches 18; Indels 0; Gaps 0;  
  
QY 1 LSLPVTGPASISCRSSQSLHSHNGYNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 60  
DB 29 LSLPITGPASISCRSSQSLKSHNGDTFLSWYQKPGQPPRLLIYKVSNRDSGVDPDRFS 88  
  
QY 61 GSGSGTDTLTKISRVEADVGIYYCMQTRPTFTFGGKTKVEIKRTVAAPSVFIIPPSDE 120  
DB 89 GSGAGTDTLTKISAVEADVGVYFCGQGTPTFTFGGKTKVEIKRTVAAPSVFIIPPSDE 148  
  
QY 121 QKSGTASVVCLLNNFYPREAKEHOK 146  
DB 149 QKSGTASVVCLLNNFYPREAKVQWK 174



```

; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teekin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-383-916-6

Query Match 80.0%; Score 621; DB 4; Length 239;
Best Local Similarity 82.9%; Pred. No. 2.8e-53;
Matches 121; Conservative 7; Mismatches 18; Indels 0; Gaps 0

Qy 1 LSLPTTGPASISICRSQSLLHSNGVNYLDWLYQKGGQSPQLLIYLGNSRAGVDPRES 60
Db 29 LSLPTTGPASISICRSQSLLHSNGDTFLSLWYQQKPGQPRLLIYKVNRSRGVDPRES 88
Qy 61 GSGGTDTFLKISVAEADGVGYCMOTROTPTTFGGTKVEIKRTVAAPSVFIFPPSDE 120
Db 89 GSGGTDTFLKISVAEADGVGYCGGTPTPTTFGGTKVEIKRTVAAPSVFIFPPSDE 148
Qy 121 QLKSGTASVVCLLNNFYPREAKEHQK 146
Db 149 QLKSGTASVVCLLNNFYPREAKVQWK 174

RESULT 7
US-09-698-705-10
; Sequence 10, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P177R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 10
; LENGTH: 238

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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-10

Query Match          78.5%; Score 609; DB 4; Length 238;
Best Local Similarity 81.4%; Pred. No. 4.3e-52;
Matches 118; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 2 LSLPVTGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFS 61
Db 29 SVPVTPGESVTSICRSSKSLHNSGNTLYLWFLQRPQSPQLLIYRMSNLASGVDPDRFS 88

Qy 62 GSGGTDFTLKISRVEAEDVGIYCMQTRQTRTFGQGTKEIKRTVAAPSVFIFPPSDEQ 121
Db 89 GSGGTAFTLRISRVEAEDVGVYICLQHLEYPTFGGTKLEIKRTVAAPSVFIFPPSDEQ 148

Qy 122 LKSGTASVVCLLNNFYPREAKEHQK 146
Db 149 LKSGTASVVCLLNNFYPREAKVQWK 173

RESULT 8
US-09-472-087-25
; Sequence 25, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; FILE REFERENCE: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-25

Query Match          76.2%; Score 591; DB 4; Length 139;
Best Local Similarity 83.3%; Pred. No. 1.3e-50;
Matches 115; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 LSLPVTGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFS 60
Db 2 LSLPVTLGQPASISCRSSQSLVSDGNTYLNWFOQRPQSPRRLIYKVSNWDSGVDPDRFS 61

Qy 61 GSGGTDFTLKISRVEAEDVGIYCMQTRQTRTFGQGTKEIKRTVAAPSVFIFPPSDE 120
Db 62 GSGGTDFTLKISRVEAEDVGVYICMQGSHWPPPTFGQGTKEIKRTVAAPSVFIFPPSDE 121

Qy 121 QKSGTASVVCLLNNFYP 138
Db 122 QKSGTASVVCLLNNFYP 139

RESULT 10
US-09-698-705-12
; Sequence 12, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; FILE REFERENCE: PI777R1
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-12

Query Match          75.4%; Score 585; DB 4; Length 218;
Best Local Similarity 78.8%; Pred. No. 8.7e-50;
Matches 115; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Qy 1 LSLPVTGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFS 60
Db 9 LLSVITIGQPASISCKSSQSLSDSGKTYLNWLLQRPQSPKRLIYLVSTLDSGVDPDRFT 68

Qy 61 GSGGTDFTLKISRVEAEDVGIYCMQTRQTRTFGQGTKEIKRTVAAPSVFIFPPSDE 120
Db 69 GSGGTDFTLKISRVEAEDLVGYICWQGHFPTFGGTKLEIKRTVAAPSVFIFPPSDE 128
```

```
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-114

Query Match          76.2%; Score 591; DB 4; Length 139;
Best Local Similarity 83.3%; Pred. No. 1.3e-50;
Matches 115; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 LSLPVTGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFS 60
Db 2 LSLPVTLGQPASISCRSSQSLVSDGNTYLNWFOQRPQSPRRLIYKVSNWDSGVDPDRFS 61

Qy 61 GSGGTDFTLKISRVEAEDVGIYCMQTRQTRTFGQGTKEIKRTVAAPSVFIFPPSDE 120
Db 62 GSGGTDFTLKISRVEAEDVGVYICMQGSHWPPPTFGQGTKEIKRTVAAPSVFIFPPSDE 121

Qy 121 QKSGTASVVCLLNNFYP 138
Db 122 QKSGTASVVCLLNNFYP 139

RESULT 10
US-09-698-705-12
; Sequence 12, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; FILE REFERENCE: PI777R1
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-12

Query Match          75.4%; Score 585; DB 4; Length 218;
Best Local Similarity 78.8%; Pred. No. 8.7e-50;
Matches 115; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Qy 1 LSLPVTGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFS 60
Db 9 LLSVITIGQPASISCKSSQSLSDSGKTYLNWLLQRPQSPKRLIYLVSTLDSGVDPDRFT 68

Qy 61 GSGGTDFTLKISRVEAEDVGIYCMQTRQTRTFGQGTKEIKRTVAAPSVFIFPPSDE 120
Db 69 GSGGTDFTLKISRVEAEDLVGYICWQGHFPTFGGTKLEIKRTVAAPSVFIFPPSDE 128
```

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; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
; TITLE OF INVENTION: Treatment of Inflammatory Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,612A
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-Mar-1995
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-398-612A-56
;
; Query Match 75.4%; Score 585; DB 1; Length 242;
; Best Local Similarity 77.4%; Pred. No. 9.9e-50;
; Matches 113; Conservative 12; Mismatches 21; Indels 0; Gaps 0
;
; Qy 1 LSLPVTPEGPASISCRSSQSLHNGNYYLDWYLQKPGQSPQLLIYLGSNRAGVDPDRFS 60
; Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
; 32 LSLPSVLGDAQASISCRSSQSLVHGIGNTYLHWYLLQKPGQSPKLLIYKVSNRFGVDPDRFS 91
;
; Qy 61 GSGSGTDTLKLISRVEADLVCIYCMQTRQTPRTFGQGTKEIKRTVAAPSVEIFPPSDE 120
; Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
; 92 GSGSGTDTLKLISRVEADLVGLYFCQSQTHVPLTFGAGTKLELKRAVAAPTIVFIPTPSSE 151
;
; Qy 121 QLKSGTASVVCLLNNFYPREAKEHQK 146
; Db 152 QLKSGTASVVCLLNNFYPREAKVQWK 177
;
; RESULT 13
; US-08-398-611A-56
; Sequence 56, Application US/08398611A
; Patent No. 5702946
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
; TITLE OF INVENTION: of Inflammatory Disorders

```

```
;
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,611A
; FILING DATE: 01-Mar-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-398-611A-56

Query Match 75.4%; Score 585; DB 1; Length 242;
Best Local Similarity 77.4%; Pred. No. 9.9e-50;
Matches 113; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPOLLIIYLGNSRAGVDPDRFS 60
DB 32 LSLPVLGDAQSISCRSSQSLVHGIGNTYLLHWYLOKPGQSPKLLIYKVSNGFSGVDPDRFS 91
QY 61 GSGSGTDFTLKISRVEADGVIIYCMQTRPTFTGQTKVEIKRTVAAPSFIIPPSDE 120
DB 92 GSGSGTDFTLISRVEADGLYFCQSQSTHVPLTFGAGTKLEKRAVAAPTIVFIIPPSSE 151
QY 121 QKSGTASVCLNNFYPREAKEHQK 146
DB 152 QKSGTASVCLNNFYPREAKVQWK 177

RESULT 14
US-08-491-334A-56
; Sequence 56, Application US/08491334A
; Patent No. 5874080
; GENERAL INFORMATION:
; APPLICANT: Hebert, Caroline A.
; APPLICANT: Kabakoff, Rhona C.
; APPLICANT: Moore, Mark W.
; TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
; TITLE OF INVENTION: Disorders and Asthma
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,334A
; FILING DATE: 27-Jun-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-491-334A-56

Query Match 75.4%; Score 585; DB 2; Length 242;
Best Local Similarity 77.4%; Pred. No. 9.9e-50;
Matches 113; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPOLLIIYLGNSRAGVDPDRFS 60
DB 32 LSLPVLGDAQSISCRSSQSLVHGIGNTYLLHWYLOKPGQSPKLLIYKVSNGFSGVDPDRFS 91
QY 61 GSGSGTDFTLKISRVEADGVIIYCMQTRPTFTGQTKVEIKRTVAAPSFIIPPSDE 120
DB 92 GSGSGTDFTLISRVEADGLYFCQSQSTHVPLTFGAGTKLEKRAVAAPTIVFIIPPSSE 151
QY 121 QKSGTASVCLNNFYPREAKEHQK 146
DB 152 QKSGTASVCLNNFYPREAKVQWK 177

RESULT 15
US-09-027-449-42
; Sequence 42, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
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; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-027-449-42

Query Match 75.4%; Score 585; DB 3; Length 242;
Best Local Similarity 77.4%; Pred. No. 9.9e-50;
Matches 113; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 LSLPVTGPSPASTICRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLGSNRASGVDPDRFS 60
   |||: |: |||||: |||: |||||: |||: |||||: |||: |||||: |||: |||||:
Db 32 LSLPWSLQDASISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNRFSGVDPDRFS 91
QY 61 GSGSGTDFTLKISRVEAEDVGIIYCMQTRPTFCQGTKEIKRTVAAPSVEFIPPPSDE 120
   |||||: |||||: |||||: |||: |: |||||: |||: |||||: |||: |||||:
Db 92 GSGSGTDFTLRISRVEAEDGLYFCSQSTHVPLTFGAGTKLELKRAVAAPTVEFIPPPSSE 151
QY 121 QLKSGTASVVCLNNFYPREAKEHOK 146
   |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 152 QLKSGTASVVCLNNFYPREAKVQWK 177
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Search completed: March 8, 2005, 05:53:52  
Job time : 17.2736 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 14.0007 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-25

Perfect score: 1039

Sequence: 1 LVKPSSETLSLTCTVSGGSIS.....SQVLLPSKDVMOGTDEHKVC 197

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	900.5	86.7	231	2 B23746	Ig Fab region IV-J
2	709	68.2	627	2 S14683	Ig mu chain precu
3	569	54.8	592	2 S25705	Ig mu chain - shee
4	544.5	52.4	220	2 A49444	Ig gamma-i heavy c
5	520	50.0	140	2 I37782	Ig variable region
6	520	50.0	143	2 B49028	Ig heavy chain V-I
7	515	49.6	288	2 S29690	Ig heavy chain VDJ
8	507	48.8	130	2 S31690	Ig heavy chain V r
9	491	47.3	155	2 S31511	Ig heavy chain - h
10	489	47.1	155	2 S31512	Ig heavy chain - h
11	486	46.8	147	2 S33519	Ig heavy chain V r
12	484.5	46.6	139	2 S31586	Ig heavy chain V r
13	481.5	46.3	137	2 S31676	Ig heavy chain V r
14	480.5	46.2	130	2 S30534	Ig heavy chain V r
15	479	46.1	140	2 A49045	Ig heavy chain V r
16	471	45.3	121	2 S44113	Ig heavy chain V r
17	471	45.3	139	2 S31696	Ig heavy chain V r
18	469.5	45.2	118	2 S20780	Ig heavy chain V r
19	469.5	45.2	140	2 S78052	Ig heavy chain pre
20	463.5	44.6	568	2 A34891	Ig heavy chain pre
21	463	44.6	116	2 S37456	Ig mu chain - huma
22	462.5	44.5	110	2 S44110	Ig heavy chain V-D
23	460.5	44.3	470	2 S22080	Ig heavy chain pre
24	460	44.3	135	2 S78051	Ig heavy chain pre
25	459.5	44.2	139	2 S44114	Ig heavy chain V r
26	458	44.1	124	2 S54906	Ig heavy chain V r
27	457	44.0	105	2 S44125	Ig lambda chain V
28	457	44.0	109	2 PH1673	Ig heavy chain V r
29	456	43.9	97	2 S26906	Ig heavy chain V r

30	455	43.8	116	2 B26340	Ig heavy chain pre
31	455	43.8	123	2 S30530	Ig heavy chain V r
32	454.5	43.7	126	2 S47010	Ig heavy chain V r
33	453	43.6	97	2 S12416	Ig heavy chain V r
34	452	43.5	146	2 S09711	Ig heavy chain V r
35	452	43.5	452	1 MHHU	Ig mu chain C regi
36	452	43.5	453	2 S37768	Ig mu chain C regi
37	452	43.5	473	1 MHHUM	Ig mu chain C regi
38	452	43.5	474	2 S15590	Ig heavy chain - h
39	451.5	43.5	145	2 S78055	Ig heavy chain pre
40	445.5	42.9	118	2 S24443	Ig heavy chain V r
41	444	42.7	118	2 A26340	Ig heavy chain pre
42	441	42.4	146	2 S09710	Ig heavy chain V r
43	439.5	42.3	231	2 PC4155	Ig heavy chain V r
44	438	42.2	99	2 S12412	Ig heavy chain V r
45	437	42.1	114	2 I72667	cold agglutinin FS

ALIGNMENTS

RESULT 1

B23746

Ig Fab region IV-J (H4)-C (KAU cold agglutinin) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000

C:Accession: B23746

R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.

J. Biol. Chem. 266, 2836-2842, 1991

A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin

A:Reference number: A23746; MUID:91131575; PMID:1993660

A:Accession: B23746

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-231 <LEO>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F140-209/Domain: immunoglobulin homology <IMW>

Query Match 86.7%; Score 900.5; DB 2; Length 231;

Best Local Similarity 88.9%; Pred. No. 8e-62;

Matches 176; Conservative 5; Mismatches 16; Indels 1; Gaps 1;

Qy	1	LVKPSSETLSLTCTVSGGSIS	YNNWIROPKGLWIGYIYSGSTNNP	SLKSRVTIS	60
Db	10	LLKPSSETLSLTGAVYGGSF	SDYYNSWIRPPKGLWIGIHNHSGSTNNP	SLKSRVTIS	69
Qy	61	VDTSKNQPSLKLSVTAADTAV	YVCAR-DRGVGATGFDYWGQGLTV	VSSGSASAPTLFP	119
Db	70	VDTSKNQPSLKLSVTAADTAV	YVCARPPHDTSGHYWYWGQGLTV	VSSGSASAPTLFP	129
Qy	120	LVSCNSPDSSTSSVAVGCLAQ	DFLPDSITFSWKYKNNSDIS	TRGFPVSLRGKYAATSQ	179
Db	130	LVSCNSPDSSTSSVAVGCLAQ	DFLPDSITFSWKYKNNSDIS	TRGFPVSLRGKYAATSQ	189
Qy	180	VLLPSKDVMOGTDEHKVC	197		
Db	190	VLLPSKDVMOGTDEHVVC	207		

RESULT 2

S14683

Ig mu chain precursor, membrane-bound (clone 201) - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999

C:Accession: S14683; S08047

R:Friedlander, R.M.; Nussenzeig, M.C.; Leder, P.

Nucleic Acids Res. 18, 4278, 1990

A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.

A:Reference number: S14683; MUID:90332450; PMID:2115996

A:Accession: S14683

A:Molecule type: mRNA

A:Residues: 1-827 <PRI>

A:Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451





	100%	Conservative	37	Mismatches	19	Indels	10	Gaps	2
Qy	1	LVKSETLSLTCTVSGSISYYNNWIRQPGKGLEWTGYIYVGSTNYPNLSKSRVTIS	60	:					
Db	11	LLKPESETLSLTCAYVGGFSGYYSWIRQPPKGREWGTEINHSGSTNYPNLSKSRVTIS	70	:					
Qy	61	VDTSEKNQPSLKSSVTAADTAVVYCARD-----RGVG-ATGFDYWGOGTLVTVSSG	110	:					
Db	71	VDTSEKNQPSLKSSVTAADTAVVYCARGPIVVVPAMRGRGWIDYWGOGTVTVTVSSG	130	:					
Qy	111	SASAPTLFPPLVSC	123	:					
Db	131	SRSAPTLFPPLVSC	143	:					

RESULT 9  
S31511  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C/Accession: S31511  
R:Chastagner, P.; Demaison, C.; These, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto-  
A:Reference number: S31509  
A:Accession: S31511  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-155 <CHA>  
A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PTD:g33095  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:47-129/Domain: immunoglobulin homology <IMM>

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Query Match      47.3%; Score 491; DB 2; Length 155;
Best Local Similarity 83.2%; Pred. No. 1e-30;
Matches 94; Conservative 5; Mismatches 10; Indels 4; Gaps 1;

Qy 1 LVKSETLSLCTVSGGSISSYYWNIROPPKGLIEWIGYIYSGSNYNPSLKSRTVIS 60
    |||||
Db 43 LVKPSETLSLCTVSGGSISSYYWNIROPPKGLIEWIGYIYSGSNYNPSLKSRTVIS 102
    |||||

Qy 61 VDTSKNQPSFLKLSSTVAADTAVYYCARDRGVGA---TGFDFYMGQGLFTVTVSS 109
    |||||
Db 103 VDTSKNQPSFLKVVSTVAADTAVYYCARGGGISWYDYNGMDVMGQGLTFTVTVSS 155
    |||||

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Submitted to the EMBO Data Library, December, 1992  
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies in murine SLE  
A:Reference number: S31509  
A:Accession: S31512

A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <CHA>  
A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 47.1%; Score 489; DB 2; Length 155;  
Best Local Similarity 82.3%; Pred. No. 1.4e-30;  
Matches 93; Conservative 6; Mismatches 10; Indels 4; Gaps 1;

Qy 1 LVKPSLTLCTCTVSGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVTIS 60  
Db 43 LVKPSLTLCTCTVSGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVTIS 102  
Qy 61 VDTSKNQFSLKLSVTAADTAATVYCCARDRGVGA----TGFDPVWGQGLTVTVSS 109  
Db 103 VDTSKNQFSLKLSVTAADTAATVYCCARGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVTIS 155

RESULT 11  
S31519  
Ig heavy chain V region precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31519  
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked  
A;Reference number: S31519; MUID:91187691; PMID:2011536  
A;Accession: S31519  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-147 <MOR>  
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 46.8%; Score 486; DB 2; Length 147;  
Best Local Similarity 88.3%; Pred. No. 2.3e-30;  
Matches 98; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

Qy 1 LVKPSLTLCTCTVSGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVT 58  
Db 37 LVKPSLTLCTCTVSGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVT 96  
Qy 59 ISVDTSKNQFSLKLSVTAADTAATVYCCARDRGVGAATGPDYWGQGLTVTVSS 109  
Db 97 ISVDTSKNQFSLKLSVTAADTAATVYCCARPLWFGELFDYWGQGLTVTVSS 147

RESULT 12  
S31586  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31586  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31586  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-139 <CUI>  
A;Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 46.6%; Score 484.5; DB 2; Length 139;

Best Local Similarity 86.4%; Pred. No. 2.8e-30;  
Matches 95; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

Qy 1 LVKPSLTLCTCTVSGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVTIS 60  
Db 30 LVKPSLTLCTCTVSGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVTIS 89  
Qy 61 VDTSKNQFSLKLSVTAADTAATVYCCARDRGVGAATGPDYWGQGLTVTVSS 109  
Db 90 VDTSKNQFSLKLSVTAADTAATVYCCARGGLIRGAFDINGQGTWTVTVSS 139

RESULT 13  
S31676  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31676  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31676  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-137 <CUI>  
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 46.3%; Score 481.5; DB 2; Length 137;  
Best Local Similarity 87.2%; Pred. No. 4.7e-30;  
Matches 95; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Qy 1 LVKPSLTLCTCTVSGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVTIS 60  
Db 30 LVKPSLTLCTCTVSGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVTIS 89  
Qy 61 VDTSKNQFSLKLSVTAADTAATVYCCARDRGVGAATGPDYWGQGLTVTVSS 109  
Db 90 VDTSKNQFSLKLSVTAADTAATVYCCARDAPL-MYGMVDYWGQGLTVTVSS 137

RESULT 14  
S30534  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Aug-1996  
C;Accession: S30534  
R;Mariette, X.  
submitted to the EMBL Data Library, October 1992  
A;Reference number: S30520  
A;Accession: S30534  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-130 <MAP>  
A;Cross-references: EMBL:Z18320  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 46.2%; Score 480.5; DB 2; Length 130;  
Best Local Similarity 80.8%; Pred. No. 5.3e-30;  
Matches 97; Conservative 5; Mismatches 7; Indels 11; Gaps 2;

Qy 1 LVKPSLTLCTCTVSGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVT 58  
Db 11 LVKPSLTLCTCTVSGGSISSYYWNIROPKGLWIGYIYSGSTNPNPSLKSRVT 70  
Qy 59 ISVDTSKNQFSLKLSVTAADTAATVYCCARDRGVGAATG-----FDYWGQGLTVTVSS 109  
Db 71 ISVDTSKNQFSLKLSVTAADTAATVYCCARDGGFWGYYTRNSRAAFDINGQGTWTVTVSS 130

## RESULT

F/34-116/DOMAIL: IMMUNOGLOBULIN MONOCLONAL <IMM>

Job time : 15.0507 sec8

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 73.5696 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-25

Perfect score: 1039

Sequence: 1 LVKPSSETLSLCTVSGSGSIS.....SQVLLPSKVMQGTDEHKVC 197

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_eprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	925.5	89.1	620	Q96EY0	Q96EY0 homo sapien
2	892	85.9	595	Q8WUX4	Q8WUX4 homo sapien
3	892	85.9	597	Q6GMX5	Q6GMX5 homo sapien
4	892	85.9	597	Q9BU10	Q9BU10 homo sapien
5	892	85.9	625	Q96AA6	Q96AA6 homo sapien
6	886	85.3	597	Q9BQB8	Q9BQB8 homo sapien
7	760.5	73.2	613	Q8WUK1	Q8WUK1 homo sapien
8	760	73.1	597	Q96BB9	Q96BB9 homo sapien
9	759.5	73.1	606	Q6GMV2	Q6GMV2 homo sapien
10	614	59.1	465	Q6GMX6	Q6GMX6 homo sapien
11	596.5	57.4	476	Q6GMX1	Q6GMX1 homo sapien
12	562	54.1	477	Q6GMX7	Q6GMX7 homo sapien
13	554.5	53.4	614	Q7TWT6	Q7TWT6 mus musculus
14	554	53.3	576	Q6P4I8	Q6P4I8 homo sapien
15	553	53.2	478	Q72379	Q72379 homo sapien
16	542	52.2	613	Q8VCX7	Q8VCX7 mus musculus
17	541	52.1	496	Q96KX8	Q96KX8 homo sapien
18	526.5	50.7	492	Q72374	Q72374 homo sapien
19	518.5	49.9	478	Q6NYH3	Q6NYH3 homo sapien
20	512.5	49.3	473	Q8TC63	Q8TC63 homo sapien
21	500.5	48.2	150	Q95973	Q95973 homo sapien
22	498	47.9	119	Q9UL73	Q9UL73 homo sapien
23	494	47.5	479	Q99M22	Q99M22 mus musculus
24	492	47.4	476	Q6MZK7	Q6MZK7 homo sapien
25	462	44.5	139	Q86SX2	Q86SX2 homo sapien
26	462	44.5	605	Q6GN83	Q6GN83 xenopus lae
27	457.5	44.0	482	Q91X92	Q91X92 mus musculus
28	452	43.5	454	1 MUC_HUMAN	P01871 homo sapien
29	434.5	41.8	464	Q6MZU6	Q6MZU6 homo sapien
30	433.5	41.7	593	Q6INM5	Q6INM5 xenopus lae
31	431.5	41.5	146	1 HV21_HUMAN	P06331 homo sapien

#### RESULT 1

ID	Q96EY0	PRELIMINARY;	PRT;	620 AA.
AC	Q96EY0.			
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DE	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	IGHM protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RX	MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RA	Strausberg R.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC011857; AAH1857.2; -.			
DR	PIR; S15590; S15590.			
DR	HSSP; P01820; 1G7J.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig.C1.			
DR	InterPro; IPR003006; Ig.MHC.			
DR	InterPro; IPR003596; Ig.V.			
DR	Pfam; PF07654; C1-set; 4.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGc1; 4.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 5.			

#### ALIGNMENTS

32	428.5	41.2	225	2	Q6PAF5	Q6paf5 xenopus lae
33	420.5	40.5	572	2	Q66IQ7	Q66iq7 xenopus lae
34	419.5	40.4	465	2	Q6P6C4	Q6p6c4 homo sapien
35	418.5	40.3	130	2	Q8IZD7	Q8izd7 homo sapien
36	418	40.2	614	2	Q6DDO7	Q6ddq7 xenopus lae
37	416.5	40.1	466	2	Q6IN78	Q6in78 homo sapien
38	416	40.0	129	1	HV2F_HUMAN	P01824 homo sapien
39	415.5	40.0	470	2	Q6PJA4	Q6pja4 homo sapien
40	411.5	39.6	518	2	Q6N030	Q6n030 homo sapien
41	408	39.3	116	2	Q723Y6	Q723y6 homo sapien
42	406.5	39.1	480	2	Q6N094	Q6n094 homo sapien
43	402	38.7	473	2	Q6MZV7	Q6mzv7 homo sapien
44	399	38.4	544	2	Q6PJ95	Q6pj95 homo sapien
45	398.5	38.4	472	2	Q6N089	Q6n089 homo sapien



```

DR Pfam: PF00047; ig: 4.
DR SMART: SM00409; ig: 2.
DR SMART: SM00407; igc1: 4.
DR SMART: SM00406; igv: 1.
DR PROSITE: PS00835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6ABD85230 CRC64;

Query Match      85.9%; Score 892; DB 2; Length 597;
Best Local Similarity 86.7%; Pred. No. 1.1e-70;
Matches 176; Conservative 3; Mismatches 18; Indels 6; Gaps 2;

QY 1 LKPSSETLSLCTCTVGGSGISSYWNWIRPPKGLWIGIYIYSGSTNNPSLKSRTVIS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 30 LKPSSETLSLCTCGVYGGSPGYWWSIRPPKGLWIGIYIYSGSTNNPSLKSRTVIS 89
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VDTSKNQPSLKLSSVTAADTAVYYCAR-----DRGV-GATGPDYWGQGLTVTVSSGSASA 114
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 90 VDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMVWGQGLTVTVSSGSASA 149
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 PTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSSTRGFPVSLRGKKY 174
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 150 PTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSSTRGFPVSLRGKKY 209
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 AATSOVLLPSKDVMOGQTDHKKVC 197
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 210 AATSOVLLPSKDVMOGQTDHKKVC 232
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
Q9BU10 PRELIMINARY; PRT; 597 AA.
ID Q9BU10
AC Q9BU10;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC02963; AA02963.1; -.
DR HSSP; F01861; IADQ.

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[2]
RA SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC020240; RAH20240.1; -.
DR PIR: F36005; F36005.
DR PIR: G36005; G36005.
DR PIR: PH1642; PH1642.
DR PIR: PH1643; PH1643.
DR PIR: PH1645; PH1645.
DR PIR: PH1646; PH1646.
DR PIR: PH0098; PH0098.
DR PIR: PH0120; PH0120.
DR PIR: S15590; S15590.
DR PIR: S31116; S31116.
DR PIR: S31119; S31119.
DR PIR: S70442; S70442.
DR HSP: F01861; LADQ.
DR Pfam: PF07654; Cl-set; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 3.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67295 MW; 60CF5950671E315 CRC64;

Query Match 73.2%; Score 760.5; DB 2; Length 613;
Best Local Similarity 74.2%; Pred. No. 5.4e-59;
Matches 147; Conservative 15; Mismatches 35; Indels 1; Gaps 1;

QY 1 LVKPSSETLCTVSGGSISSYWNWIRQPGKGLEWIGYIYSGSTN-YNPSLKSRTVI 59
DB 30 VVQPGSLRLSCAASGFTSFSSYGMHWVRQAPGKLEWVAISYDGSNKYIADSVKGRFTI 89
QY 60 SVDTSKNPSLKSSTVAADTAIVYCARDRGVGTGFDYWGQGLTVTVSSGSASAPTLP 119
DB 90 SRDNSKNTLYLQNSLRADTAIVYCAKDWSGVETFDWGQGTWTVSSGSASAPTLP 149
QY 120 LVSCNSPSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQ 179
DB 150 LVSCNSPSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQ 209
QY 180 VLLPSKDVMOGTDEHKVC 197
DB 210 VLLPSKDVMOGTDEHVVC 227

RESULT 8
Q36BB9 PRELIMINARY; PRT; 597 AA.
AC Q36BB9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-NAR-2004 (Tremblrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

[2]
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015760; AAH15760.1; -.
DR PIR: S05271; S05271.
DR PIR: S24260; S24260.
DR HSP: F01861; LADQ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF07654; Cl-set; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 3.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E263D9 CRC64;

Query Match 73.1%; Score 760; DB 2; Length 597;
Best Local Similarity 75.4%; Pred. No. 5.8e-59;
Matches 153; Conservative 14; Mismatches 30; Indels 6; Gaps 3;

QY 1 LVKPSSETLCTVSGGSISSYWNWIRQPGKGLEWIGYIYSGSTN-YNPSLKSRTVI 59
DB 30 LVQPGSLRLSCAASGFTSFSSYGMHWVRQAPGKLEWVAISYDGSNKYIADSVKGRFTI 89
QY 60 SVDTSKNPSLKSSTVAADTAIVYCARD-RGVGTG----FDYWGQGLTVTVSSGSASA 114
DB 90 SRDNSRDTLYLQNSLRADTAIVYCAKDPGYSASGNVYTRDYWGQGLTVTVSSGSASA 149
QY 115 PTLFPLVSCNSPSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGPPSVLRGGKY 174
DB 150 PTLFPLVSCNSPSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGPPSVLRGGKY 209
QY 175 AATSQVLLPSKDVMOGTDEHKVC 197
DB 210 AATSQVLLPSKDVMOGTDEHVVC 232

RESULT 9
Q6GMV2 PRELIMINARY; PRT; 606 AA.
AC Q6GMV2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
```

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC TISSUE=Primary B-Cells;
RP Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B638B51114E4C55 CRC64;

Query Match 73.1%; Score 759.5; DB 2; Length 606;
Best Local Similarity 71.7%; Pred. No. 6.6e-59;
Matches 152; Conservative 12; Mismatches 33; Indels 15; Gaps 3;

QY 1 LVKPSLTLCTVSGSGSSSYNNWIRPPGKGLWIGIYSGS-TYNPPLSKSRVTI 59
DB 30 LVKPGSLRLSCAAGSPTFDYMWIRQAPGKGLWISYSSSSYNYADSVKGRFTI 89
QY 60 SVDTSKNQPSLKLSSVTAADTAVVYCAR-DRGVGAT-----GFDYWGQGTIV 105
DB 90 SRDNAKSLYLQWNLRAEDTAVVYCARGGNGIAAGRVVYAEYDYYVGMVWGQGTIV 149
QY 106 TVSSGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGF 165
DB 150 TVSSGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGF 209
QY 166 PSVLGGKYAATSQVLLPSKDVMOGTDHVKC 197
DB 210 PSVLGGKYAATSQVLLPSKDVMOGTDHVKC 241

RESULT 10
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC TISSUE=Primary B-Cells;
RP Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 59.1%; Score 614; DB 2; Length 465;
Best Local Similarity 64.1%; Pred. No. 4.1e-46;
Matches 127; Conservative 20; Mismatches 41; Indels 10; Gaps 6;

QY 1 LVKPSLTLCTVSGSGSSSYNNWIRPPGKGLWIGIYSGSTYNPPLSKSRVTIS 60
DB 30 LVKPSLTLCTVSGSGSSSYNNWIRPPGKGLWIGIYSGSTYNPPLSKSRVTIS 89
QY 61 VDTSKNQPSLKLSSVTAADTAVVYCARDRGVGATGFDYWGQGTIVTVSSGSASAPTLFPL 120
DB 90 VDTSKNQPSLKLSSVTAADTAVVYCARGR---FTYFDYWGQGTIVTVSSASTKGPSVPL 146
QY 121 VSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPSVLR-GGKYAATSQ 179
DB 147 APSSKSTSG-GTAAAGCLVKDIFPEPVTWSV-NSGALTSGVHTFPAVLQSSGLYSLSSV 203
QY 180 VLLPSKDVMOGTDHVKC 197
DB 204 VTFSSSL--GTQTY-IC 218

RESULT 11
Q6GMX1 PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RC TISSUE-Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Spleen;  
RA Strausberg R.;  
DR EMBL; BC073773; AAH73773.1; -  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF00047; IG; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;  
Query Match 57.4%; Score 596.5; DB 2; Length 476;  
Best Local Similarity 59.7%; Pred. No. 1.5e-44;  
Matches 123; Conservative 26; Mismatches 42; Indels 15; Gaps 7;  
QY 1 LVKPSSETLSLCTVSGSGTSS--YYNNWIRQPPGKLEWIGYIYSGSTNNPNSLKSRVT 58  
DB 30 LVKPSQTLSTCTVSGSGISSGGDYNSWIRQPPGKLEWIGYIYSGSTNNPNSLKSRVT 89  
QY 59 ISVDTSKNQFSLKLSVTAADTAVYICARD-----RGVATGFDYWGQGLTVTVSSGSA 112  
DB 90 ISLDTSKNQFSLKMSVTAADTAVFCARAGWGSFRSWAIDGFIWGGTWTWVSSAST 149  
QY 113 SAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSTFTFSWKYKNSDIDSTRGFPVLR-G 171  
DB 150 KGPSVFPPLAPSSKSTSG-GTAAIGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSS 206  
QY 172 GKVAATSOVLPLSKDVMQGTDEHKV 197  
DB 207 GLYSUSSVVTVFPSSSL--GTQTY-IC 229  
RESULT 12  
ID Q6GMX7 PRELIMINARY; PRT; 477 AA.  
AC Q6GMX7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Primary B-Cells;  
RA Strausberg R.;  
DR EMBL; BC073765; AAH73765.1; -  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR Pfam; PF07654; Cl-set; 2.  
DR Pfam; PF00047; IG; 3.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;  
Query Match 54.1%; Score 562; DB 2; Length 477;  
Best Local Similarity 60.6%; Pred. No. 1.8e-41;  
Matches 120; Conservative 22; Mismatches 38; Indels 18; Gaps 7;  
QY 1 LVKPSSETLSLCTVSGSGTSS--YYNNWIRQPPGKLEWIGYIYSGSTNNPNSLKSRVTIS 60  
DB 30 LVKPSSETLSLCTVSGSGTSS--YYNNWIRQPPGKLEWIGYIYSGSTNNPNSLKSRVTLS 89  
QY 61 VDTSKNQFSLKLSVTAADTAVYICARDGVGAT---GFDYWGQGLTVTVSSGSAAPTL 117  
DB 90 LDTSKNQFSLRLNSVTAADTAVYICAH---GSSWDFAFDYGQGLTVTVSSASPTSPKV 145  
QY 118 PFLVSCNSPDSSTSSVAVGCLAQDFLPD---SITFSWKYKNSDIDSTRGFP--SVLRGG 172  
DB 146 PFL-SLSDTPD-GNVVAVCLVQGFPPQEPFLSVTWSESGQN----VTARNFPSPQDASGD 199  
QY 173 KYAATSOVLPLSKDVMQOG 190  
DB 200 LYTTSSQLTLPATQCPDG 217  
RESULT 13  
ID Q7TWT6 PRELIMINARY; PRT; 614 AA.  
AC Q7TWT6;

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DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE MG60843 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAH53409.1; -.
DR HSSP; P01820; 1G77.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
DR SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;

Query Match 53.4%; Score 554.5; DB 2; Length 614;
Best Local Similarity 52.8%; Pred. No. 1.1e-40;
Matches 105; Conservative 39; Mismatches 52; Indels 3; Gaps 3;

Qy 1 LVKPSLTLCTVSGSGSISSYYNNWIRQPPGKLEWIGYIY-YSGSTNYPNPSLKSRTYI 59
Db 30 LVKPGASVKISCKASGYAFSSSMWVQRPGKLEWIGRVYPGDNTYNGKFGKATL 89
Qy 60 SVDTSKNQFSLKLSVTAADTAVYVCARDRGVGTGPDYWGQGTLLVTVSSGSASAPTLP 119
Db 90 TADKSSSTAYMQLSLTSEDSAVYFCARDYG--SSYRFAYWGQGTLLVTVSAESQSFPNVP 148
Qy 120 LVSCNPSDTSVAVGCLAQDFLPSDITFSWKYKNNSD-LSSTRGPPSVLRGGKYAATS 178
Db 149 LVSCPSLSDKNLVAMGCLARDFLPSITISFTWYQNNAEVIQGITFTFLTGGKYLATS 208
Qy 179 QVLLPSKDVMOQTDEHKVC 197
Db 209 QVLLSPKSILEGSDYLVC 227

PRELIMINARY; PRT; 576 AA.

RESULT 14
Q6P4I8
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AC Q6P4I8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE IGHD protein.
GN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00407; Igv; 1.
DR SMART; SM00409; Igv; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Query Match 53.3%; Score 554; DB 2; Length 576;
Best Local Similarity 59.9%; Pred. No. 1.1e-40;
Matches 118; Conservative 16; Mismatches 57; Indels 6; Gaps 4;

Qy 1 LVKPSLTLCTVSGSGSI-SSYYNNWIRQPPGKLEWIGYIYSGSTNYPNPSLKSRTYI 59
Db 37 LVKPSGTLTLCAVSGSGSISSSNWVQRPPGKLEWIGIYHSGSTNYPNPSLKSRTYI 96
Qy 60 SVDTSKNQFSLKLSVTAADTAVYVCARDRGVGTGPDYWGQGTLLVTVSSGSASAPTLP 119
Db 97 SVDKSKNQFSLKLSVTAADTAVYVCASLGIYYGMDVWGQGTFTVTSSAPTAPDVP 156
Qy 120 LVSCNPSDTSVAVGCLAQDFLPSDITFSWKYKNNSDISSTRGFPVLRGGKYAAT-S 178
Db 157 IISGRHPKNSPVVLACLITGYHTSVTVTWYMGTS--QPQRTFPIQRDSYWTSS 214
Qy 179 QVLLPSKDVMOQTDEHK 195

PRELIMINARY; PRT; 576 AA.
```



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 91.3346 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-25

Perfect score: 1039  
Sequence: 1 LVKPSFTLSLCTVSGGIS.....SQVLLPSKDVNQGTDEHKVC 197

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1039	100.0	197	2 AAY34300	Aay34300 IgM antib
2	889.5	85.6	205	2 AAY34299	Aay34299 IgM antib
3	880.5	84.7	190	2 AAY34304	Aay34304 IgM antib
4	854.5	82.2	202	2 AAY34303	Aay34303 IgM antib
5	753.5	72.5	223	2 AAY08598	Aay08598 Anti-huma
6	751	72.3	266	8 ADP69305	Adp69305 Human lun
7	750.5	72.2	596	4 ADL23924	Adl23924 Human EST
8	747.5	71.9	223	8 ADL70773	Adl70773 Anti-TNFA
9	746.5	71.8	588	2 AAW71880	Aaw71880 Anti-huma
10	746.5	71.8	588	3 AAB12917	Aab12917 Anti-huma
11	743	71.5	228	8 ADL70776	Adl70776 Anti-TNFA
12	732.5	70.5	588	2 AAW71881	Aaw71881 Anti-huma
13	732.5	70.5	588	3 AAB12918	Aab12918 Anti-huma
14	730.5	70.3	533	7 ADB65070	Adb65070 Human lmm
15	709	68.2	627	7 ADE97370	Ade97370 Human lmm
16	708.5	68.2	595	7 ADM05427	Adm05427 Human pro
17	702.5	67.6	571	8 ADP84970	Adp84970 Chimeric
18	698	67.2	199	2 AAY34302	Aay34302 IgM antib
19	698	67.2	203	2 AAY34301	Aay34301 IgM antib
20	692.5	66.7	569	8 ADL19330	Adl19330 Chimeric
21	689	66.3	570	8 ADL19329	Adl19329 Chimeric
22	634	61.0	466	7 ADE28419	Ade28419 Human ant
23	633.5	61.0	241	8 ADE584432	Ade584432 Human ant
24	633.5	61.0	241	8 ADR68574	Adr68574 Human ant
25	633	60.9	466	7 ADE28479	Ade28479 Human ant

26	631	60.7	466	7 ADE28471	Ade28471 Human ant
27	626.5	60.3	230	7 ADJ32118	Adj32118 Human int
28	622.5	59.9	241	8 ADS84467	Ads84467 Human ant
29	622.5	59.9	241	8 ADR68609	Adr68609 Human ant
30	620.5	59.7	239	8 ADS84461	Ads84461 Human ant
31	620.5	59.7	239	8 ADR68603	Adr68603 Human ant
32	618	59.5	464	7 ADE28411	Ade28411 Human ant
33	615	59.2	473	4 AAB36206	Aab36206 Human lmm
34	613	59.0	446	8 ADK52356	Adk52356 Human ant
35	610	58.7	450	6 ABP96294	Abp96294 4A5-3.1.1
36	609	58.6	580	6 AAO30915	Aao30915 dI-NHS76
37	607.5	58.5	241	8 ADS84449	Ads84449 Human ant
38	607.5	58.5	241	8 ADR68591	Adr68591 Human ant
39	604.5	58.2	580	6 AAO30913	Aao30913 dI-NHS76
40	601	57.8	462	3 AAB26884	Aab26884 Human lmm
41	598	57.6	223	7 ADJ32112	Adj32112 Human int
42	596	57.4	221	7 ADJ32126	Adj32126 Human int
43	594.5	57.2	453	6 ABP96295	Abp96295 4A5-3.1.1
44	593	57.1	251	5 ABG80712	Abg80712 Amyloid p
45	593	57.1	254	5 ABG80713	Abg80713 Amyloid p

ALIGNMENTS

RESULT 1  
AAY34300  
ID AAY34300 standard; protein; 197 AA.

XX AC AAY34300;

XX DT 19-NOV-1999 (first entry)

XX DE Igm antibody CEM 10.1 G10 heavy chain sequence.

XX KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.

XX PN WO9945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX DR WPI; 1999-540816/45.

XX DR N-PSDB; AAZ20401.

XX PT New monoclonal antibody, used for treating e.g. graft versus host

PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 60; Fig 25; 245pp; English.

XX CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 MAb  
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes. e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g. blood  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

```
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 197 AA;
Query Match 100.0%; Score 1039; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 9.4e-65;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LVKPSLTLCTCTVSGSGSISSYYWNWIRQPPGKLEWIGYIYSGSTNNPNSLSKSRVTIS 60
Dy 1 LVKPSLTLCTCTVSGSGSISSYYWNWIRQPPGKLEWIGYIYSGSTNNPNSLSKSRVTIS 60
Qy 61 VDTSKNQPSLKLSSVTAADTAVYICARDRGVGTGDFYWGQGLTVTVSSGSASAPTLFPL 120
Dy 61 VDTSKNQPSLKLSSVTAADTAVYICARDRGVGTGDFYWGQGLTVTVSSGSASAPTLFPL 120
Qy 121 VSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGGKYAATSQV 180
Dy 121 VSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGGKYAATSQV 180
Qy 181 LLPSKDVMOGTDEHKVC 197
Dy 181 LLPSKDVMOGTDEHKVC 197
RESULT 2
AA34299
ID AA34299 standard; protein; 205 AA.
XX
AC AA34299;
XX
DT 19-NOV-1999 (first entry)
XX
DE IgM antibody CEM 10.1 C3 heavy chain sequence.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 150
FT /label= unknown
FT /note= "encoded by TYC"
XX
FN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
XX
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
DR WPI; 1999-540816/45.
DR N-PSDB; AAZ20400.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Claim 60; Fig 24; 245pp; English.
XX
CC This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
```

```
CC by the IgM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 205 AA;
Query Match 85.6%; Score 889.5; DB 2; Length 205;
Best Local Similarity 87.2%; Pred. No. 2.5e-54;
Matches 177; Conservative 3; Mismatches 12; Indels 11; Gaps 2;
Qy 1 LVKPSLTLCTCTVSGSGSISSYYWNWIRQPPGKLEWIGYIYSGSTNNPNSLSKSRVTIS 60
Dy 2 LLKPSLTLCTCAVYGGFSGYWSWIRQPPGKLEWIGIENHSGSTNNPNSLSKSRVTIS 61
Qy 61 VDTSKNQPSLKLSSVTAADTAVYICARDRGVGT-----GPDYWGQGLTVTVSSGSAS 113
Dy 62 VDTSKNQPSLKLSSVTAADTAVYICAR---GTEYYYYYGGMDVWGQGLTVTVSSGSAS 117
Qy 114 APTLPLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGGK 173
Dy 118 APTLPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNSDISSTRGFPSPVLRGGK 177
Qy 174 YAATSQVLLPSKDVMOGTDEHKV 196
Dy 178 YAATSQVLLPSKDVMOGTDEHV 200
RESULT 3
AA34304
ID AA34304 standard; protein; 190 AA.
XX
AC AA34304;
XX
DT 19-NOV-1999 (first entry)
XX
DE IgM antibody CEM 13.5 heavy chain sequence.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
FN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
XX
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
DR WPI; 1999-540816/45.
DR N-PSDB; AAZ20405.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Claim 60; Fig 29; 245pp; English.
XX
CC This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
```



CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IGM MAb ABX-CBL, providing that the antibody is not CBL1. The MAb  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX  
SQ Sequence 190 AA;

Query Match 84.7%; Score 880.5; DB 2; Length 190;  
Best Local Similarity 90.6%; Pred. No. 9.9e-54;  
Matches 173; Conservative 3; Mismatches 12; Indels 3; Gaps 2;  
QY 5 SETSLTCTVSGSISYYNNWIRQPPGKLEWIGYIYVSGSTNNPNSLKSRVTISVDT 64  
DB 1 SETSLTCAVYGGSGFYNNWIRQPPGKLEWIGYIYVSGSTNNPNSLKSRVTISVDT 60  
QY 65 KNPQSLKLSVTAADTAIVYICARDRGVAT--GPDYWGQGLTVTVSSGSASAPTLFPLVS 122  
DB 61 KNPQSLKLSVTAADTAIVYICARG-GTTVTDFADPWGQGTMTVTVSSGSASAPTLFPLVS 119  
QY 123 CENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSQVLL 182  
DB 120 CENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSQVLL 179  
QY 183 PSKDVMOQTDE 193  
DB 180 PSKDVMOQTDE 190

RESULT 4  
AA34303  
ID AAY34303 standard; protein; 202 AA.

AC AAY34303;  
XX  
XX 19-NOV-1999 (first entry)  
XX  
XX IGM antibody CEM 13.12 heavy chain sequence.

XX Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Misc-difference 147  
FT /label= unknown  
FT /note= "encoded by TYC"  
FT Misc-difference 151  
FT /label= unknown  
FT /note= "encoded by TYC"

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

XX Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

DR N-PSDB; AAZ20404.

XX New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX Claim 60; Fig 28; 245pp; English.

CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAb) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IGM MAb ABX-CBL, providing that the antibody is not CBL1. The MAb  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX

SQ Sequence 202 AA;

Query Match 82.2%; Score 854.5; DB 2; Length 202;  
Best Local Similarity 86.1%; Pred. No. 6.8e-52;  
Matches 173; Conservative 2; Mismatches 15; Indels 11; Gaps 2;

QY 3 KPSETLSLTCTVSGSISYYNNWIRQPPGKLEWIGYIYVSGSTNNPNSLKSRVTISVD 62  
DB 1 KLPETLSLTCAVYGGSGFYNNWIRQPPGKLEWIGYIYVSGSTNNPNSLKSRVTISVD 60

QY 63 TSKNQPSLKLSVTAADTAIVYICARDRGVAT-----GPDYWGQGLTVTVSSGSASAP 115

DB 61 TSKNQPSLKLSVTAADTAIVYICAR---GAAEYIYVYGMVDMGQGTTVTVSSGSASAP 116

QY 116 TLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYA 175

DB 117 TLFPLVSCENSPSDTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLRGGKYA 176

QY 176 ATSOVLLPSKDVMOQTDEHKV 196

DB 177 ATSOVLLPSKDVMOQTDEHVV 197

RESULT 5

AA08598

ID AAY08598 standard; protein; 223 AA.

AC AAY08598;

XX 05-AUG-1999 (first entry)

XX Anti-human TNF-alpha monoclonal antibody H-chain protein.

XX Monoclonal antibody; H chain; heavy chain; anti-human; TNF-alpha;

XX tumour necrosis factor; light chain; L chain.

XX Homo sapiens.

XX JP11127855-A.

XX 18-MAY-1999.

XX 27-OCT-1997; 97JP-00293994.

XX 27-OCT-1997; 97JP-00293994.

XX (NIHA ) JAPAN ENERGY CORP.

XX WPI; 1999-350318/30.

XX N-PSDB; AAX77407.

XX Recombinant anti-human TNF-alpha human monoclonal antibody - produced  
PT stably with a high purity, and in large amounts.

XX

PS Claim 3; Page 12-13; 22pp; Japanese.

XX This invention describes novel recombinant anti-human TNF-alpha human

CC monoclonal antibody consisting of a heavy (H) chain and a light (L)

CC chain. The recombinant anti-human TNF-alpha human monoclonal antibody can

CC be produced stably in a high purity and in a large amount

XX

SQ Sequence 223 AA;

Query Match 72.5%; Score 753.5; DB 2; Length 223;

Best Local Similarity 74.2%; Pred. No. 8.2e-45;

Matches 147; Conservative 15; Mismatches 33; Indels 3; Gaps 2;

Qy 1 LVKSETLTLCTVSGGSISSYWNWIRQPPKGLWIGYIYSGSTN-YNPSLKSRVTI 59

Db 11 VVQGRSLRLSCASGFTFSSYGHVWVRQAPKGLWAVISYDGSNKYIADSVKGRFTI 70

Qy 60 SVDTSRKNQFSLKLSVTAADTAIVYICARDRGVATGFDYWGQGLTVTVSSGSASAPTLFP 119

Db 71 SRDNSKNTLYLQMSLRAEDTAIVYICAKDS--GDLAFDWQGGTMTVTVSSGSASAPTLFP 128

Qy 120 LVSCNSPDSSTSSVAVGCLAQDFLPSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQ 179

Db 129 LVSCNSPDSSTSSVAVGCLAQDFLPSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQ 188

Qy 180 VLLPSKDVMOQGTDEHKVC 197

Db 189 VLLPSKDVMOQGTDEHVVC 206

RESULT 6

ADF69305

ID ADF69305 standard; protein; 266 AA.

XX

AC ADF69305;

XX

DT 26-FEB-2004 (first entry)

XX

DE Human lung specific protein sequence SEQ ID NO:62.

XX

KW human; lung specific nucleic acid; lung specific protein; lung cancer;

KW cytostatic; gene therapy.

XX

OS Homo sapiens.

XX

XX

PN WO2003102137-A2.

XX

XX

PD 11-DEC-2003.

XX

PF 30-MAY-2003; 2003WO-US016810.

XX

PR 31-MAY-2002; 2002US-0385301P.

XX

PA (DIAD-) DIADEXUS INC.

XX

PI Chen S, Macina RA, Sun Y, Liu C, Turner LR;

XX

FI WPI; 2004-053457/05.

DR

XX

XX

PT New human lung specific nucleic acid, useful for preparing a composition

PT for diagnosing or treating lung cancer.

XX

XX

PS Claim 11; SEQ ID NO 62; 221pp; English.

XX

CC The present invention describes a human lung specific nucleic acid

CC molecule. Also described: (1) a method for determining the presence of a

CC lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising

CC the nucleic acid molecule; (3) a host cell comprising the vector; (4) a

CC method for producing a polypeptide encoded by the nucleic acid molecule;

CC (5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody

CC or its fragment that specifically binds to the polypeptide; (7) a method

CC for determining the presence of a lung specific protein in a sample; (8)

CC a method for diagnosing and monitoring the presence and metastases of

CC lung cancer in a patient; (9) a kit for detecting a risk of cancer or

CC presence of cancer in a patient comprising a means for determining the

CC presence the nucleic acid molecule or polypeptide in a sample of a

CC patient; (10) a method of treating a patient with lung cancer; and (11) a

CC vaccine comprising the polypeptide or the nucleic acid encoding the

CC polypeptide. Human LSNA molecules and related proteins have cytostatic

CC activity, and can be used in gene therapy. They are useful for preparing

CC a composition for diagnosing or treating lung cancer. The present

CC sequence represents a human lung specific protein, which is used in the

CC exemplification of the present invention.

XX

SQ Sequence 266 AA;

Query Match 72.3%; Score 751; DB 8; Length 266;

Best Local Similarity 75.6%; Pred. No. 1.5e-44;

Matches 149; Conservative 15; Mismatches 31; Indels 2; Gaps 2;

Qy 3 KPSTLSLTCTVSGGSISSYWNWIRQPPKGLWIGYIYSGS-TYNNPBLKSRVTISV 61

Db 24 KPGSLKISCKSGSYSTSYWIGVWRQMPKGLWEMGIYPGDSITRYSPFQGVITISA 83

Qy 62 DTSKNQFSLKLSVTAADTAIVYICARDRGV-GATGFDYWGQGLTVTVSSGSASAPTLPL 120

Db 84 DKSISTAYLQWSSLKASDTAMYYCARPIAVAGHYFYFDYWGQGLTVTVSSGSASAPTLPL 143

Qy 121 VSCNSPDSSTSSVAVGCLAQDFLPSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQ 180

Db 144 VSCNSPDSSTSSVAVGCLAQDFLPSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQ 203

Qy 181 LLPSKDVMOQGTDEHKVC 197

Db 204 LLPSKDVMOQGTDEHVVC 220

RESULT 7

AAAM23924

ID AAAM23924 standard; protein; 596 AA.

XX

AC AAAM23924;

XX

DT 12-OCT-2001 (first entry)

XX

DE Human EST encoded protein SEQ ID NO: 1449.

XX

KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;

KW gene therapy; nutrition.

XX

OS Homo sapiens.

XX

PN WO200154477-A2.

XX

PD 02-AUG-2001.

XX

PF 25-JAN-2001; 2001WO-US002687.

XX

PR 25-JAN-2000; 2000US-00491404.

PR 17-JUL-2000; 2000US-00617746.

PR 03-AUG-2000; 2000US-00631451.

PR 15-SEP-2000; 2000US-00663870.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX

DR WPI; 2001-476164/51.

DR N-PSDB; AAH98583.

XX

PT Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use.

XX

PS Claim 20; Page 1011-1012; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

CC urchin and tomato. These were derived from expressed sequence tags (ESTs)

CC from the organism of interest. They can be used in diagnostics,

CC forensics, gene mapping, identification of mutations, to assess

CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention

XX Sequence 596 AA;

SQ

Query Match 72.2%; Score 750.5; DB 4; Length 596;

Best Local Similarity 73.3%; Pred. No. 3.7e-44;

Matches 148; Conservative 16; Mismatches 33; Indels 5; Gaps 2;

QY 1 LVKSETLSLCTVSGGSISSYYNNWIRQPPKGLWIGYIYSG-STNYPNLSKSRVTI 59

DB 30 LVQPGSLRLSCAASGFTFSSYMHVWVQAPKGLVWVSRINTDGSSTSYADSVKGRFTI 89

QY 60 SVDTSKNQFSLKLSVTAADTAVYYCARDRGVGATG----FDYWGQGLTVTVSSGSASAP 115

DB 90 SRDNAKNTLYLQMSLRAEDTAVYYCARADNCSTSCYKCFDYWGQGLTVTVSSGSASAP 149

QY 116 TLFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYA 175

DB 150 TLFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYA 209

QY 176 ATSQVLLPSKDVMOQTDEHKVC 197

DB 210 ATSQVLLPSKDVMOQTDEHVVC 231

RESULT 8

ADL70773

ID ADL70773 standard; protein; 223 AA.

XX

AC ADL70773;

XX

XX 03-JUN-2004 (first entry)

DT

XX

DE Anti-TNFAlfa antibody VH region, SEQ ID 46.

XX

XX Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;

KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;

KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnery;

KW Antiparkinsonian; Nootropic; Cardiant; Antinaemic; Antiatherosclerotic;

KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;

KW Tf; transferrin fusion protein; Tf fusion protein; anti-TNFAlfa;

XX antibody; VH region.

OS Unidentified.

XX

XX WO2004020588-A2.

FN

XX

PD 11-MAR-2004.

XX

XX 28-AUG-2003; 2003WO-US026779.

PF

XX

PR 30-AUG-2002; 2002US-0406977P.

PR 10-MAR-2003; 2003US-00384060.

PR 09-JUL-2003; 2003US-0485404P.

XX

XX (BIOR-) BIOREXIS PHARM CORP.

PA

XX

PI Prior CP, Turner AJ, Sadeghi H;

XX

XX WPI; 2004-239175/22.

DR

XX

XX Novel library containing several fusion proteins each of which comprises

PT first transferrin polypeptide fused to at least one second peptide,

PT useful for screening for transferrin fusion protein having the particular

PT activity.

XX Example 8; SEQ ID NO 46; 243pp; English.

XX

CC The present invention relates to a library (I) of modified fusion

CC proteins of transferrin (Tf) and therapeutic proteins with increased

CC serum half-life or serum stability. Preferred fusion proteins include

CC those modified so that the Tf moiety exhibits no or reduced

CC glycosylation, iron binding and/or Tf receptor binding. The transferrin

CC fusion proteins are useful for treating, preventing or ameliorating

CC disorders or diseases of endocrine system, nervous system, immune system,

CC respiratory system, cardiovascular system, diseases and/or disorders

CC relating to cell proliferation, and/or diseases or disorders relating to

CC blood. The modified fusion proteins are useful in diagnosis, prognosis,

CC prevention and/or treatment of autoimmune disorders; diseases and

CC disorders of haematopoietic cells (e.g., leukaemia, neutropenia, anaemia

CC and thrombocytopenia); allergic reactions such as asthma, rhinitis and

CC eczema; inflammatory conditions e.g., inflammation associated with

CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,

CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders

CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel

CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders

CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative

CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The

CC fusion protein is also useful as an adjuvant to enhance antibacterial or

CC antifungal immune responses, antiparasitic immune responses, etc. The

CC fusion protein is also useful for treating monoclonal gammopathy of

CC undetermined significance (MGUS), Waldenström's disease, plasmacytomas,

CC adult respiratory distress syndrome, for stimulating wound repair, for

CC preventing or treating infections of joints, bones, skin, etc. The fusion

CC protein is also useful for treating or preventing thrombosis, myocardial

CC infarction, cancers, thrombocytopenia, sickle cell anaemia,

CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,

CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf

CC and a specific example of a SCA that can be fused to Tf is anti-tumour

CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence

XX from an anti-TNFAlfa antibody.

XX

SQ Sequence 223 AA;

Query Match 71.9%; Score 747.5; DB 8; Length 223;

Best Local Similarity 73.7%; Pred. No. 2.1e-44;

Matches 146; Conservative 15; Mismatches 34; Indels 3; Gaps 2;

QY 1 LVKSETLSLCTVSGGSISSYYNNWIRQPPKGLWIGYIYSGSTN-YNPSLKSRTVI 59

DB 11 VVQPSRLRLSCAASGFTFSSYGHVWVQAPKGLWVAVISYDGSNKYYADSVKGRFTI 70

QY 60 SVDTSKNQFSLKLSVTAADTAVYYCARDRGVGATGFDYWGQGLTVTVSSGSASAPTLPP 119

DB 71 SRDNSKNTLYLQMSLRAEDTAVYYCAKDS--GDIAFDIWGQGTWTVTVSSGSASAPTLPP 128

QY 120 LVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSO 179

DB 129 LVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSO 188

QY 180 VLLPSKDVMOQTDEHKVC 197

DB 189 VLLPSKDVMOQTDEHVVC 206

RESULT 9

AAW71880

ID AAW71880 standard; protein; 588 AA.

XX

XX AAW71880;

AC

XX

DT 18-JAN-1999 (first entry)

XX

XX Anti-human Fas humanised antibody CH11 heavy chain HmuH.

DE

XX Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;

KW

autoimmune disease; rheumatoid arthritis; therapy; human; antibody engineering.

OS Homo sapiens.  
XX Synthetic.

Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Sig\_peptide  
FT Protein 20..588  
FT /label= Mat\_protein  
FT Region 50..54  
FT /label= CDR1  
FT /note= "complementarity determining region 1 from CH11 heavy chain"  
FT Region 69..84  
FT /label= CDR2  
FT /note= "complementarity determining region 2 from CH11 heavy chain"  
FT Region 118..124  
FT /label= CDR3  
FT /note= "complementarity determining region 3 from CH11 heavy chain"

PN EP866131-A2.

PD 23-SEP-1998.

XX 20-MAR-1998; 98EP-00302113.

XX 21-MAR-1997; 97JP-00067938.

XX (SANY ) SANKYO CO LTD.

PI Serizawa N, Haryuama H, Takahaishi T, Nakahara K, Yonehara S;

XX WPI; 1998-482965/42.  
DR N-PSDB; AAV61363.

XX Production of anti-Fas protein humanised antibodies - for use in inducing apoptosis on Fas expressing cells in the treatment of auto:immune diseases, especially rheumatoid arthritis.

XX Claim 21; Page 105-107; 187pp; English.

XX This is the amino acid sequence of a humanised anti-Fas antibody CH11 heavy chain, designated HmuH. HmuH is based on the heavy chain (see AAW71888) of murine anti-human Fas monoclonal antibody CH11. The humanised sequence was designed following selection of donor residues from CH11 to be grafted onto acceptor molecule 21.28'CL. 2 Heavy chain sequences (see AAW71880-81) have been designed, and each can be used in combination with any of 4 light chain sequences (see AAW71876-79) to provide novel, claimed humanised CH11 Igm antibodies that lack a J chain. These humanised anti-human Fas antibodies are capable of inducing apoptosis in cells expressing Fas (e.g. synovocytes) and are useful in the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA sequences encoding the humanised antibodies are claimed, as are vectors such as pMmuH5-1 including the HmuH nucleotide sequence (see AAV61363), and host cells such as Escherichia coli pMmuH5-1 (FERM BP-5863)

XX Sequence 588 AA;

Query Match 71.8%; Score 746.5; DB 2; Length 588;  
Best Local Similarity 72.4%; Pred. No. 7e-44; Mismatches 19; Indels 5; Gaps 2;  
Matches 142; Conservative 30;

Qy 3 KPSETLSLCTCTVSGGSISSYYNMWIRPPGKLEWIGYIY-YSGSTNNYNPGLKSRVTISV 61

Db 32 KPGASVKVSCASGYTFDDYNHWVRQAPGGGLEWMGVIYPNGGTGYNQFKSKATLTV 91

Qy 62 DTSKNQPSKLKLSVTAADTAVYVCARDRGVATGPDYWGQGLTVTVSSGSASAPTLFPLV 121

Db 92 DNSASTAYMELSLRSEDVAVYVCAR----SYVAMDYWGQGLTVTVSSGSASAPTLFPLV 147

Qy 122 SCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSSTRGPPSVLRGGKYAATSQVL 181  
Db 148 SCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSSTRGPPSVLRGGKYAATSQVL 207  
Qy 182 LPKXDMVMOGTDEHKVC 197  
Db 208 LPKXDMVMOGTDEHVVC 223

RESULT 10

AAAB12917

ID AAB12917 standard; protein; 588 AA.

XX AAB12917;

XX 16-NOV-2000 (first entry)

XX Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #86.

XX Antirheumatic agent; immunoglobulin M; Igm; apoptosis inducer;  
XX immunosuppression; autoimmune disease; treatment; rheumatism;  
XX anti-Fas antibody.

XX Synthetic.

XX JP2000154149-A.

XX 06-JUN-2000.

XX 17-SEP-1999; 99JP-00263984.

XX 18-SEP-1998; 98JP-00264598.

XX (SANY ) SANKYO CO LTD.

XX WPI; 2000-454476/40.  
DR N-PSDB; AAA78271.

XX Anti-human Fas humanizing antibody-containing antirheumatic agents.

XX Claim 1; Page 75-77; 109pp; Japanese.

XX The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (Igm) protein. The Igm protein does not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, especially rheumatism. The Igm molecule used in the invention has human Fas-antigen binding properties. Included in the invention are nucleotide sequences of the Igm light and heavy chains (see AAA78267-A78272) and the corresponding protein sequences (see AAB12913-B12918 and AAB12919), and nucleotide sequences of the humanised anti-human Fas Igm CH11 (see AAW78202-A78206) and protein sequences (see AAB12908-B12910). Also included are anti-human Fas antibody CDR peptides (AAB12902-B12907). Primers specific for the anti-human Fas antibody, light, heavy and kappa chains used in the invention are represented by sequences AAA78213-A78266. Primers used for sequencing the human Igm DNA used in the invention are represented by sequences AAA78277-A78318 and AAA78335-A78337, while humanised anti-Fas Igm DNA sequencing primers are represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer sequences AAA78207-A78212 are specific for murine Igm DNA, and are used in the production of the agent of the invention

XX Sequence 588 AA;

Query Match 71.8%; Score 746.5; DB 3; Length 588;  
Best Local Similarity 72.4%; Pred. No. 7e-44; Mismatches 19; Indels 5; Gaps 2;  
Matches 142; Conservative 30;

Qy 3 KPSETLSLCTCTVSGGSISSYYNMWIRPPGKLEWIGYIY-YSGSTNNYNPGLKSRVTISV 61

Db 3 KPSETLSLCTCTVSGGSISSYYNMWIRPPGKLEWIGYIY-YSGSTNNYNPGLKSRVTISV 61





AC ADB65070;  
XX 04-DEC-2003 (first entry)  
XX Human protein encoded by clone SMINT20056230.  
DE Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;  
KW cell regeneration; membrane protein; signal transduction-related protein;  
KW transduction-related protein; osteoporosis; neurological disease;  
KW cancer; tumour.  
XX Homo sapiens.  
XX EPI308459-A2.  
XX 07-MAY-2003.  
XX 28-MAR-2002; 2002EP-00007401.  
XX 05-NOV-2001; 2001JP-00379298.  
XX 25-JAN-2002; 2002US-00350978.  
XX (HELI-) HELIX RES INST.  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX WPI; 2003-450961/43.  
XX N-PSDB; ADB63100.  
XX New polynucleotides and polypeptides, useful for developing a diagnostic  
PT marker or medicines for regulation of their expression and activity, or  
PT as targets of gene therapy.  
XX Claim 1; Page; 222pp; English.  
XX The invention discloses a polynucleotide comprising a sequence selected  
CC from 1970 fully defined nucleotide sequences which encode novel  
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
CC or its partial peptide, an antibody binding to the polypeptide or peptide  
CC of the polynucleotide, immunologically assaying the polypeptide or  
CC peptide of the polynucleotide by contacting the polypeptide or peptide  
CC with the antibody of the encoded protein, and observing the binding  
CC between the two, a transformant carrying the polynucleotide in an  
CC expressible manner and an antisense polynucleotide. The oligonucleotide  
CC is useful as a primer for synthesising the polynucleotide, or as a probe  
CC for detecting the polynucleotide. The polynucleotides and encoded  
CC proteins are useful as pharmaceutical agents and many disease-related  
CC genes may be included in them, for developing a diagnostic marker or  
CC medicines for regulation of their expression and activity, or as targets  
CC of gene therapy. The genes are involved in tissue and/or cell  
CC regeneration. Membrane proteins, signal transduction-related proteins,  
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,  
CC neurological diseases, cancer, tumours). The cDNA may be used to regulate  
CC the activity or expression of the encoded protein to treat diseases. The  
CC sequence presented is a protein of the invention. Note: Some of the  
CC sequence data for this patent is not represented in the printed  
CC specification, but is based on sequence information supplied by the  
CC European Patent Office.  
XX Sequence 533 AA;  
Query Match 70.3%; Score 730.5; DB 7; Length 533;  
Best Local Similarity 72.0%; Pred. No. 8.2e-43;  
Matches 144; Conservative 15; Mismatches 38; Indels 3; Gaps 1;  
QY 1 LVKPSLTLCTGSGGSSVYNNWIRQPPGKLEWIGYIYSGSTWNPSPKSRVTIS 60  
DB 30 LVQPGGSLRLCAASGFDVSSNYSWVRQSPKGFVATWYGGNTYAESVKGRTVS 89

QY 61 VDTSKNQPSLKLSSVTAADTAIVYCARDRGVGTGFDY---WGQGLTVTVSSGSASAPTL 117  
DB 90 RDGSQNTLYLEMSLSLRPDDTAIVYCVDRHRNYADTSPYGRKWGQGLTVTVSSGSASAPTL 149  
QY 118 PFLVSCENSPSDTSGSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAAT 177  
DB 150 PFLVSCENSPSDTSGSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAAT 209  
QY 178 SQVLLPSKDVNMQGTDEHKVC 197  
DB 210 SQVLLPSKDVNMQGTDEHVVC 229  
RESULT 15  
ADE97370  
ID ADE97370 standard; protein; 627 AA.  
XX AC ADE97370;  
XX 12-FEB-2004 (first entry)  
XX Human immunoadhesin-related protein - SEQ ID 47.  
XX immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;  
KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;  
KW intercellular adhesion molecule; ICAM-1; human.  
XX Homo sapiens.  
XX WO2003064992-A2.  
XX 07-AUG-2003.  
XX 25-OCT-2002; 2002WO-US034197.  
XX 26-OCT-2001; 2001US-00047542.  
XX (PLAN-) PLANET BIOTECHNOLOGY INC.  
PA (LARR/) LARRICK J W.  
PA (WYCO/) WYCOFF K L.  
PI Larrick JW, Wycoff KL;  
XX WPI; 2003-636816/60.  
XX New immunoadhesin, useful for treating anthrax and rhinovirus, comprises  
PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and  
PT J chain and secretory component associated with the chimeric toxin  
PT receptor protein.  
XX Disclosure; SEQ ID NO 47; 288pp; English.  
XX The invention relates to a novel immunoadhesin comprising a chimeric  
CC toxin receptor protein consisting of a toxin receptor protein linked to  
CC at least a portion of an immunoglobulin heavy chain with a J (joining)  
CC chain and secretory component (SC) associated with the chimeric toxin  
CC receptor protein. The immunoadhesin comprises a chimeric bacterial or  
CC viral toxin receptor protein and the immunoadhesin has plant-specific  
CC glycosylation. The immunoadhesin of the invention demonstrates virucide  
CC and antibacterial activities and may be useful for reducing the binding  
CC of a viral or bacterial antigen to a host cell and thus for treating or  
CC preventing anthrax, as well as human rhinovirus infection which results  
CC in the common cold. The current sequence is that of the human  
CC immunoadhesin-related protein of the invention.  
XX Sequence 627 AA;  
Query Match 68.2%; Score 709; DB 7; Length 627;  
Best Local Similarity 67.0%; Pred. No. 3e-41;  
Matches 140; Conservative 19; Mismatches 36; Indels 14; Gaps 2;  
QY 3 KPSETLSLCTVSGGSSVYNNWIRQPPGKLEWI-GYIYSGSTWNPSPKSRVTIS 61  
DB 30 LVQPGGSLRLCAASGFDVSSNYSWVRQSPKGFVATWYGGNTYAESVKGRTVS 89

Db 32 KPGSSVKVCKASGGTFSSYAISWVRQAPQGQLEWVGIIPIFGTANYAQKFQGRVTITA 91  
Qy 62 DTSKNQFSLKLSSVTAADTAVYYCARDRGVGA-----TGFDYWGQGLVTVS 108  
Db 92 DESTSTAYMELSSURSEDTAVYYCAKTIILGIPYSSGWYPNSDYIYGGMDVWGQGLTVTVS 151  
Qy 109 SGSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSV 168  
Db 152 SGSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSV 211  
Qy 169 LRGKYAATSQVLLPSKDVMOGTDEHKVC 197  
Db 212 LRGKYAATSQVLLPSKDVMOGTDEHVVC 240

Search completed: March 8, 2005, 06:17:07  
Job time : 93.3346 secs



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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 104.543 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-25

Perfect score: 1039

Sequence: 1 LVKPSSETLSLTCTVSGSGSIS.....SQVLLPSKDVNQGTDEHKVC 197

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	730.5	70.3	533	15	US-10-104-047-3224
2	709	68.2	627	13	Sequence 3224, Ap
3	708.5	68.2	595	15	Sequence 47, Appl
4	634	61.0	466	15	US-10-108-260A-4112
5	633.5	61.0	241	15	Sequence 30, Appl
6	633	60.9	466	15	US-10-292-088-30
7	631	60.7	466	15	US-10-684-109-71
8	626.5	60.3	230	10	Sequence 86, Appl
9	625	60.2	179	15	US-10-292-088-70
10	622.5	59.9	241	16	US-10-309-762-171
11	620.5	59.7	239	16	Sequence 171, Appl
12	618	59.5	464	15	Sequence 106, App
13	609	58.6	580	14	US-10-684-109-100
					Sequence 100, App
					Sequence 22, Appl
					Sequence 37, Appl

14	607.5	58.5	241	16	US-10-684-109-88
15	604.5	58.2	580	14	US-10-310-719-35
16	598	57.6	223	10	Sequence 35, Appl
17	596	57.4	221	10	US-09-972-656-66
18	591	56.9	229	10	Sequence 80, Appl
19	581.5	56.0	173	15	US-09-972-656-82
20	581.5	56.0	235	16	US-10-309-762-173
21	581	55.9	172	14	Sequence 173, App
22	576	55.4	193	15	US-10-684-109-112
23	576	55.4	229	9	Sequence 21, Appl
24	573	55.1	250	14	US-10-153-382-21
25	562.5	54.1	243	16	US-10-264-049-4331
26	556	53.5	487	9	US-09-974-449-37
27	556	53.5	487	9	US-10-684-109-94
28	556	53.5	487	11	Sequence 94, Appl
29	547	52.6	467	14	Sequence 145, App
30	547	52.6	467	14	Sequence 2194, Ap
31	544.5	52.4	152	9	Sequence 8, Appli
32	542.5	52.2	476	9	Sequence 10, Appl
33	542.5	52.2	476	9	Sequence 68, Appl
34	542.5	52.2	476	13	Sequence 12, Appl
35	542.5	52.2	476	14	Sequence 12, Appl
36	542.5	52.2	476	14	Sequence 12, Appl
37	534.5	51.4	118	15	Sequence 12, Appl
38	530.5	51.1	220	16	Sequence 109, App
39	529.5	51.0	220	16	Sequence 114, App
40	528.5	50.9	220	16	Sequence 167, App
41	526	50.6	119	14	Sequence 113, App
42	521.5	50.2	122	15	Sequence 5, Appli
43	521.5	50.2	122	15	Sequence 24, Appl
44	521.5	50.2	122	15	Sequence 25, Appl
45	521.5	50.2	122	15	Sequence 27, Appl
					Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-10-104-047-3224  
; Sequence 3224, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3224  
; LENGTH: 533  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3224

Query Match	70.3%	Score	730.5;	DB	15;	Length	533;
Best Local Similarity	72.0%	Pred	No. 1.9e-46;				
Matches	144;	Conservative	15;	Mismatches	38;	Indels	3;
Gaps	1;						
Qy	1	LVKPSSETLSLTCTVSGSGSISYYNNWIRPPGKGLWIGYIYSGSTNNPPLKSRVTIS	60				
Db	30	LVQPGGSLRLSCAASGFDVSSNNYMSWRQSPCKGPWATMYGGNTYYAESVKGRFTVS	89				
Qy	61	VDTSKNQSLKSLSVTAADTAVYICARDRGVATGFDY---WGQGLTVTVSSGSASAPTL	117				
Db	90	RDGQNTLYLEMSLRDPDPTAVYICVRDHRNADTSPYGRKMGQGLTVTVSSGSASAPTL	149				
Qy	118	PFLVSCNSPDSSTSSAVGCLAQDFLPDSITFWSWKYKNSDISSTRGFPFSLVLRGGKYAAT	177				
Db	150	PFLVSCNSPDSSTSSAVGCLAQDFLPDSITFWSWKYKNSDISSTRGFPFSLVLRGGKYAAT	209				



FILE REFERENCE: 6989.US.02  
CURRENT APPLICATION NUMBER: US/10/684,109  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: 10/269,711  
PRIOR FILING DATE: 2002-10-14  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 71  
LENGTH: 241  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-684-109-71

Query Match 61.0%; Score 633.5; DB 16; Length 241;  
Best Local Similarity 67.4%; Pred. No. 1.4e-39;  
Matches 128; Conservative 20; Mismatches 31; Indels 11; Gaps 6;  
QY 1 LVKPSLTLCTVSGGSSISSYWNWIRPPCKGLEWIGYIYSGSTNNPDLKSRVTIS 60  
DB 32 LVKPSLTLCTVSGGSSISSYWNWIRPPCKGLEWIGYIYSGSTNNPDLKSRVTIS 91  
QY 61 V--DTSKNQFSLKSSVTAADTAATVYICARDR-GVGATGFDYWGQGTTLTVSSGSASAPTL 117  
DB 92 VASPTSKNQFSLKLSVTAADTAATVYICARERLIGIG----DYWGQGTTLTVSSASTKGPSV 147  
QY 118 PPLVSCNSPDTSSVAVGCLAQDFLPSITFSWKYKNSDISSTRGPFVLR-GGKYAA 176  
DB 148 PPLAPCSRSTSE--STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPVAVLQSSGLYSL 204  
QY 177 TSQVLLPSKD 186  
DB 205 SSVTVPSN 214

RESULT 6  
US-10-292-088-86  
Sequence 86, Application US/10292088  
Publication No. US20030211100A1  
GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40  
FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/10/292,088  
CURRENT FILING DATE: 2003-03-14  
PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 86  
LENGTH: 466  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-292-088-86

Query Match 60.9%; Score 633; DB 15; Length 466;  
Best Local Similarity 64.7%; Pred. No. 3e-39; Indels 14; Gaps 7;  
Matches 132; Conservative 20; Mismatches 38; Indels 14; Gaps 7;  
QY 1 LVKPSLTLCTVSGGSSISSYWNWIRPPCKGLEWIGYIYSGSTNNPDLKSRVTIS 60  
DB 30 LVKPSLTLCTVSGGSSIRGYIYWNWIRPPCKGLEWIGYIYSGSTNNPDLKSRVTIS 89  
QY 61 VDTSKNQFSLKSSVTAADTAATVYICARDGV-GATG-FDYWGQGTTLTVSSGSASAPTLF 118  
DB 90 VDTSKNQFSLKSSVTAADTAATVYICARRGGLYDYGWFPAPWGQGTTLTVSSASTKGPSV 149  
QY 119 PPLVSCNSPDTSSVAVGCLAQDFLPSITFSWKYKNSDISSTRGPFVLR-GGKYAAT 177  
DB 150 PPLAPCSRSTSE--STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPVAVLQSSGLYSL 206

QY 178 SQVLLPSKDVNQGTD-----EHK 195  
DB 207 SSVTVPSNFG--GTQTYTCNVNDHK 228  
RESULT 7  
US-10-292-088-70  
Sequence 70, Application US/10292088  
Publication No. US20030211100A1  
GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40  
FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/10/292,088  
CURRENT FILING DATE: 2003-03-14  
PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 70  
LENGTH: 466  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-292-088-70

Query Match 60.7%; Score 631; DB 15; Length 466;  
Best Local Similarity 64.2%; Pred. No. 4.3e-39;  
Matches 131; Conservative 21; Mismatches 38; Indels 14; Gaps 7;  
QY 1 LVKPSLTLCTVSGGSSISSYWNWIRPPCKGLEWIGYIYSGSTNNPDLKSRVTIS 60  
DB 30 LVKPSLTLCTVSGGSSIRGYIYWNWIRPPCKGLEWIGYIYSGSTNNPDLKSRVTIS 89  
QY 61 VDTSKNQFSLKSSVTAADTAATVYICARDGV-GATG-FDYWGQGTTLTVSSGSASAPTLF 118  
DB 90 VDTSKNQFSLKSSVTAADTAATVYICARRGGLYDYGWFPAPWGQGTTLTVSSASTKGPSV 149  
QY 119 PPLVSCNSPDTSSVAVGCLAQDFLPSITFSWKYKNSDISSTRGPFVLR-GGKYAAT 177  
DB 150 PPLAPCSRSTSE--STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPVAVLQSSGLYSL 206  
QY 178 SQVLLPSKDVNQGTD-----EHK 195  
DB 207 SSVTVPSNFG--GTQTYTCNVNDHK 228

RESULT 8  
US-09-972-656-72  
Sequence 72, Application US/09972656  
Publication No. US20030099647A1  
GENERAL INFORMATION:  
APPLICANT: Deshpande, Rajendra  
APPLICANT: Tsai, Mei-Mei  
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
TITLE OF INVENTION: Neutralizing Activity  
FILE REFERENCE: A-799  
CURRENT APPLICATION NUMBER: US/09/972,656  
CURRENT FILING DATE: 2001-10-05  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 72  
LENGTH: 230  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-972-656-72  
Query Match 60.3%; Score 626.5; DB 10; Length 230;  
Best Local Similarity 61.7%; Pred. No. 4.5e-39;



```
QY 179 QVLLPSKD 186
Db 205 VVTVPSSN 212

RESULT 12
US-10-292-088-22
; Sequence 22, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-XI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PE/3 US
; CURRENT FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-22

Query Match 59.5%; Score 618; DB 15; Length 464;
Best Local Similarity 62.9%; Pred. No. 4e-38;
Matches 127; Conservative 20; Mismatches 43; Indels 12; Gaps 5;

QY 1 LVKPSETLSLCTVSGGSISSYYNNWIROPKGLWIGYIYSGSTNNPGLKSRVTIS 60
Db 30 LVKPSETLSLCTVSGGSISSYYNNWIROPKGLWIGRVYTSSTNNPGLKSRVTMS 89

QY 61 VDTSKNQFSLKLSSTVAADTAIVYCARDRGVATGDFYWGQGTTLVTVSSGSASAPTL 120
Db 90 VDTSKNQFSLKLSSTVAADTAIVYCARDGLYRGYGMVWGQGTTLVTVSSASTKGFVPFL 149

QY 121 VSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPVLR-GGKYAATSQ 179
Db 150 APCSRSTSE-STAAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGLYLSV 206

QY 180 VLLPSKDVMOGTD-----BHK 195
Db 207 VVTVPSSNFGTQYTCNVVDHK 226

RESULT 13
US-10-310-719-37
; Sequence 37, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT FILING DATE: 2002-12-04
; PRIOR FILING DATE: 2001-12-04
; PRIOR FILING DATE: 2001-12-04
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dI-NHS76(gamma4h) (FN>AQ) -ala-IL2 (D20T) heavy chain fused to
```

```
; OTHER INFORMATION: IL-2 variant
US-10-310-719-37

Query Match 58.6%; Score 609; DB 14; Length 580;
Best Local Similarity 63.1%; Pred. No. 2.3e-37;
Matches 128; Conservative 21; Mismatches 38; Indels 16; Gaps 7;

QY 1 LVKPSETLSLCTVSGGSISS--YYNNWIROPKGLWIGYIYSGSTNNPGLKSRVTI 59
Db 11 LVKPSETLSLCTCAVSGYISGGYWGIRQPPKGLWIGSYTHSGSTYNNPGLKSRVTI 70

QY 60 SVDTSKNQFSLKLSSTVAADTAIVYCARDRGVATGDFYWGQGTTLVTVSSGSASAPTL 119
Db 71 SVDTSKNQFSLKLSSTVAADTAIVYCARGW---SKFDYWGQGTTLVTVSSASTKGFSPVP 127

QY 120 LVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPVLR-GGKYAATS 178
Db 128 LAPCSRSTSE-STAAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGLYLSL 184

QY 179 QVLLPSKDVMOGTD-----BHK 195
Db 185 VVTVPSSSL--GTYTCNVVDHK 205

RESULT 14
US-10-684-109-88
; Sequence 88, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-88

Query Match 58.5%; Score 607.5; DB 16; Length 241;
Best Local Similarity 64.2%; Pred. No. 1.2e-37;
Matches 122; Conservative 24; Mismatches 33; Indels 11; Gaps 6;

QY 1 LVKPSETLSLCTVSGGSISSYYNNWIROPKGLWIGYIYSGSTNNPGLKSRVTIS 60
Db 32 LVKPSETLSLCTVSGASISNNYNNWIROPKGLWIGYISGTYNNPGLKGRVTMS 91

QY 61 V--DTSKNQFSLKLSSTVAADTAIVYCARDR-GVGATGDFYWGQGTTLVTVSSGSASAPTL 117
Db 92 VASPTSKNQFSLKLSSTVAADTAIVYCARGLIGIG---DYWGQGTTLVTVSSASTKGFSPV 147

QY 118 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPVLR-GGKYAA 176
Db 148 PFLAPCSRSTSE-STAAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGLYSL 204

QY 177 TSQVLLPSKD 186
Db 205 SSVTVTPSSN 214

RESULT 15
US-10-310-719-35
; Sequence 35, Application US/10310719
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; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-NHS76(gamma2h)(FN>AQ)-ala-IL2(D20T) heavy chain fused to IL2
; OTHER INFORMATION: variant
; US-10-310-719-35
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Query Match          58.2%; Score 604.5; DB 14; Length 580;
Best Local Similarity 63.2%; Pred. No. 5e-37;
Matches 129; Conservative 21; Mismatches 37; Indels 17; Gaps 8;

QY      1 LVKPSSETLSLCTVSGGSISS--YYWNWIRQPPGKLEWIGYIYSGSTNYNPSLKSRYTI 59
Db      11 LVKPSSETLSLCTCAVSGYISISGYWGWIRQPPGKLEWIGSIYHSGSTYINPSLKSRYTI 70

QY      60 SVDTSKNQFSLKLSSTVAADTAVYYCARDRGVGTGFDYWGQGTILVTVSSG--SASAPTLF 118
Db      71 SVDTSKNQFSLKLSSTVAADTAVYYCARGKW---SKFDYWGQGTILVTVSSGASTKGPSVF 127

QY      119 PLVSCNSPDSITSVAVGCLAQDFLPDSITFSWKYNNNSDISSTRGFPSPVLR--GQKYAAT 177
Db      128 PLAPCSRSTSE--STAALGCLVKDYPPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLS 184

QY      178 SOVLLPSKDVMOGTD-----EHK 195
Db      185 SVTVFSSNF--GTQTYTCNVDPHK 206
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Search completed: March 8, 2005, 07:05:48  
Job time : 104.543 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 21.6614 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-25

Perfect score: 1039

Sequence: 1 LVKSEETLSLCTVSGGIS.....SQLLPKDVQGTDEHKVC 197

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	615	59.2	473	3	US-09-049-672A-4
2	581	55.9	172	4	US-09-472-087-7
3	581	55.9	172	4	US-09-472-087-86
4	572.5	55.1	472	3	US-08-793-450-8
5	556.5	53.6	832	4	US-08-630-820-7
6	556.5	53.6	832	4	US-09-273-453-7
7	556	53.5	487	4	US-09-800-729-145
8	549.5	52.9	219	3	US-09-460-384-37
9	547	52.6	467	3	US-08-523-894-8
10	547	52.6	467	3	US-08-523-894-10
11	547	52.6	467	3	US-08-523-894-12
12	542.5	52.2	476	3	US-08-487-550-12
13	542.5	52.2	476	4	US-09-526-098-12
14	542.5	52.2	476	4	US-09-383-916-12
15	526	50.6	119	3	US-09-025-769B-39
16	526	50.6	119	3	US-09-025-769B-65
17	526	50.6	119	4	US-09-490-070A-39
18	526	50.6	119	4	US-09-490-070A-65
19	526	50.6	119	4	US-09-490-153-39
20	526	50.6	119	4	US-09-490-153-65
21	526	50.6	119	4	US-09-490-324-39
22	526	50.6	119	4	US-09-490-324-65
23	521.5	50.2	118	3	US-09-025-769B-25
24	521.5	50.2	118	4	US-09-490-070A-25
25	521.5	50.2	118	4	US-09-490-153-25
26	521.5	50.2	118	4	US-09-490-324-25
27	508.5	48.9	476	3	US-08-487-550-4

Sequence 4, Appli  
Sequence 4, Appli  
Sequence 79, Appl  
Sequence 77, Appl  
Sequence 20, Appl  
Sequence 57, Appl  
Sequence 6, Appli  
Sequence 7, Appli  
Sequence 95, Appl  
Sequence 113, App  
Sequence 125, App  
Sequence 42, Appl  
Sequence 93, Appl  
Sequence 41, Appl  
Sequence 48, Appl  
Sequence 11, Appl  
Sequence 11, Appl  
Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-09-049-672A-4  
; Sequence 4, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,672A  
FILING DATE: HEREWITH  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PANCYT01

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; CLONE: 1513264
US-09-049-672A-4

Query Match      59.2%; Score 615; DB 3; Length 473;
Best Local Similarity 63.7%; Pred. No. 3e-47;
Matches 130; Conservative 20; Mismatches 40; Indels 14; Gaps 8;

Qy 1 LVKPESETLSLTCTVSGGSISS--YYNWIRPPGKLEWIGYIYSGSTNPNLSKSRVT 58
Db 30 LVKPESETLSLTCAVSGSITSGGYWNSWIRPPGKLEWIGYIYSGSTNPNLSKSRVT 89
Qy 59 ISVDTSKNQFSLKLSVTAADTAIVYICARD---RGVCGATGFDYWGQGTTLTVSSGSASA 114
Db 90 ISVDTSKNQFSLKLSVTAADTAIVYICARDVDVGLRG-GNYGMDVWGQGTTLTVSSASTKG 148
Qy 115 PTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-GGK 173
Db 149 PSVFPPLAPSSKTSG-GTAALGCLVKDYFPBPVTVSW--NSGALTSGVHTTFFPAVLQSSGL 205
Qy 174 YAATSOVLLPSKDVMOGTDEHKVC 197
Db 206 YLSVSVTVPPSSSL--GTQTY-IC 226

RESULT 2
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN B.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      55.9%; Score 581; DB 4; Length 172;
Best Local Similarity 67.4%; Pred. No. 9.5e-45;
Matches 116; Conservative 17; Mismatches 33; Indels 6; Gaps 4;

Qy 1 LVKPESETLSLTCTVSGGSISS--YYNWIRPPGKLEWIGYIYSGSTNPNLSKSRVT 58
Db 5 LVKPSQILSLTCTVSGGSISSGGHWSWIRHPGKLEWIGYIYIGNTYNPNLSKSRVT 64
Qy 59 ISVDTSKNQFSLKLSVTAADTAIVYICARDRGVCGATGFDYWGQGTTLTVSSGSASA 118
Db 65 ISVDTSKNQFSLKLSVTAADTAIVYICARDSG-DYIGIDVWGQGTTLTVSSASTKGPSVF 123
Qy 119 PLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR 170
Db 124 PLAPCSRSTSE-STAALGCLVKDYFPBPVTVSW--NSGALTSGVHTTFFPAVLQ 172

RESULT 3
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
```

```
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN B.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-86

Query Match      55.9%; Score 581; DB 4; Length 172;
Best Local Similarity 67.4%; Pred. No. 9.5e-45;
Matches 116; Conservative 17; Mismatches 33; Indels 6; Gaps 4;

Qy 1 LVKPESETLSLTCTVSGGSISS--YYNWIRPPGKLEWIGYIYSGSTNPNLSKSRVT 58
Db 5 LVKPSQILSLTCTVSGGSISSGGHWSWIRHPGKLEWIGYIYIGNTYNPNLSKSRVT 64
Qy 59 ISVDTSKNQFSLKLSVTAADTAIVYICARDRGVCGATGFDYWGQGTTLTVSSGSASA 118
Db 65 ISVDTSKNQFSLKLSVTAADTAIVYICARDSG-DYIGIDVWGQGTTLTVSSASTKGPSVF 123
Qy 119 PLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR 170
Db 124 PLAPCSRSTSE-STAALGCLVKDYFPBPVTVSW--NSGALTSGVHTTFFPAVLQ 172

RESULT 4
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312890
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABRIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 472 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-450-8

Query Match 55.1%; Score 572.5; DB 3; Length 472;  
Best Local Similarity 59.4%; Pred. No. 26-43; 49; Indels 11; Gaps 6;  
Matches 120; Conservative 22; Mismatches 22;  
QY 1 LKPSSETLSLCTVSGSGSISSYYNNWIRQPPGKGLWIGIYIYSGSTNNPNSLKSRTVIS 60  
DB 30 LKPSSETLSLCTVSGSGSISSYYNNWIRQPPGKGLWIGIYIYSGSTNNPNSLKSRTVIS 89  
QY 61 VDTSKNQSLKLSSTAAADTAVYYCAR---DRGVGATGFDYWGQGTLLVTVSSSGSASAPT 116  
DB 90 VDTSKNQSLKLSSTAAADTAVYYCARAPEYKWKYHGDWFDWQGGTITVTVSSASTKGPS 149  
QY 117 LPFLVSCENSPDTSSTAVGCLAQDFLPDSITFWSKYKNNSDISSTRGFPVLR-GGKYA 175  
DB 150 VFLAPSKSTSG-GTAAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQSSGLYS 206  
QY 176 ATSQLLPKSKDVMQGTDEHKVC 197  
DB 207 LSSVTVFPSSSL-GTQTY-IC 225

RESULT 5  
US-08-630-820-7  
Sequence 7, Application US/08630820  
Patent No. 6008023  
GENERAL INFORMATION:  
APPLICANT: OPPER, Martin  
APPLICANT: BOSSLET, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 832 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-820-7  
Query Match 53.6%; Score 556.5; DB 3; Length 832;  
Best Local Similarity 58.6%; Pred. No. 1.1e-41;  
Matches 116; Conservative 27; Mismatches 46; Indels 9; Gaps 6;  
QY 1 LKPSSETLSLCTVSGSGSISSYYNNWIRQPPGKGLWIGIYIYSGSTNNPNSLKSRTVI 59  
DB 12 LVRPSQTLSLCTVSGFTISSGYSHWVRQPPGKGLWIGIYIYSGIINYNPNSLKSRTVI 71  
QY 60 SVDTSKNQSLKLSSTAAADTAVYYCARDRGVATGFDYWGQGTLL--VTVSSGSASAPT 117  
DB 72 LVDTSKNQSLRLSSVTAAADTAVYYCAREDDYHWFVDMVGQGLVTVTVSSASTKGPSV 131  
QY 118 FPLVSCENSPDTSSTAVGCLAQDFLPDSITFWSKYKNNSDISSTRGFPVLR-GGKYAA 176  
DB 132 FPLAPSKSTSG-GTAAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQSSGLYS 188  
QY 177 TSQVLLPSPKDVMOGTDEH 194  
DB 189 SSVTVFPSSSL-GTQTY 204  
RESULT 6  
US-09-273-453-7  
Sequence 7, Application US/09273453  
Patent No. 6602688  
GENERAL INFORMATION:  
APPLICANT: OPPER, Martin  
APPLICANT: BOSSLET, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/273,453  
FILING DATE: 23-Mar-1999  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/630,820  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 832 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-273-453-7



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;
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 06-SEP-1995
; APPLICATION NUMBER: US/08/523,894
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-523-894-8

Query Match 52.6%; Score 547; DB 3; Length 467;
Best Local Similarity 57.8%; Pred. No. 3.9e-41;
Matches 118; Conservative 23; Mismatches 49; Indels 14; Gaps 7;

QY 1 LVKPSETLSLCTVSGGSGIS-SYYNWIRQPPGKLEWIGIYIYS-GSTNYPNPSLKSRVT 58
DB 30 LVKPSETLSLCTSVSGSGISGDYWFIRQSPGKLEWIGIYIYGGGGTNYNPSLNNRVS 89
QY 59 ISVDTSKNQFSLKLSVTAADTAVVYCARDRGVGTGFDYWGQGLTVTVSSGSASAPTLF 118
DB 90 ISIDTSKQLFSLKLSRVTAAADTAVVYCASNLKYLHLLYWGQGLTVTVSSASTKGPSVF 149
QY 119 PLVSCENSPDTSVVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLR-GGKYAAT 177
DB 150 PLAPCSRSTSE-STAAAGCLVKDYFPEPTVSM--NSGALTSGVHTFPAVLQSSGLYSL 206
QY 178 SQVLLPSKDVMOGTD-----EHK 195
DB 207 SVTVTPSSSL--GTKYTCNVDPHK 228

RESULT 10
US-08-523-894-10
; Sequence 10, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 06-SEP-1995
; APPLICATION NUMBER: US/08/523,894
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-523-894-10

Query Match 52.6%; Score 547; DB 3; Length 467;
Best Local Similarity 57.8%; Pred. No. 3.9e-41;
Matches 118; Conservative 23; Mismatches 49; Indels 14; Gaps 7;

QY 1 LVKPSETLSLCTVSGGSGIS-SYYNWIRQPPGKLEWIGIYIYS-GSTNYPNPSLKSRVT 58
DB 30 LVKPSETLSLCTSVSGSGISGDYWFIRQSPGKLEWIGIYIYGGGGTNYNPSLNNRVS 89
QY 59 ISVDTSKNQFSLKLSVTAADTAVVYCARDRGVGTGFDYWGQGLTVTVSSGSASAPTLF 118
DB 90 ISIDTSKQLFSLKLSRVTAAADTAVVYCASNLKYLHLLYWGQGLTVTVSSASTKGPSVF 149
QY 119 PLVSCENSPDTSVVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLR-GGKYAAT 177
DB 150 PLAPCSRSTSE-STAAAGCLVKDYFPEPTVSM--NSGALTSGVHTFPAVLQSSGLYSL 206
QY 178 SQVLLPSKDVMOGTD-----EHK 195
DB 207 SVTVTPSSSL--GTKYTCNVDPHK 228

RESULT 11
US-08-523-894-12
; Sequence 12, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 06-SEP-1995
; APPLICATION NUMBER: US/08/523,894
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
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; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-12

Query Match 52.6%; Score 547; DB 3; Length 467;
Best Local Similarity 57.8%; Pred. No. 3.9e-41;
Matches 118; Conservative 23; Mismatches 49; Indels 14; Gaps 7;

Qy 1 LVKPESTLSLTCTVSGGIS-SYYWNWIRQPPGKLEWIGYIYS-GSTNNPNSLKSRVT 58
Db 30 LVKPESTLSLTCSVSGGISGDIYFWIRQSPGKLEWIGYIYGGGGTNNPNSLNRRVS 89
Qy 59 ISVDTSKNQPSLKLSVTAADTAIVYICARDRGVGTGFDYWGQGLTVTVSSGSASAPTLF 118
Db 90 ISIDTSKNLFLSKLRSVTAADTAIVYICASNILKYLHLLYWGQGLTVTVSSASTKGPSVF 149
Qy 119 PLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLR-GGKYAAT 177
Db 150 PLAFCSRSTSE-STAAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTFFPAVLQSSGLYLS 206
Qy 178 SQVLLPSKDVMOGTD-----EHK 195
Db 207 SWVTVPSSSL--GTNTYTCNVDDHK 228

RESULT 12
US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-526-098-12
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US-08-487-550-12

Query Match 52.2%; Score 542.5; DB 3; Length 476;
Best Local Similarity 56.8%; Pred. No. 1e-40;
Matches 117; Conservative 22; Mismatches 52; Indels 15; Gaps 8;

Qy 1 LVKPESTLSLTCTVSGGIS-SYYWNWIRQPPGKLEWIGYIY-YSGSTNNPNSLKSRVT 58
Db 30 LVKPESTLSLTCAVSGGISGGYGMWIRQPPGKLEWIGSYSSGNTYNNPSLKSQVT 89
Qy 59 ISVDTSKNQPSLKLSVTAADTAIVYICARDRGVGTG-----FDYWGQGLTVTVSSGSA 112
Db 90 ISDTSKNQPSLKLSNMTAADTAIVYICVRDLFSVGMVNNWFDVMPGVLVTVSSAST 149
Qy 113 SAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLR-G 171
Db 150 KGPSVFPLAPSSKTSG-GTAAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTFFPAVLQSS 206
Qy 172 GKYAATSQVLLPSKDVMOGTDDEHKVC 197
Db 207 GLYSLSSVTVTPSSSL--GTQTY-IC 229

RESULT 13
US-09-526-098-12
; Sequence 12, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-526-098-12

Query Match 52.2%; Score 542.5; DB 4; Length 476;
Best Local Similarity 56.8%; Pred. No. 1e-40;
Matches 117; Conservative 22; Mismatches 52; Indels 15; Gaps 8;
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Qy      1  LVKPSLTLSTCTVSGSIS-SYYWNWIRQPGKLEWIGIYI-YSGSTNNPSLKSRVT 58
Db      30  LVKPSLTLSTCAVSGSGSISGGYGWGWIRQPPGKLEWIGSFYSSSGNTYNNPSLKSOVT 89
Qy      59  ISVDTSKNQPSLKLKSLSVTAADTAVYYCARDRGVGATG-----FDYWGOGTLVTVSSGSA 112
Db      90  ISDTSKNQPSLKLKSLNWTAAADTAVYYCYDRDLRFVVGWYNNWFVDWPGVLVTVSSAST 149
Qy     113  SAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPSDITFGWKYKNSDISSTRGFPSVLR-G 171
Db     150  KGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPTVSM--NSGALTSGVHTFPAVLQSS 206
Qy     172  GKTAATSOVLPLPSKQVMQGTDEHKVC 197
Db     207  GLYSLSVVTPSSSL--GTQTY-IC 229

RESULT 14
US-09-383-916-12
; Sequence 12, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-383-916-12

Query Match          52.2%; Score 542.5; DB 4; Length 476;
Best Local Similarity 56.8%; Pred.No.1e-40;
Matches 117; Conservative 22; Mismatches 52; Indels 15; Gaps 8;

Qy      1  LVKPSLTLSTCTVSGSIS-SYYWNWIRQPGKLEWIGIYI-YSGSTNNPSLKSRVT 58
Db      30  LVKPSLTLSTCAVSGSGSISGGYGWGWIRQPPGKLEWIGSFYSSSGNTYNNPSLKSOVT 89
Qy     59  ISVDTSKNQPSLKLKSLSVTAADTAVYYCARDRGVGATG-----FDYWGOGTLVTVSSGSA 112

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.4472 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-26

Perfect score: 783

Sequence: 1 SQSPSSLSASVGERVTTCR.....VVCLLNNFYPREAKEHOKSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	552.5	72.4	215	2 JE0242	Ig kappa chain NIG
3	541.5	71.0	215	2 JE0243	Ig kappa chain NIG
4	512.5	67.2	215	2 A23746	Ig kappa chain V-I
5	496	65.0	125	2 S40353	Ig kappa chain V-J
6	490	64.2	230	2 S33161	Ig kappa chain - s
7	487	63.8	123	2 S40313	Ig kappa chain V-J
8	485	63.6	234	2 S14237	Ig kappa chain pre
9	481	63.0	141	2 A49134	Ig kappa chain V-I
10	481	63.0	240	2 S06084	Ig kappa chain pre
11	478	62.6	108	1 K1HUGL	Ig kappa chain V-I
12	478	62.6	216	2 JE0241	Ig kappa chain Am3
13	478	62.6	234	2 S01320	Ig kappa chain pre
14	475	62.3	214	2 S68212	Ig kappa chain (Ma
15	468	61.3	108	1 K1HWE	Ig kappa chain V-I
16	462	60.6	132	2 S40334	Ig kappa chain - h
17	459	60.2	126	2 S40335	Ig kappa chain V-J
18	458	60.0	144	2 P0106	Ig kappa chain pre
19	458	60.0	220	2 A31790	Ig kappa chain V r
20	457	59.9	210	2 A56169	Ig kappa chain V r
21	454	59.5	131	2 S40352	Ig kappa chain V-J
22	453.5	59.4	235	2 S25058	Ig kappa chain - m
23	453	59.4	218	2 JC5810	monoclonal antibody
24	452	59.2	107	2 S36262	Ig lambda chain V
25	452	59.2	125	2 S40349	Ig kappa chain V-J
26	451.5	59.2	225	2 S37484	Ig kappa chain - m
27	450	59.0	218	2 S68241	Ig kappa chain V r
28	449	58.8	117	2 S41809	Ig kappa chain V r
29	448	58.7	125	2 S40333	Ig kappa chain V-J

RESULT 1  
JE0244  
Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Te  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 556.5; DB 2; Length 215;  
Best Local Similarity 74.0%; Pred. No. 5e-38;  
Matches 108; Conservative 15; Mismatches 22; Indels 1; Gaps 1;

Qy 1 SQSPSSLSASVGERVTTCRASQIRDELGHVQKPKAPKRLIYVASSLSQSGVSPRSG 60  
Db 5 TQSPATLSVSGERATLSCRASQSVHNSLAWYQKPGQAPRLIYRSTRATGIPARFSG 64  
Qy 61 SCSGTFTLTSSLOPEFATYVCLQNGY-PRTFGQGTKEIKRTVAAPSVFIPPPSDE 119  
Db 65 SCSGTDFILITSSLOSEDFALYYCQYNTWPLTFGGGTKEIKRTVAAPSVFIPPPSDE 124  
Qy 120 QLKSGTASVVCLLNNFYPREAKEHOK 145  
Db 125 QLKSGTASVVCLLNNFYPREAKVQWK 150

RESULT 2  
JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mult  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 552.5; DB 2; Length 215;  
Best Local Similarity 74.0%; Pred. No. 1e-37;  
Matches 108; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

ALIGNMENTS





Ig kappa chain V-I region (ISE) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: A49134; S25115  
R;Rocca, A.; Khamlichi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.L  
Clin. Exp. Immunol. 91, 506-509, 1993  
A;Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light  
A;Reference number: A49134; MUID:93185310; PMID:7680298  
A;Accession: A49134  
A;Status: preliminary  
A;Molecule type: mRNA; protein  
A;Residues: 1-141 <ROC>  
A;Cross-references: EMBL:X67322; NID:G33258; PIDN:CAA47736.1; PID:G33259  
A;Note: sequence extracted from NCB1 backbone (NCBIP:127088)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match	63.0%;	Score 481;	DB 2;	Length 141;
Best Local Similarity	81.7%;	Pred. No. 4.1e-32;		
Matches	94;	Conservative	8;	Mismatches 13; Indels 0; Gaps 0;
QY	1	SQSPSSLSASGGERVTITCRASQGRDELGWQQKPGKAPKRLIYVASSLSQSGVPSRFSG	60	
DB	27	TQSPSTLSASVGDRVTITCRASLGINILAWTQQKPGKAPNLLIYKATNLQSGVPSRPSA	86	
QY	61	SGSGTEFTLISSLPQDFATYYICLQHNQYPRTFGQTKVEIKRTVAAPSVFIFP	115	
DB	87	SGSGTEFTLIISGLQDPDFATYYICHOYDYPWTFGQTKVEIKRTVAAPSVFIFP	141	

RESULT 10  
S06084  
Ig kappa chain precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C;Accession: S06084  
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.  
Nucleic Acids Res. 17, 7992, 1989  
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA  
A;Reference number: S06084; MUID:90016888; PMID:2508067  
A;Accession: S06084  
A;Molecule type: mRNA  
A;Residues: 1-240 <CRO>  
A;Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-240/Product: Ig kappa chain #status predicted <MAT>  
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match	63.0%;	Score 481;	DB 2;	Length 240;
Best Local Similarity	64.8%;	Pred. No. 6.9e-32;		
Matches	94;	Conservative	19;	Mismatches 26; Indels 6; Gaps 1;
QY	1	SQSPSSLSASGGERVTITCRASQGI-----RDELGWYQKPGKAPKRLIYVASSLSQGV	54	
DB	25	TQSPSSLSASGGEIVTINCKSSQSLFYSGNQKNLAWYQKPGQSPKLLIYWASTRQSGV	84	
QY	55	PSRFGSGSGTEFTLTIISSLPQDFATYYICLQHNQYPRTFGQTKVEIKRTVAAPSVFIF	114	
DB	85	PDRFIGSGSGTDFLTIISSVQAEDLAIYVCLQYETPYTFGAGTKLEKRAADAAPTVSIF	144	
QY	115	PPSDEQLKSGTASVVCVLLNNFYPR	139	
DB	145	PPSTEQLATGASVVCVLMNNFYPRD	169	

RESULT 11  
K1HUGL  
Ig kappa chain V-I region (Gal) - human (tentative sequence)  
C;Species: Homo sapiens (man)  
C;Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004

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C;Accession: A01867
R;Laure, C.J.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973
A;Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gall), I
A;Reference number: A01867; MUID:75059122; PMID:4215718
A;Accession: A01867
A;Molecule type: protein
A;Residues: 1-108 <LAU>
A;Cross-references: UNIPROT:P01599
A;Note: The C region of this chain has the Inv (3) marker
C;Comment: This chain was isolated from a Waldenstrom's macroglobulin.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 62.6%; Score 478; DB 1; Length 108;
Best Local Similarity 87.5%; Pred. No. 5.6e-32;
Matches 91; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 TQSPSSLSASVGDRTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 64
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SGSSTFTLTSSSQPEDFATYYCLOHNGYPRTEFGQTKVEIKR 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 SGAGTFTLTSSSQPEDFATYYCLOHNGYPRTEFGQTKVEIKR 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
JE0241
Ig kappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0241
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JFID, November 1998
A;Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0241
A;Molecule type: protein
A;Residues: 1-216 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>

Query Match 62.6%; Score 478; DB 2; Length 216;
Best Local Similarity 65.8%; Pred. No. 1.1e-31;
Matches 98; Conservative 18; Mismatches 27; Indels 6; Gaps 3;

Qy 1 SQSPSSLSASVGERVTITCRASQGI-----RDELGWYQKPGKAPKRLIYVASSLSQSGVPS 56
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 TQSPDFLAVSGERATINCKSSQSVLYNKNFLAWYQKPGQ-PKLLIW-ANVRESGVDP 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 57 RFGSGSGTFTLTSSSQPEDFATYYCLOHNGYPRTEFGQTKVEIKRTVAAPSVFIPPP 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 RFRGSGVGTDFLTITSNLAELVAVYQQYYSTPSPFGQGRLEIKRTVAAPSVFIPPP 122
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 117 SDEQLKSGTASVVCLLNNFYPREAKEHOK 145
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 SDEQLKSGTASVVCLLNNFYPREAKVQWK 151
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
S01320
Ig kappa chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
```

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C;Accession: S01320
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed at
A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01320
A;Molecule type: mRNA
A;Residues: 1-234 <DE1>
A;Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579,1; PID:g51785
A;Note: This sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-234/Product: Ig kappa chain #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 62.6%; Score 478; DB 2; Length 234;
Best Local Similarity 66.2%; Pred. No. 1.2e-31;
Matches 92; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 TQSPASLSVSVGESVTITCRASENIYSNLAWYQKQKSPQLLYVATKLVGDVPSRFSG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SGSSTFTLTSSSQPEDFATYYCLOHNGYPRTEFGQTKVEIKRTVAAPSVFIPPPSEQ 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 SGSSTYSLKINSIQSEDFGSIYQHFWDPTFTFGSGTKLEMKRADAAPTYSIFPPSSEQ 144
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 LKSGTASVVCLLNNFYPRE 139
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 145 LTSGGASVVCFLNNFYPKD 163
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C;Accession: S68212
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68212
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-214 <TAK>
A;Cross-references: EMBL:D29668
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 62.3%; Score 475; DB 2; Length 214;
Best Local Similarity 62.1%; Pred. No. 1.9e-31;
Matches 90; Conservative 24; Mismatches 25; Indels 6; Gaps 1;

Qy 1 SQSPSSLSASVGERVTITCRASQGI-----RDELGWYQKPGKAPKRLIYVASSLSQSGV 54
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 TQSPSSLSASVGVKVTMSCKSSQSLNRSQKNLAWYQKPGQSPKLLVYFASRFSGV 64
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 55 PSRFSGSGSGTFTLTSSSQPEDFATYYCLOHNGYPRTEFGQTKVEIKRTVAAPSVFI 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 PDRFISGSGTDFLTITSTVQAEADLADYFCQHYSTPYTFGGTGKLEIKRADAAPTYSIF 124
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 115 PPSDEQLKSGTASVVCLLNNFYPRE 139
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 PPSDEQLTSGGASVVCFLNNFYPKD 149
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
K1HUWE
Ig kappa chain V-I region (WEA) - human
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A01876
```

Search completed: March 8, 2005, 06:39:22  
Job time : 10.4972 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 54.8971 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-26

Perfect score: 763

Sequence: 1 SQSSSSLSASVGRVTTCR.....VVCLLNFPYPRAEKHQKSP 147

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	665	87.2	236	2	Q6GMW1	Q6gmw1 homo sapien
2	633	83.0	236	2	Q6GMX8	Q6gmw8 homo sapien
3	631	82.7	236	2	Q6PIT5	Q6pit5 homo sapien
4	628	82.3	236	2	Q6PIH7	Q6pih7 homo sapien
5	621	81.4	236	2	Q723V4	Q723v4 homo sapien
6	620	81.3	236	2	Q6GMX9	Q6gmw9 homo sapien
7	606	79.4	236	2	Q6GMX0	Q6gmw0 homo sapien
8	604	79.2	234	2	Q72473	Q72473 homo sapien
9	601	78.8	236	2	Q6PIH4	Q6pih4 homo sapien
10	552.5	72.4	235	2	Q6GMW0	Q6gmw0 homo sapien
11	536	70.2	236	2	Q6PIL8	Q6pil8 homo sapien
12	530.5	69.5	235	2	Q6GMV9	Q6gmw9 homo sapien
13	530.5	69.5	235	2	Q6PJP2	Q6pjf2 homo sapien
14	527	69.1	236	2	Q6P5S8	Q6p5s8 homo sapien
15	503	65.9	236	2	Q7TS98	Q7ts98 mus musculus
16	497.5	65.2	239	2	Q8NEK0	Q8nek0 homo sapien
17	496.5	65.1	239	2	Q8TCD0	Q8tcd0 homo sapien
18	484	63.4	240	2	Q6PIH6	Q6pih6 homo sapien
19	478	62.6	108	1	KV1G_HUMAN	P01599 homo sapien
20	476.5	62.5	239	2	Q6P491	Q6p491 homo sapien
21	468	61.3	108	1	KV1R_HUMAN	P01610 homo sapien
22	446	58.5	238	2	Q66JS7	Q66js7 mus musculus
23	442	57.9	108	2	Q9UL70	Q9ul70 homo sapien
24	433	56.7	108	1	KV1V_HUMAN	P04430 homo sapien
25	431.5	56.6	219	2	Q65ZC0	Q65zc0 mus musculus
26	429.5	56.3	243	2	Q6NTU5	Q6ntu5 xenopus lae
27	428	56.1	244	2	Q65ZC8	Q65zc8 homo sapien
28	426	55.8	108	2	Q9UL77	Q9ul77 homo sapien
29	424	55.6	108	1	KV1H_HUMAN	P01600 homo sapien
30	421	55.2	237	2	Q75Z36	Q75z36 xenopus lae
31	420.5	55.1	107	2	Q96SA9	Q96sa9 homo sapien

RESULT 1

Q6GMW1	PRELIMINARY;	PRT;	236 AA.
AC	Q6GMW1;		
DT	05-JUL-2004 (Tremblrel. 27, Created)		
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)		
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Spleen;		
RX	MEDLINE=24388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RC	SEQUENCE FROM N.A.		
RC	TISSUE=Spleen;		
RA	Strausberg R.;		
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.		
DR	EMBL; BC073791; AAH73791.1; -		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003597; IG c1.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF07654; Cl-set; 1.		
DR	SMART; SM00407; IG; 2.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGcl; 1.		
DR	SMART; SM00406; IGv; 1.		
DR	PROSITE; PS50835; IG_LIKE; 2.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.		

Q65zcc9 homo sapien  
P01598 homo sapien  
Q9ul79 homo sapien  
P01594 homo sapien  
Q96pf6 homo sapien  
P01605 homo sapien  
P01604 homo sapien  
P01611 homo sapien  
P01603 homo sapien  
P04431 homo sapien  
P01596 homo sapien  
Q63zxx4 mus musculus  
P01607 homo sapien  
P01597 homo sapien

```
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 87.2%; Score 665; DB 2; Length 236;
Best Local Similarity 89.7%; Pred. No. 1.4e-58;
Matches 130; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 SQSPSSLSASGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 60
Db 27 TQSPSSLSASVGDRTVITCRASQIGISNDLGNWYQKPGKAPKLLIYAASSLSQGVPSRFSG 86
QY 61 SSGSGTEFTLTSSQLPEDFATYYCLQHNHGYPRTEGQGTQKVKIRKTAAPSFIPIPPSDEQ 120
Db 87 SSGSGTDFLTSSQLPEDFATYYCLQVNYEPTWTEGQGTQKVKIRKTAAPSFIPIPPSDEQ 146
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 147 LKSGTASVVCLLNNFYPREAKVQWK 171

RESULT 2
Q6GMX8 PRELIMINARY; PRT; 236 AA.
ID Q6GMX8 AC Q6GMX8
AC Q6GMX8 AC Q6GMX8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG. 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
```

```
DR PROSITE; PS00290; IG.MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 83.0%; Score 633; DB 2; Length 236;
Best Local Similarity 85.5%; Pred. No. 2.2e-55;
Matches 124; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 SQSPSSLSASGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 60
Db 27 TQSPSSLSASVGDRTVITCRASQIGISNLGNWYQKPGKAPKLLIYAASSLSQGVPSRFSG 86
QY 61 SSGSGTEFTLTSSQLPEDFATYYCLQHNHGYPRTEGQGTQKVKIRKTAAPSFIPIPPSDEQ 120
Db 87 SSGSGTDFLTSSQLPEDFATYYCQAHSPFTFTGPGTKVDIKRTVAAPSFIPIPPSDEQ 146
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 147 LKSGTASVVCLLNNFYPREAKVQWK 171

RESULT 3
Q6PITS PRELIMINARY; PRT; 236 AA.
ID Q6PITS AC Q6PITS
AC Q6PITS AC Q6PITS
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029444; AAH29444.1; -.
DR HSP; P01607; IAR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
```

```
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEE351 CRC64;

Query Match 82.7%; Score 631; DB 2; Length 236;
Best Local Similarity 84.8%; Pred.No. 3.6e-55;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SQSPSSLSASGGERVTITCRASQGIIRDELGWYQKPGKAPKELIYVASSLSQSGVPSRFSG 60
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 TQSPSSLSASGGERVTITCRASQGISSALAWYQKPGKPKLLIYDASTMESGVPSRFSG 86
QY 61 SSGSGTEFTLTSSLOPEDFATYICLQHGNYPRTFQGGTKVEIKRTVAAPSVFIPPPSDEQ 120
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 SSGSGTEFTLTSSLOPEDFATYICQFKSYPRTFQGGTKVEIKRTVAAPSVFIPPPSDEQ 146
QY 121 LKSGTASVVCLLNNFPYPREAKEHOK 145
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 LKSGTASVVCLLNNFPYPREAKVQWK 171

RESULT 4
Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; 1AB2.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; I.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213P CRC64;

Query Match 82.3%; Score 628; DB 2; Length 236;
Best Local Similarity 86.2%; Pred.No. 7.2e-55;
Matches 125; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 1 SQSPSSLSASGGERVTITCRASQGIIRDELGWYQKPGKAPKELIYVASSLSQSGVPSRFSG 60
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 TQSPSSLSASGGERVTITCRASQGISSALAWYQKPGKPKLLIYDASTMESGVPSRFSG 86
QY 61 SSGSGTEFTLTSSLOPEDFATYICLQHGNYPRTFQGGTKVEIKRTVAAPSVFIPPPSDEQ 120
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 SSGSGTEFTLTSSLOPEDFATYICQQLNSPPTFGGTKVEIKRTVAAPSVFIPPPSDEQ 146
QY 121 LKSGTASVVCLLNNFPYPREAKEHOK 145
DQ :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 LKSGTASVVCLLNNFPYPREAKVQWK 171

RESULT 5
Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; I.
DR SMART; SM00406; IGV; 1.
DR SMART; PS00835; IG_LIKE; 2.
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DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFBE4ED23084BC6 CRC64;

Query Match 81.4%; Score 621; DB 2; Length 236;
Best Local Similarity 84.1%; Pred. No. 3.6e-54;
Matches 122; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 SQSPSSLSASGVGVTTTCRASQGIIRDELGHVQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
27 TQSPSSLSASGVGVTTTCRASQDISLNLAWFQKPGKAPKSLIYVASSLSQSGVQSKFSG 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SSGSGTEFTLTSSLOPEDFATYYCLQHNGYPRTFQGGTKVEIKRTVAAPSVFIPPPSDEQ 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
87 SSGSGTDFLTLTSSLOPEDFATYYCQYKSYPTVTFGGTKLEIKRTVAAPSVFIPPPSDEQ 146
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LKSGTASVCLNNFYPREAKEHQK 145
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
147 LKSGTASVCLNNFYPREAKVQWK 171
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q6GMX9 PRELIMINARY; PRT; 236 AA.
ID Q6GMX9
AC Q6GMX9;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalious D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;

Query Match 81.3%; Score 620; DB 2; Length 236;
Best Local Similarity 84.1%; Pred. No. 4.6e-54;
Matches 122; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 SQSPSSLSASGVGVTTTCRASQGIIRDELGHVQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
27 TQSPSSLSASGVGVTTTCRASQNVRLAWYQORPEKAPKSLIYATSSLSGVPSRFSG 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SSGSGTEFTLTSSLOPEDFATYYCLQHNGYPRTFQGGTKVEIKRTVAAPSVFIPPPSDEQ 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
87 SSGSGTDFLTLTSSLOPEDFATYYCQYNTYPLTFGGTKVEIKRTVAAPSVFIPPPSDEQ 146
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LKSGTASVCLNNFYPREAKEHQK 145
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
147 LKSGTASVCLNNFYPREAKVQWK 171
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q6GMX0 PRELIMINARY; PRT; 236 AA.
ID Q6GMX0
AC Q6GMX0;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalious D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 79.4%; Score 606; DB 2; Length 236;
Best Local Similarity 82.8%; Pred. No. 1.2e-52;
Matches 120; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
27 TQSPSSLSASVGERVTITCRASQGINNNYLNWYQLKPGKAPNLLIYVASSLSQSGVPSRFSG 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGTEFTLTSSLOPEDFATYICLOHNGYRPTFGQGTKEIKRTVAAPSVFIFPPSDEQ 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
87 SSGSGTDFLTSSLRPDDFATYICQSYNIPLTFGGNTNVEIKRTVAAPSVFIFPPSDEQ 146
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 LKSGTASVVCLLNNFYPREAKEHQK 145
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 LKSGTASVVCLLNNFYPREAKEVQWK 171
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 79.2%; Score 604; DB 2; Length 234;
Best Local Similarity 82.1%; Pred. No. 1.8e-52;
Matches 119; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
25 TQSPSSPSASGDRVTITCRASQSIGSLAWYQKPGKAPOLLIYAASTLQSGVPSRFSG 84
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGTEFTLTSSLOPEDFATYICLOHNGYRPTFGQGTKEIKRTVAAPSVFIFPPSDEQ 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
85 SASGTDFTLTSSLSQSGEDFATYICQYYTYPWTFGQGTKEIKRTVAAPSVFIFPPSDEQ 144
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 LKSGTASVVCLLNNFYPREAKEHQK 145
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 145 LKSGTASVVCLLNNFYPREAKEVQWK 169
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
Q6PIH4 PRELIMINARY; PRT; 236 AA.
AC Q6PIH4
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034146; AAH34146.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25871 MW; BE01A28CD06BEE26 CRC64;

Query Match 78.8%; Score 601; DB 2; Length 236;
Best Local Similarity 82.1%; Pred. No. 3.7e-52;
Matches 119; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASGVGVTTTCRASQIGIRDELGWYQKPKAPKRLIYVASSLSQSGVPSRFSG 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 27 TQSPSTLSASGVDRVTIACRASQISDWLAWYQKPKAPKRLIYDASRLSLSGVPSRFSG 86
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 SSGSTETLTSSLOPEDFATYICLOHNGY-PRTFGGTKVKEIKRTVAAPSVFIPPSDEQ 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 87 SSGSTETLTSSIGLPDDFATYICQYNSNSPFGQGTKEIKRTVAAPSVFIPPSDEQ 146
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 147 LKSGTASVVCLLNNFYPREAKVQWK 171
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 10
Q6GMW0 PRELIMINARY; PRT; 235 AA.
ID Q6GMW0
AC Q6GMW0;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IG; 2.
DR SMART; SM00407; IGc1; 1.

DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 72.4%; Score 552.5; DB 2; Length 235;
Best Local Similarity 74.0%; Pred. No. 2.8e-47;
Matches 108; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

Qy 1 SQSPSSLSASGVGVTTTCRASQIGIRDELGWYQKPKAPKRLIYVASSLSQSGVPSRFSG 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 25 TQSPATLSVSGERATLSCRASQISNNLAWYQORPGQAPRLIYGASSRVITGIPRFSG 84
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 SSGSTETLTSSLOPEDFATYICLOHNGY-PRTFGGTKVKEIKRTVAAPSVFIPPSDE 119
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 85 SSGSTETLTSSISQSEDFAVIFCOQYNDMLLYTFGGTKLEIKRTVAAPSVFIPPSDE 144
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 120 QKSGTASVVCLLNNFYPREAKEHQK 145
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 145 QKSGTASVVCLLNNFYPREAKVQWK 170
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
Q6PIL8 PRELIMINARY; PRT; 236 AA.
ID Q6PIL8
AC Q6PIL8;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032451; AAH32451.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
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```
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 69.5%; Score 530.5; DB 2; Length 235;
Best Local Similarity 70.5%; Pred. No. 4.5e-45;
Matches 103; Conservative 17; Mismatches 25; Indels 1; Gaps 1;

QY 1 SQSPSSLSASVGERVTITCRASQGRDE-LGWYQKPGKAPKRLIYVASSLQSGVPSRFS 59
DB 25 TQSPATLSLSPGERATLSRASQIVSSAYLAWYQKPGQAPRLIMFGSSSRATGIPDRFS 84

QY 60 GSGSGTEFTLTISLQPEDFATYYCLOHNGYPRFTFGQGTKEIKRTVAAPSVFIFFPSDE 119
DB 85 GSGSGTDFLTITSLRLEPEDFAVYCCQYSGQTFGPGTKVDIKRTVAAPSVFIFFPSDE 144

QY 120 QLKSGTASVCLNNFYPREAKEHOK 145
DB 145 QLKSGTASVCLNNFYPREAKVQWK 170

RESULT 14
Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=glandular pool- thyroid;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Kryzinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2];
RP SEQUENCE FROM N.A.
RC TISSUE=glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; 1KCU;
DR InterPro; IPR003599; IG;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003006; IG_MHC.
```

```
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BBB4PF527 CRC64;

Query Match 69.1%; Score 527; DB 2; Length 236;
Best Local Similarity 70.7%; Pred. No. 1e-44;
Matches 104; Conservative 16; Mismatches 25; Indels 2; Gaps 2;

QY 1 SQSPSSLSASVGERVTITCRASQGI-RDELGWYQKPGKAPKRLIYVASSLQSGVPSRFS 59
DB 25 TQSPGTLSLSPGERATLSRASQIVSSHLAWYQORPGQAPRLIYGASSRATGIPDRFS 84

QY 60 GSGSGTEFTLTISLQPEDFATYYCLOHNGYPR-TFGQGTKEIKRTVAAPSVFIFFPSD 118
DB 85 GSGSGTDFLTITRLEPEDFAVYCCQYGTSPSLTFGGGTRVEIKRTVAAPSVFIFFPSD 144

QY 119 EQLKSGTASVCLNNFYPREAKEHOK 145
DB 145 EQLKSGTASVCLNNFYPREAKVQWK 171

RESULT 15
Q7TS98 PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=93383497; PubMed=8372513;
RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 1116NS19.9 heavy and light chain
RT cDNAs and expression of antibody fragments in Escherichia coli.";
RL Year Immunol. 7:56-62 (1993).
DR EMBL; S65921; AAB28160.1; -.
DR HSSP; P01837; 1KB5.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 26454 MW; 2C586BFB5EA10F4C CRC64;

Query Match 65.9%; Score 503; DB 2; Length 236;
Best Local Similarity 69.1%; Pred. No. 2.7e-42;
Matches 96; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 1 SQSPSSLSASVGERVTITCRASQGRDELGWYQKPGKAPKRLIYVASSLQSGVPSRFS 60
DB 27 TQSPSSMTASLSPGERVTITCRASQDINSYLSWFOQPGKSPKTIYRANRLVDGVPDRFS 86

QY 61 GSGSGTEFTLTISLQPEDFATYYCLOHNGYPRFTFGQGTKEIKRTVAAPSVFIFFPSDEQ 120
DB 87 GSGGQDYSLTISLSEYEDMGIIYCLQYDEPRFTFGGTKLEIKRADRAPTVSIFFPSSEQ 146

QY 121 LKSGTASVCLNNFYPRE 139
DB 147 LTSGGASVVCFLNNFYPKD 165
```

Search completed: March 8, 2005, 06:35:47  
Job time : 55.8971 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 68.1532 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-26

Perfect score: 763

Sequence: 1 SQSPSSLASVGERVTTCR.....VVCLLNPNYPREAKEHQKSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	763	100.0	147	2	AAY34310 IgM antib
2	698	91.5	236	5	ABG77164 Germline
3	698	91.5	236	8	ADR28586 Human ant
4	697	91.3	184	8	ADSR4439 Human ant
5	697	91.3	184	8	ADR68581 Human ant
6	696	91.2	236	5	ABG77160 Germline
7	696	91.2	236	8	ADR28582 Human ant
8	695	91.1	147	2	AAY34312 IgM antib
9	691	90.6	234	8	ADSR4470 Human ant
10	691	90.6	234	8	ADR68612 Human ant
11	690	90.4	215	8	ADH10328 Anti-HIV-
12	690	90.4	234	8	ADSR44464 Human ant
13	690	90.4	234	8	ADR68606 Human ant
14	689	90.3	152	8	ADK52390 Human ant
15	688	90.2	234	8	ADSR4476 Human ant
16	688	90.2	234	8	ADSR4452 Human ant
17	688	90.2	234	8	ADR68618 Human ant
18	688	90.2	234	8	ADR68594 Human ant
19	686	89.9	236	8	ADP07905 Human imm
20	683	89.5	152	8	ADK52354 Human ant
21	682	89.4	234	8	ADSR4458 Human ant
22	682	89.4	234	8	ADR68600 Human ant
23	675	88.5	236	5	ABG77163 Amino aci
24	675	88.5	236	8	ADR28585 Human ant
25	670	87.8	236	5	ABG77159 Amino aci

26	670	87.8	236	8	ADR28581	Adr28581 Human ant
27	665	87.2	164	7	ADD28242	Ad28242 Human het
28	662	86.8	212	6	AAO31100	Aao31100 Human A2-
29	653	85.6	233	8	ADR46823	Adr46823 Human ant
30	651	85.3	214	7	ADF11431	Adf11431 18B2 anti
31	649	85.1	236	5	AAU74297	Aau74297 Anti-huma
32	648.5	85.0	234	2	AAK38162	Aak38162 Human imm
33	646	84.7	224	4	AAW75043	Aaw75043 TRO005 Hu
34	644	84.4	214	2	AAV08600	Aav08600 JP1112785
35	642	84.1	214	8	ADF11669	Adf11669 anti-CD11
36	642	84.1	224	4	AAW75040	Aaw75040 TRO005 Hu
37	642	84.1	236	2	AAK42065	Aak42065 Human ant
38	641	84.0	136	5	ABG77135	Abg77135 Anti-IGF-
39	641	84.0	136	8	ADR28536	Adr28536 Human ant
40	640	83.9	224	4	AAW75044	Aaw75044 TRO005 Hu
41	640	83.9	224	4	AAW75041	Aaw75041 TRO005 Hu
42	639	83.7	234	7	ADM47073	Adm47073 Mouse ant
43	638	83.6	164	2	AAV34317	Aav34317 IgG antib
44	638	83.6	214	7	ADF11423	Adf11423 2B11 anti
45	636.5	83.4	241	4	AAW82912	Aaw82912 Human imm

#### ALIGNMENTS

RESULT 1  
AAY34310  
ID AAY34310 standard; protein; 147 AA.  
XX  
AC AAY34310;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE Igm antibody CEM 10.1 G10 kappa chain sequence.  
XX

KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

XX WO9945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX WPI; 1999-540816/45.

XX N-PSDB; AA220411.

XX New monoclonal antibody, used for treating e.g. graft versus host  
XX disease, cancers, autoimmune diseases and inflammatory diseases.  
XX Claim 61; Fig 25; 245pp; English.

XX This sequence represents the kappa chain of an antibody of the invention.

CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood





ischaemia or neurodegenerative disorder) in a mammal. The method comprises administering to the mammal an amount of a human anti-insulin-like growth factor I receptor (IGF-IR) antibody. Also described is a pharmaceutical composition for treating or preventing the above-mentioned disorder in a mammal, comprising an amount of the human anti-IGF-IR antibody and a pharmaceutical carrier. The composition has cytostatic, immunosuppressive, endocrine, vasotropic, neuroprotective, trophic and antithyroid activities, and can be used in vaccines and in gene therapy. The method and composition are useful for preventing or treating aging or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus disorder, T-cell-mediated autoimmune disease, endocrinological disorder, ischaemia or neurodegenerative disorder) in mammals, such as humans. The human IGF-IR antibody is used in preparing a composition for the treatment or prevention of the above-mentioned disorders. The present sequence represents a human anti-IGF-IR antibody light chain amino acid sequence, which is used in the exemplification of the present invention.

Sequence 236 AA;

```

Query Match      91.5%; Score 698; DB 8; Length 236;
Best Local Similarity 93.1%; Pred. No. 1.1e-43;
Matches 135; Conservative 4; Mismatches 6; Indels 0; Gaps 0

Qy      1  SOSPSLSASVGERVTTTCRASQGRDLGWYQOKPKGKAPRLIYVASSIQSGVPSRSG 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      27  TOSPSLSASVGDRTVTTTCRASQGRDLGWYQOKPKGKAPRLIYAASLQSGVPSRSG 86

Qy      61  SSGSGTEFLTITSSLPQDPATYYCLQHNGYPRVFGQTKVEIKRTVAAPSVFIPPPSDQ 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      87  SSGSGTEFLTITSSLPQDPATYYCLQNSVPWFVFGQTKVEIKRTVAAPSVFIPPPSDQ 146

Qy      121  LKSGTASVVCLLNNFYPREAKEHQK 145
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      147  LKSGTASVVCLLNNFYPREAKVOMK 171
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 4	
ADS84439	
ID	ADS84439 standard; protein; 184 AA.
XX	
AC	ADS84439;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Human anti-EPO-R antibody Ab12 light chain SEQ ID NO:78.
XX	
KW	human; erythropoietin receptor; EPO receptor;
KW	erythropoietin receptor binding antibody; EPO receptor binding antibody;
KW	antianemic; neuroprotective; vulnerable; gene therapy; aplasia; anaemia;
KW	wound healing; neural cell damage protection;
KW	neural tissue damage protection; brain injury; spinal cord injury;
KW	stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
XX	
OS	Homo sapiens.
XX	
PN	WO2004035603-A2.
XX	
PD	29-APR-2004.
XX	
PF	14-OCT-2003; 2003WO-US032243.
XX	
PR	14-OCT-2002; 2002US-00269711.
PR	10-OCT-2003; 2003US-00684109.
XX	
PA	(ABBO ) ABBOTT LAB.
XX	
PI	Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
XX	
WPI	2004-348433/32.
DR	N-PSDB; ADS84437, ADS84438.
XX	
PT	New antibodies that bind to or activate an endogenous human
PT	erythropoietin receptor, useful for diagnosing, preventing or treating

disorders associated with dysfunctional erythropoietin receptor, e.g. anemia.

Claim 41; SEQ ID NO 78; 192pp; English.

The present invention describes an antibody or its fragment that binds to or activates an endogenous activity of a human erythropoietin (EPO) receptor in a mammal, but does not interact with a peptide having a sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1) methods of modulating or activating an endogenous activity of a human EPO receptor in a mammal, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (2) a method of treating a mammal suffering from aplasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) an isolated and purified polynucleotide sequence, and their fragments, complements and degenerate codon equivalents; and (5) an isolated and purified amino acid sequence, and their fragments. The EPO receptor binding antibody has antianemic, neuroprotective and vulnerable activities, and can be used in gene therapy. The compositions and methods from the present invention can be used for modulating an endogenous activity of a human EPO receptor or for treating mammals suffering from aplasia or anaemia. They may also be used for identifying mammals having a dysfunctional EPO receptor. The composition may also be used in promoting wound healing or in protecting against neural cell and/or tissue damage resulting from brain/spinal cord injury, stroke and the like. The present sequence represents a human anti-EPO-R antibody light chain, which is given in the exemplification of the present invention.

Sequence 184 AA;

Sequence 184 AA;

Query Match	91.3%;	Score 697;	DB 8;	Length 184;
Best Local Similarity	93.1%;	Pred. No. 1e-43;		
Matches 135;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0
QY	1	SQSPSSLSASVGERVTITCRASQGIIRDLCWYQKPGKAPKRLIYVASSLQSGVPSRFSG	60	
Db	27	TQSPSSLSASVGDRTVITCRASQGIIRDLCWYQKPGKAPKRLIYVASSLQSGVPSRFSG	86	
QY	61	SGSGTEFTLTISLQPEDFATYCYLQHGYPRTFGQGTKEIKRTVAAPSVFIFFPSDSQ	120	
Db	87	SGSGTEFTLTISLQPEDFATYCYLQHTYPTFFGQGTKEIKRTVAAPSVFIFFPSDSQ	146	
QY	121	LKSGTASVVCLLNNFYPREAKEHQK	145	
Db	147	LKSGTASVVCLLNNFYPREAKVQWK	171	

XX	ADRB68581 standard; protein; 184 AA.
XX	ADRB68581;
XX	02-DEC-2004 (first entry)
XX	Human antibody Ab12 light chain polypeptide seqid 78.
XX	antianemic; respiratory; vulnerary; gene therapy; vaccine;
XX	erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
XX	hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
XX	wound healing; neural cell damage; tissue damage; brain injury;
XX	spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;
XX	AB12.
XX	Homo sapiens.
XX	OS
XX	PN
XX	US2004175379-A1.
XX	09-SEP-2004.
XX	

PF 10-OCT-2003; 2003US-00684109.  
PR 14-OCT-2002; 2002US-0418031P.  
XX  
XX (DEVIR) DEVRIES P J.  
FA (OSTR) OSTROW D H.  
PA (REIL) REILLY E B.  
PA (GREE) GREEN L L.  
PA (WIEL) WIELER J.  
XX  
PI Devries PJ, Ostrow DH, Reilly BB, Green LL, Wieler J;  
XX  
XX WPI; 2004-661369/64.  
DR N-PSDB; ADR68579, ADR68586.  
XX  
XX New antibody or its antibody fragment that activates an endogenous  
PT activity or is capable of binding to a human erythropoietin receptor in a  
PT mammal, useful for treating a mammal suffering aplasia or anemia.  
XX  
XX Claim 41; SEQ ID NO 78; 156pp; English.  
XX  
XX The invention describes an antibody or its fragment that activates an  
CC endogenous activity or capable of binding to a human erythropoietin  
CC receptor in a mammal, or that comprises at least one heavy or light chain  
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
CC given in the specification. Also described are: a method of activating or  
CC modulating an endogenous activity of a human erythropoietin receptor in a  
CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
CC isolated and purified polynucleotide sequence selected from 28 sequences  
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in  
CC the specification, and their fragments, complements, and degenerate codon  
CC equivalents; and an isolated and purified amino acid sequence selected  
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between  
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
CC their fragments. The antibody or its antibody fragment that activates or  
CC modulates the activity of the receptor is useful in a method of treating  
CC a mammal suffering aplasia or anemia. The antibodies are also useful for  
CC treating disorders characterised by decreased or subnormal levels of  
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
CC hypoxia and/or diseases characterised by inadequate blood circulation or  
CC reduced blood flow. They are also useful for promoting wound healing or  
CC for protecting against neural cell and/or tissue damage, resulting from  
CC brain/spinal cord injury, stroke and the like. The antibodies are also  
CC useful for identifying or diagnosing mammals having dysfunctional  
CC erythropoietin receptor. This is the amino acid sequence of a human Ab12  
XX antibody light chain polypeptide.  
XX  
XX Sequence 184 AA;  
Query Match 91.3%; Score 697; DB 8; Length 184;  
Best Local Similarity 93.1%; Pred. No. 1e-43;  
Matches 135; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 1 SQSPSSLSASGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 60  
Db 27 TQSPSSLSASVGDRTVITCRASQGIIRNDLWYQKPGKAPKRLIYVASSLSQGVPSRFSG 86  
QY 61 SSGSGTEFTLTISLQPEDFATYYCLQHNQYPRTEGQGTKEIKRTVAAPSFIFFPSDEQ 120  
Db 87 SSGSGTEFTLTISLQPEDFATYYCLQHNQYPTTGGQGTKEIKRTVAAPSFIFFPSDEQ 146  
QY 121 LKSGTASVCLLNFPYPREAKEHOK 145  
Db 147 LKSGTASVCLLNFPYPREAKVQWK 171  
RESULT 6  
ABG77160  
ID ABG77160 standard; protein; 236 AA.  
XX

AC ABG77160;  
XX  
XX 24-OCT-2002 (first entry)  
XX  
XX Germline protein sequence of anti-IGF-IR antibody AJ30/Jk2.  
XX  
XX Insulin-like growth factor I receptor; antibody; human; cytostatic;  
KW osteopathic; antiatherosclerotic; antiapoptotic; IGF-IR; tumour;  
KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;  
KW acromegaly; gigantism; psoriasis; atherosclerosis.  
XX  
XX Homo sapiens.  
XX  
XX WO200253596-A2.  
XX  
XX 11-JUN-2002.  
XX  
XX 20-DEC-2001; 2001WO-US0511113.  
XX  
XX 05-JAN-2001; 2001US-0259927P.  
XX  
XX (PFIZ ) PFIZER INC.  
FA (ABGE-) ABGENIX INC.  
XX  
XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;  
PI  
XX WPI; 2002-575410/61.  
XX  
XX Novel humanized, chimeric monoclonal antibody that specifically binds to  
PT insulin-like growth factor I (IGF-I) receptor useful for inhibiting  
PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.  
XX  
XX Disclosure; Fig 19C; 172pp; English.  
XX  
XX This invention relates to a novel humanised, chimeric or human monoclonal  
CC antibody or its antigen binding portion that specifically binds to  
CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the  
CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-  
CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine  
CC phosphorylation. The antibodies of the invention are useful for  
CC diagnosing the presence or location of an IGF-IR-expressing tumour in a  
CC subject. The antibody or its antigen-binding portion is also useful for  
CC treating cancer in a human. The method for this further involves an anti  
CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The  
CC antibodies may also be useful for increasing IGF-IR activity and thus  
CC restoring IGF-IR activity in a condition characterised by low IGF-IR  
CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is  
CC also useful for inducing apoptosis of specific cells in a patient, and to  
CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,  
CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies  
CC minimise the immunogenic and allergic responses intrinsic to mouse or  
CC mouse-derivatised monoclonal antibodies and thus increase the efficacy  
CC and safety of the administered antibodies. The present sequence  
CC represents an anti-insulin-like growth factor I receptor antibody of the  
XX invention  
XX  
XX Sequence 236 AA;  
Query Match 91.2%; Score 696; DB 5; Length 236;  
Best Local Similarity 92.4%; Pred. No. 1.5e-43;  
Matches 134; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
QY 1 SQSPSSLSASGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 60  
Db 27 TQSPSSLSASVGDRTVITCRASQGIIRNDLWYQKPGKAPKRLIYVASSLSQGVPSRFSG 86  
QY 61 SSGSGTEFTLTISLQPEDFATYYCLQHNQYPRTEGQGTKEIKRTVAAPSFIFFPSDEQ 120  
Db 87 SSGSGTEFTLTISLQPEDFATYYCLQHNQYPTTGGQGTKEIKRTVAAPSFIFFPSDEQ 146  
QY 121 LKSGTASVCLLNFPYPREAKEHOK 145  
Db 147 LKSGTASVCLLNFPYPREAKVQWK 171





RESULT 11	
ADH10328	
ID	ADH10328 standard; protein; 215 AA.
XX	
AC	ADH10328;
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	Anti-HIV-gp120-antibody light chain sequence.
XX	
XX	Glycoprotein; gp120; anti-HIV; vaccine; antibody S8; human; antibody S19;
XX	antibody S20.
KW	
XX	
OS	Homo sapiens.
XX	
PN	EP1371660-A1.
XX	
PD	17-DEC-2003.
XX	
PF	14-JUN-2002; 2002EP-00380126.
XX	
PR	14-JUN-2002; 2002EP-00380126.
XX	
PA	(CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX	( PHAA ) PHARMACIA SPAIN.
PA	
XX	
PI	Toran JL, Martinez Alonso C;
XX	

DR	WPI; 2004-055251/06.
DR	N-PSDB; ADH10327.
XX	
PT	Novel antibody or its fragment comprising a light chain and/or heavy
PT	chain which is capable of binding to glycoprotein gp120 of human
PT	immunodeficiency virus (HIV) useful for treating HIV infection.
XX	
XX	Claim 1; SEQ ID NO 2; 56pp; English.
PS	
CC	The invention relates to an antibody (I) or its fragment comprising heavy
CC	chain and/or light chain, capable of binding to glycoprotein gp120
CC	protein of HIV, anti-HIV vaccine (I) or a chemical compound identified by
CC	(I) is useful for preventing and treating HIV infections. They are also
CC	useful for inhibiting binding of HIV to a viral co-receptor. The present
CC	sequence represents the light chain sequence of anti-HIV-gp120 antibody
CC	S8, S19 and S20.
XX	
XX	Sequence 215 AA;
Qy	Query Match 90.4%; Score 690; DB 8; Length 215;
Dd	Best Local Similarity 91.7%; Pred. No. 3.8e-43;
Dd	Matches 133; Conservative 4; Mismatches 8; Indels 0; Gaps 0
Qy	1 SQSPSSLSASVGERVTITCRASQIRDELGWYQQPGKAPKRLIYVAASSLQSQGVPSRFSG 60
Dd	: :       :       :       :       :       :
Qy	3 TQSPSSLSASVGRVTITCRASQIRDDLGWYQQPGKAPKRLIYAASNLSQSGVPSRFSG 62
Dd	: :       :       :       :       :       :
Qy	61 SGSGTEFTLTISSLQPEDFATYYCLOHGVPRTFGQGTVKEIKRTVAAPSVEIFPPSDEQ 120
Dd	: :       :       :       :       :       :
Qy	63 GSGSGTEFTLTISSLQPEDFATYYCLOHNSYPLTFGGGTKEIKRTVAAPSVEIFPPSDEQ 122
Dd	: :       :       :       :       :       :
Qy	121 LKSGTASVVCLNNFYPREAKEHQK 145
Dd	: :       :       :       :       :       :
Qy	123 LKSGTASVVCLNNFYPREAKVQWK 147
Dd	: :       :       :       :       :       :
RESULT 12	
ADS84464	ID ADS84464 standard; protein; 234 AA.
XX	
AC	ADS84464;
XX	
XX	18-NOV-2004 (first entry)
XX	
XX	Human anti-EPO-R antibody Ab430 light chain SEQ ID NO:103.
XX	
KW	human; erythropoietin receptor; EPO receptor;
KW	erythropoietin receptor binding antibody; EPO receptor binding antibody;
KW	antianemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;
KW	wound healing; neural cell damage protection;
KW	neural tissue damage protection; brain injury; spinal cord injury;
KW	stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
XX	Homo sapiens.
XX	WO2004035603-A2.
PN	
XX	29-APR-2004.
PD	
XX	14-OCT-2003; 2003WO-US032243.
PF	
XX	
PR	14-OCT-2002; 2002US-00269711.
PR	10-OCT-2003; 2003US-00684109.
XX	
PA	(ABBO ) ABBOTT LAB.
XX	
PI	Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
XX	
XX	WPI; 2004-348433/32.
DR	N-PSDB; ADS84462, ADS84463.
XX	
PT	New antibodies that bind to or activate an endogenous human
PT	erythropoietin receptor. useful for diagnosing, preventing or treating





Db 25 TQSPSSLGASVGDRTTTCRTSQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSG 84  
Qy 61 SSGTTEFTLTSSLOPEDFATYYCLOHNGYPRTFGGGTKEIKRTVAAPSVFIPPPSDEQ 120  
Db 85 SSGTTEFTLTSSLOPEDFATYYCLOHNSYPPTFGGGTKEIKRTVAAPSVFIPPPSDEQ 144  
Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145  
Db 145 LKSGTASVVCLLNNFYPREAKVQWK 169

Search completed: March 8, 2005, 06:17:08  
Job time : 69.1532 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 78.009 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-26

Perfect score: 763

Sequence: 1 SQSPSSLSASVGERVTTCR.....VVCLLNPFYPREAKEHQKSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	698	91.5	236	15	US-10-038-591-52
2	697	91.3	184	16	US-10-684-109-78
3	696	91.2	236	15	US-10-038-591-48
4	692	90.7	233	15	US-10-309-762-245
5	691	90.6	234	15	US-10-684-109-109
6	690	90.4	215	16	US-10-462-040A-2
7	690	90.4	234	16	US-10-684-109-103
8	688	90.2	234	16	US-10-684-109-91
9	688	90.2	234	16	US-10-684-109-115
10	682	89.4	234	16	US-10-684-109-97
11	675	88.5	236	15	US-10-038-591-51
12	670	87.8	232	15	US-10-038-591-47
13	662	86.8	212	14	US-10-320-231A-77

14	651	85.3	214	15	US-10-408-901-44	Sequence 44, Appl
15	649.5	85.1	163	15	US-10-364-743-20	Sequence 20, Appl
16	649	85.1	236	9	US-09-859-053-30	Sequence 30, Appl
17	649	85.1	236	16	US-10-625-105-30	Sequence 3, Appl
18	642	84.1	214	15	US-10-423-299-3	Sequence 2, Appl
19	641	84.0	136	15	US-10-038-591-2	Sequence 36, Appl
20	638	83.6	214	15	US-10-408-901-36	Sequence 1, Appl
21	636.5	83.4	241	14	US-10-221-945-1	Sequence 66, Appl
22	636	83.4	223	16	US-10-693-629-66	Sequence 150, App
23	631	82.7	233	16	US-10-663-244-150	Sequence 19, Appl
24	630	82.6	214	14	US-10-153-382-19	Sequence 166, App
25	628	82.3	211	15	US-10-379-392-166	Sequence 11, Appl
26	628	82.3	214	15	US-10-364-953-11	Sequence 170, App
27	628	82.3	214	16	US-10-379-392-170	Sequence 48, Appl
28	628	82.3	234	15	US-10-292-088-48	Sequence 8, Appl
29	628	82.3	237	14	US-10-020-786-8	Sequence 4, Appl
30	628	82.3	237	14	US-10-227-694-4	Sequence 5, Appl
31	628	82.3	237	17	US-10-754-212-5	Sequence 2, Appl
32	625	81.9	214	9	US-09-940-166A-2	Sequence 11, Appl
33	625	81.9	214	9	US-09-811-384-11	Sequence 11, Appl
34	625	81.9	214	15	US-10-404-286-11	Sequence 6, Appl
35	625	81.9	214	16	US-10-762-967-2	Sequence 1, Appl
36	625	81.9	237	9	US-09-940-166A-6	Sequence 144, App
37	625	81.9	237	14	US-10-227-694-1	Sequence 128, App
38	625	81.9	237	16	US-10-762-967-6	Sequence 128, App
39	625	81.9	237	17	US-10-754-212-2	Sequence 4, Appl
40	624	81.8	208	15	US-10-634-581-1	Sequence 2, Appl
41	624	81.8	211	16	US-10-379-392-144	Sequence 1, Appl
42	624	81.8	214	9	US-09-949-559-128	Sequence 144, App
43	624	81.8	214	10	US-09-875-221A-128	Sequence 128, App
44	624	81.8	214	14	US-10-310-454-4	Sequence 4, Appl
45	624	81.8	214	17	US-10-728-420B-113	Sequence 113, App

ALIGNMENTS

RESULT 1

US-10-038-591-52  
; Sequence 52, Application US/10038591  
; Publication No. US20040086503A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Bruce D.  
; APPLICANT: Beebe, Jean  
; APPLICANT: Miller, Penelope E.  
; APPLICANT: Moyer, James D.  
; APPLICANT: Corvalan, Jose R.  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
; FILE REFERENCE: ABX-PF2  
; CURRENT APPLICATION NUMBER: US/10/038,591  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,927  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 52  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-038-591-52

Query Match	91.5%	Score 698;	DB 15;	Length 236;
Best Local Similarity	93.1%	Pred. No. 5.5e-43;		
Matches 135;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0;
QY	1	SQSPSSLSASVGERVTTCRASQGRIRDELGWYQKPGKAPKRLIYVASSLQSGVSRFSG	60	
Db	27	TQSPSSLSASVGDRTTTCRASQGRIRDELGWYQKPGKAPKRLIYVASSLQSGVSRFSG	86	
QY	61	SGSGTEFTLTSSLOPEDFATYVCLQHNYPWTFCQGTKEIKRTVAAPSVFIFPPSDEQ	120	
Db	87	SGSGTEFTLTSSLOPEDFATYVCLQHNYPWTFCQGTKEIKRTVAAPSVFIFPPSDEQ	146	



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; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-109

Query Match
Best Local Similarity 90.6%; Score 691; DB 16; Length 234;
Matches 133; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 25 TQSPSSLSASVGDRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 84

Qy 61 SSGTTEFTLTSSLOPEDFATYVCLQHNQYPRTFQGTKEIKRTVAAPSFIFFPSDEQ 120
Db 85 SSGTTEFTLTSSLOPEDFATYVCLQHNQYPRTFQGTKEIKRTVAAPSFIFFPSDEQ 144

Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 145 LKSGTASVVCLLNNFYPREAKEHOK 169

RESULT 6
US-10-462-040A-2
; Sequence 2, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Light chain
US-10-462-040A-2

Query Match
Best Local Similarity 90.4%; Score 690; DB 16; Length 215;
Matches 133; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 3 TQSPSSLSASVGDRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 62

Qy 61 SSGTTEFTLTSSLOPEDFATYVCLQHNQYPRTFQGTKEIKRTVAAPSFIFFPSDEQ 120
Db 63 SSGTTEFTLTSSLOPEDFATYVCLQHNQYPRTFQGTKEIKRTVAAPSFIFFPSDEQ 122

Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 123 LKSGTASVVCLLNNFYPREAKEHOK 147

RESULT 7
US-10-684-109-103
; Sequence 103, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-103

Query Match
Best Local Similarity 90.2%; Score 688; DB 16; Length 234;
Matches 132; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 25 TQSPSSLSASVGDRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 84

Qy 61 SSGTTEFTLTSSLOPEDFATYVCLQHNQYPRTFQGTKEIKRTVAAPSFIFFPSDEQ 120
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; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-47

Query Match      87.8%; Score 670; DB 15; Length 236;
Best Local Similarity 89.0%; Pred. No. 5.7e-41;
Matches 129; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 27 TQFPSSLSASVGDRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 86

Qy 61 SGSCTEFTLTSSLOPEDFATYYCLOHNGYPRTFQGTKEIKRTVAAPSFIIPPSDEQ 120
Db 87 SGSCTEFTLTSSLOPEDFATYYCLOHNSYPCSGQGTKEIKRTVAAPSFIIPPSDEQ 146

Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 147 LKSGTASVVCLLNNFYPREAKVQWK 171

RESULT 13
US-10-320-231A-77
; Sequence 77, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-77

Query Match      86.8%; Score 662; DB 14; Length 212;
Best Local Similarity 89.7%; Pred. No. 2e-40;
Matches 130; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 3 TQSPSSLSASVGDRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 62

Qy 61 SGSCTEFTLTSSLOPEDFATYYCLOHNGYPRTFQGTKEIKRTVAAPSFIIPPSDEQ 120
Db 63 SGSCTEFTLTSSLOPEDFATYYCQYSGMPYTFQGTKEIKRTVAAPSFIIPPSDEQ 122

Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 123 LKSGTASVVCLLNNFYPREAKVQWK 147

RESULT 14
US-10-408-901-44
; Sequence 44, Application US/10408901
; Publication No. US20040023313A1
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; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-44

Query Match      85.3%; Score 651; DB 15; Length 214;
Best Local Similarity 88.3%; Pred. No. 1.2e-39;
Matches 128; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
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Qy 61 SGSCTEFTLTSSLOPEDFATYYCLOHNGYPRTFQGTKEIKRTVAAPSFIIPPSDEQ 120
Db 65 SGSCTEFTLTSSLOPEDFATYYCQYNSYPTTQGTKEIKRTVAAPSFIIPPSDEQ 124

Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 15
US-10-364-743-20
; Sequence 20, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178Alan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 163
; TYPE: PRT
; ORGANISM: human
US-10-364-743-20

Query Match      85.1%; Score 649.5; DB 15; Length 163;
Best Local Similarity 87.6%; Pred. No. 1.2e-39;
Matches 127; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 7 TQSPSSLSASVGDRTITCRASQIGVRNALVWY-QKPGKAPERLIYAASILQSGVPSRFSG 65

Qy 61 SGSCTEFTLTSSLOPEDFATYYCLOHNGYPRTFQGTKEIKRTVAAPSFIIPPSDEQ 120
Db 66 SGSCTEFTLTIGGLQPEDFATYYCLOHNSYPTTQGTKEIKRTVAAPSFIIPPSDEQ 125
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Job time : 79.009 secs

GenCore version 5.1.6  
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678.897 Million cell updates/sec

Title: US-09-784-950-26

Perfect score: 763

Sequence: 1 SQSPSSLASVGERVTITCR.....VVCLLNYPREAKEHQKSP 147

Scoring table: BLOSUM62DX

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pep:\*
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- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649	85.1	236	4	US-09-859-053-30
2	642	84.1	236	1	US-08-157-101A-5
3	630	82.6	214	4	US-09-472-087-96
4	627	82.2	214	2	US-07-934-373C-39
5	627	82.2	214	3	US-08-437-642B-39
6	627	82.2	214	5	PCT-US93-07832-39
7	625	81.9	214	2	US-07-934-373C-40
8	625	81.9	214	2	US-08-788-800-11
9	625	81.9	214	3	US-08-437-642B-40
10	625	81.9	214	3	US-09-097-309-2
11	625	81.9	214	3	US-09-097-171A-2
12	625	81.9	214	3	US-09-460-587-2
13	625	81.9	214	4	US-09-940-166A-2
14	625	81.9	214	5	PCT-US93-07832-40
15	625	81.9	233	2	US-07-934-373C-25
16	625	81.9	233	3	US-08-437-642B-25
17	625	81.9	233	4	US-08-146-206C-25
18	625	81.9	233	4	US-09-705-686-25
19	625	81.9	233	4	US-09-705-392A-25
20	625	81.9	233	4	US-09-705-398-25
21	625	81.9	233	5	PCT-US93-07832-25
22	625	81.9	237	3	US-09-097-309-6
23	625	81.9	237	3	US-09-097-171A-10
24	625	81.9	237	3	US-09-422-712B-2
25	625	81.9	237	3	US-09-607-756-2
26	625	81.9	237	3	US-09-460-587-6
27	625	81.9	237	4	US-09-940-166A-6

28	619	81.1	139	4	US-09-472-087-22	Sequence 22, Appl
29	619	81.1	139	4	US-09-472-087-96	Sequence 96, Appl
30	619	81.1	491	4	US-10-011-125A-2	Sequence 2, Appl
31	618	81.0	233	4	US-08-030-175-43	Sequence 43, Appl
32	616.5	80.8	233	3	US-08-812-586-45	Sequence 45, Appl
33	616.5	80.8	233	4	US-09-535-832A-42	Sequence 42, Appl
34	615	80.6	214	3	US-09-679-397-1	Sequence 1, Appl
35	615	80.6	214	4	US-09-680-148-1	Sequence 1, Appl
36	615	80.6	214	4	US-09-304-465A-1	Sequence 1, Appl
37	615	80.6	237	2	US-08-463-587A-25	Sequence 25, Appl
38	615	80.6	237	2	US-08-463-667A-3	Sequence 3, Appl
39	615	80.6	237	3	US-08-923-854-25	Sequence 25, Appl
40	615	80.6	237	5	PCT-US91-09133-26	Sequence 26, Appl
41	613	80.3	218	5	PCT-US96-13152-2	Sequence 2, Appl
42	611	80.1	218	2	US-08-887-352B-15	Sequence 15, Appl
43	611	80.1	218	2	US-08-887-352B-17	Sequence 17, Appl
44	611	80.1	218	2	US-08-887-352B-19	Sequence 19, Appl
45	611	80.1	218	2	US-08-887-352B-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-859-053-30  
; Sequence 30, Application US/09859053  
; Patent No. 6803039  
; GENERAL INFORMATION:  
; APPLICANT: Teuji, Takashi  
; APPLICANT: Tezuka, Tatsunari  
; APPLICANT: Horii, No. 6803039uaki  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A  
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND  
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF  
; FILE REFERENCE: 06501-079001  
; CURRENT APPLICATION NUMBER: US/09/859,053  
; CURRENT FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: JP 2001-99508  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-147116  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-859-053-30

Query Match	85.1%	Score 649;	DB 4;	Length 236;
Best Local Similarity	88.3%;	Pred. No. 3.5e-55;		
Matches 128;	Conservative	5;	Mismatches 12;	Indels 0;
Gaps	0;			
QY	1	SQSPSSLASVGERVTITCRASQGRDELGWYQKPGKAPKLLIYVASSLQSGVPSRFSG	60	
DB	27	TQSPSSVSASGDRVTITCRASQGISRLLAWYQKPGKAPKLLIYVASSLQSGVPSRFSG	86	
QY	61	SGSGTEFTLTSSLOPEDFATVYCLQHNQYPRTPGQGTKEIKRTVAAPSVFIFPPSDEQ	120	
DB	87	SGSGTDFLTSSLOPEDFATVYCCQANSFFWTFQGTKEIKRTVAAPSVFIFPPSDEQ	146	
QY	121	LKSGTASVCLLNFPYPREAKEHQK	145	
DB	147	LKSGTASVCLLNFPYPREAKVQWK	171	

RESULT 2

US-08-157-101A-5  
; Sequence 5, Application US/08157101A  
; Patent No. 5808032  
; GENERAL INFORMATION:  
; APPLICANT: KURIHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU

APPLICANT: TSURUOKA, NOBUO  
APPLICANT: ARIMA, KENJI  
APPLICANT: NISHIHARA, TATSURO  
TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION  
TITLE OF INVENTION: PLASMIDS THEREFOR  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILLSBURY, MADISON & SUTRO  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/157,101A  
FILING DATE: 05-APR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: TITUS, MARLANA K  
REGISTRATION NUMBER: 35843  
REFERENCE/DOCKET NUMBER: 9437/204199  
TELEPHONE: 202-861-3711  
TELEFAX: 202-822-0944  
TELEX: 6714627 CUCH

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 236 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-157-101A-5

Query Match 84.1%; Score 642; DB 1; Length 236;  
Best Local Similarity 85.5%; Pred. No. 1.7e-54;  
Matches 124; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 SQSPSSLSASVGRVTITCRASQGRDELGWQKPGKAPKRLIYVASSLSQSGVPSRFSG 60  
DB 27 TQSPSAMSASVGRVTITCRASQGRDELGWQKPGKAPKRLIYVASSLSQSGVPSRFSG 86  
QY 61 SSGSGTEFTLTISLQPEDFATYCYCLOHNGYPRTFQGGTKVEIKRTVAAPSVFIFPPSDEQ 120  
DB 87 SSGSGTEFTLTISLQPEDFATYCYCLOHNGYPRTFQGGTKVEIKRTVAAPSVFIFPPSDEQ 146  
QY 121 LKSGTASVCLNNFYPREAKEHOK 145  
DB 147 LKSGTASVCLNNFYPREAKEVQWK 171

## RESULT 3

US-09-472-087-71  
Sequence 71, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, EILEEN E.  
APPLICANT: HANKE, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFFREY  
APPLICANT: CORVALAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PFI  
CURRENT APPLICATION NUMBER: US/09/472,087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647

PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 71  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-472-087-71

Query Match 82.6%; Score 630; DB 4; Length 214;  
Best Local Similarity 86.2%; Pred. No. 2.1e-53;  
Matches 125; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 SQSPSSLSASVGRVTITCRASQGRDELGWQKPGKAPKRLIYVASSLSQSGVPSRFSG 60  
DB 5 TQSPSSLSASVGRVTITCRASQGRDELGWQKPGKAPKRLIYVASSLSQSGVPSRFSG 64  
QY 61 SSGSGTEFTLTISLQPEDFATYCYCLOHNGYPRTFQGGTKVEIKRTVAAPSVFIFPPSDEQ 120  
DB 65 SSGSGTEFTLTISLQPEDFATYCYCLOHNGYPRTFQGGTKVEIKRTVAAPSVFIFPPSDEQ 124  
QY 121 LKSGTASVCLNNFYPREAKEHOK 145  
DB 125 LKSGTASVCLNNFYPREAKEVQWK 149

## RESULT 4

US-07-934-373C-39  
Sequence 39, Application US/07934373C  
Patent No. 5821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-39

Query Match 82.2%; Score 627; DB 2; Length 214;  
Best Local Similarity 84.8%; Pred. No. 4.2e-53;





```

RESULT 7
US-07-934-373C-40
; Sequence 40, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: 07/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-40

Query Match      81.9%; Score 625; DB 2; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 SOSPSLSASVGERVTITCRASQGIKRWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 TQSPSSLSASVGDRTVITCRASQDINNLYNQKPGKAPKLLIYTTLSHSGVPSRFSG 64

Qy 61 SSGSGTEFTLTSSLOPEDFATYICLQHNQYPRFTQGGTKVEIKRTVAAPSVFIPPSPDEQ 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 SSGSGTDYTLTSSLOPEDFATYICQGGNTLPTFTQGGTKVEIKRTVAAPSVFIPPSPDEQ 124

Qy 121 LKSGTASVCLNNFYPREAKEHQK 145
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 LKSGTASVCLNNFYPREAKVQWK 149

US-07-934-373C-40

Query Match      81.9%; Score 625; DB 2; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 SOSPSLSASVGERVTITCRASQGIKRWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 TQSPSSLSASVGDRTVITCRASQDINNLYNQKPGKAPKLLIYTTLSHSGVPSRFSG 64

Qy 61 SSGSGTEFTLTSSLOPEDFATYICLQHNQYPRFTQGGTKVEIKRTVAAPSVFIPPSPDEQ 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 SSGSGTDYTLTSSLOPEDFATYICQGGNTLPTFTQGGTKVEIKRTVAAPSVFIPPSPDEQ 124

Qy 121 LKSGTASVCLNNFYPREAKEHQK 145
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 LKSGTASVCLNNFYPREAKVQWK 149

RESULT 8
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-11

Query Match      81.9%; Score 625; DB 2; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 SOSPSLSASVGERVTITCRASQGIKRWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 TQSPSSLSASVGDRTVITCRASQDINNLYNQKPGKAPKLLIYTTLSHSGVPSRFSG 64

Qy 61 SSGSGTEFTLTSSLOPEDFATYICLQHNQYPRFTQGGTKVEIKRTVAAPSVFIPPSPDEQ 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 SSGSGTDYTLTSSLOPEDFATYICQGGNTLPTFTQGGTKVEIKRTVAAPSVFIPPSPDEQ 124

Qy 121 LKSGTASVCLNNFYPREAKEHQK 145
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 LKSGTASVCLNNFYPREAKVQWK 149

RESULT 9
US-08-437-642B-40
; Sequence 40, Application US/08437642B
; Patent No. 6054397
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA: PCT/US92/05126
; APPLICATION NUMBER: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-437-642B-40

Query Match      81.9%; Score 625; DB 3; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQQKPGKAPKELIYVASSLSQGVPSRFSG 60
Db 5 TQSPSSLSASVGDVRTITCRASQDINNLYNQKPGKAPKLLIYTTSLHSGVPSRFSG 64
QY 61 SSGSTEFTLTISLQPEDFATYYCLQHNQYPRTFQGGTKVEIKRTVAAPSVEIFFPPSDEQ 120
Db 65 SSGGTDYTLTISLQPEDFATYYCOQGNLPTPTFGQGTKEIKRTVAAPSVEIFFPPSDEQ 124
QY 121 LKSGTASVCLNNFYPREAKEHOK 145
Db 125 LKSGTASVCLNNFYPREAKVQWK 149

RESULT 10
US-09-784-950-26
; Sequence 2, Application US/09097309
; Patent No. 6121428
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,309
; FILING DATE: 12-Jun-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050951
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P110SR1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-097-309-2

Query Match      81.9%; Score 625; DB 3; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQQKPGKAPKELIYVASSLSQGVPSRFSG 60
Db 5 TQSPSSLSASVGDVRTITCRASQDINNLYNQKPGKAPKLLIYTTSLHSGVPSRFSG 64
QY 61 SSGSTEFTLTISLQPEDFATYYCLQHNQYPRTFQGGTKVEIKRTVAAPSVEIFFPPSDEQ 120
Db 65 SSGGTDYTLTISLQPEDFATYYCOQGNLPTPTFGQGTKEIKRTVAAPSVEIFFPPSDEQ 124
QY 121 LKSGTASVCLNNFYPREAKEHOK 145
Db 125 LKSGTASVCLNNFYPREAKVQWK 149

RESULT 11
US-09-097-171A-2
; Sequence 2, Application US/09097171A
; Patent No. 6171586
; GENERAL INFORMATION:
; APPLICANT: Lam, Xanthe M.
; APPLICANT: Oeswein, James Q.
; APPLICANT: Ongpipattanakul, Boonsri
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Wang, Sharon X.
; APPLICANT: Weissburg, Robert P.
; APPLICANT: Wong, Rita L.
; TITLE OF INVENTION: Antibody Formulation
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,171A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/874897
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1089R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-171A-2

Query Match      81.9%; Score 625; DB 3; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQKPGKAPKELIYVASSLOSQVPSRFSG 60
Db 5 TQSPSSLSASVGDVRTITCRASQDINNLYNWTQKPGKAPKLLIYTTLSHSGVPSRFSG 64
QY 61 SGSGETFTLTISLQPEDFATYYCLOHNGYPRTFQGGTKVEIKRTVAAPSFIFFPSDEQ 120
Db 65 SGSGETDVTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSFIFFPSDEQ 124
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 12
US-09-460-587-2
; Sequence 2, Application US/09460587
; Patent No. 6322997
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,587
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/097,309
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-460-587-2

Query Match      81.9%; Score 625; DB 3; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQKPGKAPKELIYVASSLOSQVPSRFSG 60
Db 5 TQSPSSLSASVGDVRTITCRASQDINNLYNWTQKPGKAPKLLIYTTLSHSGVPSRFSG 64
QY 61 SGSGETFTLTISLQPEDFATYYCLOHNGYPRTFQGGTKVEIKRTVAAPSFIFFPSDEQ 120
Db 65 SGSGETDVTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSFIFFPSDEQ 124
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 13
US-09-940-166A-2
; Sequence 2, Application US/09940166A
; Patent No. 6716598
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/940,166A
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/097,309
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-940-166A-2

Query Match      81.9%; Score 625; DB 4; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQKPGKAPKELIYVASSLOSQVPSRFSG 60
Db 5 TQSPSSLSASVGDVRTITCRASQDINNLYNWTQKPGKAPKLLIYTTLSHSGVPSRFSG 64
QY 61 SGSGETFTLTISLQPEDFATYYCLOHNGYPRTFQGGTKVEIKRTVAAPSFIFFPSDEQ 120
Db 65 SGSGETDVTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSFIFFPSDEQ 124
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 14
PCT-US93-07832-40
; Sequence 40, Application PC/TUS9307832
; GENERAL INFORMATION:
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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-171A-2

Query Match      81.9%; Score 625; DB 3; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQKPGKAPKELIYVASSLOSQVPSRFSG 60
Db 5 TQSPSSLSASVGDVRTITCRASQDINNLYNWTQKPGKAPKLLIYTTLSHSGVPSRFSG 64
QY 61 SGSGETFTLTISLQPEDFATYYCLOHNGYPRTFQGGTKVEIKRTVAAPSFIFFPSDEQ 120
Db 65 SGSGETDVTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSFIFFPSDEQ 124
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 13
US-09-940-166A-2
; Sequence 2, Application US/09940166A
; Patent No. 6716598
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/940,166A
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/097,309
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-940-166A-2

Query Match      81.9%; Score 625; DB 4; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQKPGKAPKELIYVASSLOSQVPSRFSG 60
Db 5 TQSPSSLSASVGDVRTITCRASQDINNLYNWTQKPGKAPKLLIYTTLSHSGVPSRFSG 64
QY 61 SGSGETFTLTISLQPEDFATYYCLOHNGYPRTFQGGTKVEIKRTVAAPSFIFFPSDEQ 120
Db 65 SGSGETDVTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSFIFFPSDEQ 124
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 14
PCT-US93-07832-40
; Sequence 40, Application PC/TUS9307832
; GENERAL INFORMATION:
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 14.4271 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-27

Perfect score: 1085

Sequence: 1 KPGASVKVSKASGYTFTS.....QVLLPSKDVMOQTDEHVVCK 203

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	894	82.4	627	S14683	Ig mu chain precu
2	695.5	64.1	231	B23746	Ig Fab region IV-J
3	598	55.1	288	S29690	Ig heavy chain VDJ
4	525.5	48.4	110	PH1670	Ig heavy chain V r
5	510	47.0	127	S34014	Ig heavy chain V r
6	507.5	46.8	136	S31600	Ig heavy chain V r
7	501.5	46.2	246	S38950	Ig heavy chain V r
8	501.5	46.2	446	S40295	Ig gamma chain - m
9	491	45.3	160	PL0105	anti-PR2 erythrocy
10	486	44.8	592	S25705	Ig mu chain - shee
11	485.5	44.7	118	PH1666	Ig heavy chain V r
12	483	44.5	469	S37483	Ig gamma-2a chain
13	482.5	44.5	132	S31596	Ig heavy chain V r
14	479	44.1	171	S23623	Ig heavy chain V r
15	473.5	43.6	241	S69131	Ig heavy chain (DO
16	468.5	43.2	568	A34891	Ig heavy chain pre
17	465	42.9	129	A246393	Ig heavy chain V r
18	463	42.7	452	1 MHU	Ig mu chain C regi
19	463	42.7	453	S37768	Ig mu chain C regi
20	463	42.7	473	1 MHUM	Ig mu chain C regi
21	463	42.7	474	S15590	Ig heavy chain - h
22	462	42.6	98	S28918	Ig heavy chain V r
23	454	41.8	129	S36260	Ig heavy chain V r
24	453.5	41.8	118	S36265	Ig heavy chain V r
25	451.5	41.6	135	S49530	anti-Sm antibody V
26	451	41.6	475	S01321	Ig gamma-2b chain
27	449.5	41.4	114	PH1667	Ig heavy chain V r
28	449	41.4	123	D33548	Ig heavy chain V-1
29	449	41.4	142	A32483	Ig heavy chain V r

30	447	41.2	131	2	S26792	Ig heavy chain V r
31	444.5	41.0	474	1	G2MS11	Ig gamma-2b chain
32	443	40.8	109	2	PH1668	Ig heavy chain V r
33	439	40.5	549	2	S04845	Ig heavy chain pre
34	438.5	40.4	214	2	PC4202	monoclonal antibod
35	437.5	40.3	110	2	PH1669	Ig heavy chain V r
36	437	40.3	119	2	PH0961	Ig heavy chain V r
37	436	40.2	160	2	S05271	Ig heavy chain pre
38	431	39.7	133	2	C33548	Ig heavy chain V-1
39	429.5	39.6	136	2	PH0960	Ig heavy chain V r
40	424.5	39.1	120	2	S31999	Ig heavy chain V r
41	424.5	39.1	132	2	PH0954	Ig heavy chain V r
42	423	39.0	125	2	S68170	Ig heavy chain V r
43	422	38.9	122	2	S36271	Ig heavy chain V r
44	419	38.6	127	2	PH0955	Ig heavy chain V r
45	418.5	38.6	124	2	S19665	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S14683  
Ig mu chain precursor, membrane-bound (clone 201) - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
C:Accession: S14683; S08047  
R:Friedlander, R.M.; Nussenzeig, M.C.; Leder, P.  
Nucleic Acids Res. 18, 4278, 1990  
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.  
A:Reference number: S14683; MUID:90332450; PMID:2115996  
A:Accession: S14683  
A:Molecule type: mRNA  
A:Residues: 1-627 <PRI>  
A:Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin; membrane protein  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-627/Product: Ig mu chain #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match	82.4%	Score	894	DB 2	Length	627
Best Local Similarity	83.4%	Pred. No.	3.1e-62			
Matches	176	Conservative	7	Mismatches	20	Indels 8; Gaps 1;
Qy	1	KPGASVKVSKASGYTFTSYDINNVROATGQGLEWMGMWPNPNSGNTGYAQKFQGRVTWN	60			
Db	31	KPGSSVKVSKASGCTFSSVAISWRQAPQGQLEWMGGIPIFGTANYAQKFQGRVTIT	90			
Qy	61	RNTSISTAYMELSSLRSEDTAVYYCARGHGGSYF-----YSYIGMDVMVGQTTVTY	112			
Db	91	ADESTSTAYMELSSLRSEDTAVYYCAKTIILGPYSSGWPNSDYYYGMDVMVGQTTVTY	150			
Qy	113	SSGSASAPTLPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPS	172			
Db	151	SSGSASAPTLPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPS	210			
Qy	173	VLRGKYAATSOVLPLSKDVMOQTDEHVVCK	203			
Db	211	VLRGKYAATSOVLPLSKDVMOQTDEHVVCK	241			

RESULT 2

B23746  
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: B23746  
J:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin.  
A:Reference number: A23746; MUID:91131575; PMID:1993660  
A:Accession: B23746

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-231 <LEO>  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;140-209/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 695.5; DB 2; Length 231;  
Best Local Similarity 68.8%; Pred. No. 3.2e-47;  
Matches 139; Conservative 22; Mismatches 36; Indels 5; Gaps 2;

Qy 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMNR 61  
Db 12 KPSETLSLTGAVYGSFSDYMSWIRQPPGKGLWIGIN-HSGSTNYNPSLKSRVTISV 70  
Qy 62 NTSISTAYMELSSLRSEDATVYVCARGGHGGSFYFYCYMDVWGQGTITVTSSGSASAPT 121  
Db 71 DTSKNQFSLKLSVTAADATVYCARPHDTSGHYWNV----WGQGTITVTSSGSASAPT 126  
Qy 122 LPPLVSCNSPDSSTSSAVGCLAQDFLPSITFTFSWKYKNNSDISSTRGFPSPVLRGGKYAA 181  
Db 127 LPPLVSCNSPDSSTSSAVGCLAQDFLPSITFTFSWKYKNNSDISSTRGFPSPVLRGGKYAA 186  
Qy 182 TSQVLLPSKDVNQGTDEHVCK 203  
Db 187 TSQVLLPSKDVNQGTDEHVCK 208

RESULT 3  
S29690  
Ig heavy chain VDJ region - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 06-Jan-1995 #sequence\_revision 30-Jan-1998 #text\_change 20-Jun-2000  
C;Accession: S29690  
R;Dammer, P.M.; Bos, N.A.; Kroese, F.G.M.  
submitted to the EMBL Data Library, October 1992  
A;Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.  
A;Reference number: S29690  
A;Accession: S29690  
A;Molecule type: mRNA  
A;Residues: 1-288 <DM>  
A;Cross-references: EMBL:X68782; NID:G56442; PID:gl334294  
A;Experimental source: strain D2B  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 55.1%; Score 598; DB 2; Length 288;  
Best Local Similarity 55.7%; Pred. No. 1.6e-39;  
Matches 113; Conservative 37; Mismatches 45; Indels 8; Gaps 2;

Qy 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMNR 61  
Db 10 RPSGVKISCKASGYTFTSYDYNHWVKQRPQEGVLWIGRINPANGNTEYAEKPKSRATLTA 69  
Qy 62 NTSISTAYMELSSLRSEDATVYVCARGGHGGSFYFYCYMDVWGQGTITVTSSGSASAPT 121  
Db 70 DKSSNTAYQLSSLTSEDATVTFCTING-----TVVPFDYWGQGVNVTVSSQSQST 122  
Qy 122 LPPLVSCNSPDSSTSSAVGCLAQDFLPSITFTFSWKYKNNSDI-SSTRGFPSPVLRGGKYA 180  
Db 123 VLPLVSCSPISDENLVAMGCLARDFLPSISFSFNWYQNTEVMQGVRTFTLRTGDKYT 182  
Qy 181 ATSQVLLPSKDVNQGTDEHVCK 203  
Db 183 ATSQVLLSAKNLVGSDYLVCK 205

RESULT 4  
PH1670  
Ig heavy chain V region (clone 2A12) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C;Accession: PH1670

R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
A;Reference number: PH1642; MUID:93301610; PMID:8315388  
A;Accession: PH1670  
A;Molecule type: mRNA  
A;Residues: 1-110 <HIL>  
A;Experimental source: B cell  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 48.4%; Score 525.5; DB 2; Length 110;  
Best Local Similarity 86.8%; Pred. No. 2.6e-34;  
Matches 99; Conservative 3; Mismatches 5; Indels 7; Gaps 1;

Qy 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMNR 60  
Db 4 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMT 63  
Qy 61 RNTSISTAYMELSSLRSEDATVYVCARGGHGGSFYFYCYMDVWGQGTITVTSS 114  
Db 64 RNTSISTAYMELSSLRSEDATVYVCARGKGGEF-----DIWGQGTITVTSS 110

RESULT 5  
S34014  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C;Accession: S34014; S30535  
R;Mariette, X.; Teapla, A.; Brouet, J.C.  
Eur. J. Immunol. 23, 846-851, 1993  
A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal antibodies of the IgG1 class  
A;Reference number: S34001; MUID:93209281; PMID:7681398  
A;Accession: S34014  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-127 <MAR>  
A;Cross-references: EMBL:Z18321  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 47.0%; Score 510; DB 2; Length 127;  
Best Local Similarity 83.2%; Pred. No. 5e-33;  
Matches 99; Conservative 5; Mismatches 7; Indels 8; Gaps 2;

Qy 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMNR 60  
Db 12 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMT 71  
Qy 61 RNTSISTAYMELSSLRSEDATVYVCARGGHG-----SYFYCYMDVWGQGTITVTSS 114  
Db 72 RNTSISTAYMELSSLRSEDATVYFCARALSIGVIRGY---YYALDVGQGTITVS 127

RESULT 6  
S31600  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31600  
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnel, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the germ-line to the mature B cell  
A;Reference number: S31585  
A;Accession: S31600  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-136 <CU>  
A;Cross-references: EMBL:Z14165; NID:G30994; PID:CAA78534.1; PID:G30995  
C;Superfamily: immunoglobulin V region; immunoglobulin homology



C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 46.8%; Score 507.5; DB 2; Length 136;  
Best Local Similarity 84.3%; Pred. No. 8.3e-33;  
Matches 97; Conservative 2; Mismatches 7; Indels 9; Gaps 1;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAOKFQGRVTMNR 60  
DB 31 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAOKFQGRVTMT 90  
QY 61 RNTSISTAYMELSLRSEDATVYICARGHGGSFYFYYGMDVWGQGTQVTVSSG 115  
DB 91 RNTSISTAYMELSLRSEDATVYICARWRD-----AFDIWGQGTMTVTVSSG 136

RESULT 7  
S38950

IG gamma chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999  
C:Accession: S38950  
R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bielefeld, Chem. Hoppe-Seyler 374, 993-1000, 1993  
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha 1 chain of IgG2a  
A:Reference number: S38950; MUID:94128242; PMID:8297501  
A:Accession: S38950  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-246 <KLE>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 46.2%; Score 501.5; DB 2; Length 246;  
Best Local Similarity 51.6%; Pred. No. 4.6e-32;  
Matches 99; Conservative 33; Mismatches 41; Indels 19; Gaps 6;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAOKFQGRVTMNR 61  
DB 13 RFGASVKISCKASGYTFTDYIHWVKQRPGELEWIGWYIPGSGNTKYNEKFKGKATLV 72  
QY 62 NTSISTAYMELSLRSEDATVYICARGHGGSFYFYYGMDVWGQGTQVTVSSGSASPT 121  
DB 73 DTSSSTAYMQLSLTSEDSAVYFCARGGK-----FAMDYWGQGTSTVTVSSAKTTAPS 124  
QY 122 LPPLVS-CENSPSDT--SSVAVGCLAQDFLPDSITFSWKYKNSDISS--TRGPPSVLRGG 177  
DB 125 VYPLAPVC-----GDTTGSSTVLGCLVKGYFPEPVLTLW---NSGSLSSGVHTFPVAVLQSD 177  
QY 178 KYAATSOVLPLS 189  
DB 178 LYTLSSTVTVTS 189

RESULT 8  
S40295

IG gamma-2a chain (mAb735) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bielefeld, submitted to the EMBL Data Library, January 1993  
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha 1 chain of IgG2a  
A:Reference number: S40295  
A:Accession: S40295  
A:Molecule type: protein  
A:Residues: 1-446 <KLE>  
A:Cross-references: UNIPROT:Q99L25  
C:Genetics:  
A:Map position: 12  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>  
F:1-117/Domain: V-D-J region <VDJ>  
F:118-446/Domain: C region <CHR>  
F:118-214/Domain: C1 region <CH1>  
F:215-230/Region: hinge  
F:231-340/Domain: C2 region <CH2>  
F:341-446/Domain: C3 region <CH3>  
F:360-427/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyroglutamic acid (Gln) #status experimental  
F:112-96,144-199,261-321,367-425/Disulfide bonds: #status predicted  
F:132/Disulfide bonds: interchain (to light chain) #status predicted  
F:224,227,229/Disulfide bonds: interchain #status predicted  
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 46.2%; Score 501.5; DB 2; Length 446;  
Best Local Similarity 51.6%; Pred. No. 8.7e-32;  
Matches 99; Conservative 33; Mismatches 41; Indels 19; Gaps 6;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAOKFQGRVTMNR 61  
DB 13 RFGASVKISCKASGYTFTDYIHWVKQRPGELEWIGWYIPGSGNTKYNEKFKGKATLV 72  
QY 62 NTSISTAYMELSLRSEDATVYICARGHGGSFYFYYGMDVWGQGTQVTVSSGSASPT 121  
DB 73 DTSSSTAYMQLSLTSEDSAVYFCARGGK-----FAMDYWGQGTSTVTVSSAKTTAPS 124  
QY 122 LPPLVS-CENSPSDT--SSVAVGCLAQDFLPDSITFSWKYKNSDISS--TRGPPSVLRGG 177  
DB 125 VYPLAPVC-----GDTTGSSTVLGCLVKGYFPEPVLTLW---NSGSLSSGVHTFPVAVLQSD 177  
QY 178 KYAATSOVLPLS 189  
DB 178 LYTLSSTVTVTS 189

RESULT 9  
P10105

anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 26-Apr-1996  
C:Accession: P10105  
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.  
J. Exp. Med. 169, 1631-1643, 1989  
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma secretory cell line to the human B cell lymphoma secretory cell line  
A:Reference number: P10106; MUID:89235583; PMID:2541221  
A:Accession: P10105  
A:Molecule type: mRNA  
A:Residues: 1-160 <SIL>  
A:Note: The authors translated the codon GAC for residues 108 and 109 as Glu  
C:Comment: The antibody is one of the cold agglutinins that preferentially bind red blood cells  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: autoantibody; hemagglutinin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:49-54/Region: complementarity-determining 1  
F:69-84/Region: complementarity-determining 2  
F:118-131/Domain: D region <DRG>  
F:132-144/Domain: J4 segment <JSG>  
F:145-160/Domain: C region <CRG>

Query Match 45.3%; Score 491; DB 2; Length 160;  
Best Local Similarity 74.2%; Pred. No. 1.9e-31;  
Matches 98; Conservative 9; Mismatches 19; Indels 6; Gaps 3;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAOKFQGRVTMNR 61  
DB 32 KPGASVKVSKASGYTFTSYGISWVRQAPGQGLEWGISVYNGDTNYAQNIGQRTMTT 91  
QY 62 NTSISTAYMELSLRSEDATVYICARG--GH--GGSFYFYYGMDVWGQGTQVTVSSGSAS 118  
DB 92 DTSTSTAYMELNLRSDATVYICARAPGYCSGGG---CYRGGDYWGQGTTLTVSSGSRS 148  
QY 119 APTLPFLVSCEN 130



```
RESULT 14
S23623
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S23623
R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gal, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A:Reference number: S23623; MUID:92156804; PMID:1740665
A:Accession: S23623
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <OLE>
A:CROSS-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 44.1%; Score 479; DB 2; Length 171;
Best Local Similarity 63.9%; Pred. No. 1.8e-30;
Matches 94; Conservative 13; Mismatches 28; Indels 12; Gaps 3;

Qy 1 KKPASVVKVCKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
Db ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| :
31 KKPASVVKVCKSGSYTFTAYQHWVRQAPQGLEWGMWNPNSGNTGYGQKFGQRTVLT 90
Qy 61 RNTSISTAYMELSLRSDTAVYYCARGHGGSFYFYYGM-----DVGQGTITVTVSS 114
Db ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| |||||
91 RDTSISTAYMELSLRSDTAVYYCAI-----EYFDGDLKPSDVFQDVGQGTITVTVSS 145

Qy 115 GSASAPTLFPLVSCNSPDSSTSSVAVG 141
Db |::||| ||||| :|||
146 ASTKGPSVFPLAPSSKSTSG-GTAALG 171

RESULT 15
S69131
Ig heavy chain (DOT) - human (fragment)
N:Alternate names: anti-riboflavin IgG Fd fragment
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C:Accession: S69131
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins
A:Reference number: S69130; MUID:95255298; PMID:7737190
A:Accession: S69131
A:Molecule type: protein
A:Residues: 1-241 <STO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAT>
F:140-205/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyroldione carboxylic acid (Gln) #status experimental

Query Match 43.6%; Score 473.5; DB 2; Length 241;
Best Local Similarity 50.0%; Pred. No. 6.9e-30;
Matches 96; Conservative 34; Mismatches 53; Indels 9; Gaps 5;

Qy 1 KKPASVVKVCKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
Db ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| :
12 KVPASVRAISCKASGAPENYYIHWVRQAPGLGLEWGMGIFNPVAGAVS--SEKFRDRLYMS 70

Qy 61 RNTSISTAYMELSLRSDTAVYYCARGHGGSFYFYYGMVWGQGTITVTVSSGSASAP 120
Db ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| |||||
71 SDTSANTVSMQLRNLRSDTGRYFCAR----VSYDFSQYGMVWGQGTITVTVSSASTKGP 126

Qy 121 TLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISTSRTGFPVLR-GGKY 179
Db ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| |||||
127 SVFPLAPCSRSTSE-STAAAGCLVKDYPPEPVTVSW--NSGALTSGVHTFPAVLQSSGLY 183

Qy 180 AATSOVLPLPSKD 191
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Db 184 SLSSVTVTPSSN 195

Search completed: March 8, 2005, 06:39:23  
Job time : 15.4771 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 75.8103 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-27

Perfect score: 1085

Sequence: 1 KPGNSVKVSKASGYTFTS.....QVLLPSKDVMOQTDEHVCK 203

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	828.5	76.4	606	2	Q6GMV2	Q6gm22 homo sapien
2	784	72.3	597	2	Q96BB9	Q96bb9 homo sapien
3	765.5	70.6	613	2	Q8WUK1	Q8wuk1 homo sapien
4	724	66.7	595	2	Q8WUX4	Q8wux4 homo sapien
5	724	66.7	597	2	Q6GMX5	Q6gmx5 homo sapien
6	724	66.7	597	2	Q9BU10	Q9bu10 homo sapien
7	724	66.7	625	2	Q96AA6	Q96aa6 homo sapien
8	720	66.4	597	2	Q9QB88	Q9qb88 homo sapien
9	687.5	63.4	620	2	Q96EY0	Q96ey0 homo sapien
10	624	57.5	613	2	Q8VCX7	Q8vcx7 mus musculus
11	609.5	56.2	614	2	Q7TMT6	Q7tmt6 mus musculus
12	537.5	49.5	497	2	Q8WY24	Q8wy24 homo sapien
13	535.5	49.4	518	2	Q6N030	Q6n030 homo sapien
14	521	48.0	498	2	Q6N041	Q6n041 homo sapien
15	508.5	46.9	469	2	Q7Z7P5	Q7z7p5 homo sapien
16	507	46.7	470	2	Q7TMK1	Q7tmk1 mus musculus
17	506	46.6	500	2	Q9BRV0	Q9brv0 homo sapien
18	498.5	45.9	475	2	Q6N095	Q6n095 homo sapien
19	490	45.2	481	2	Q91WT1	Q91wt1 mus musculus
20	480.5	44.3	500	2	Q6N091	Q6n091 homo sapien
21	478	44.1	484	2	Q99LA6	Q99la6 mus musculus
22	477.5	44.0	473	2	Q9DLA4	Q9dla4 mus musculus
23	477.5	44.0	480	2	Q6P089	Q6p089 homo sapien
24	476.5	43.9	482	2	Q8K172	Q8k172 mus musculus
25	474.5	43.7	463	2	Q99LC4	Q99lc4 mus musculus
26	474	43.7	480	2	Q6PJF1	Q6pjf1 homo sapien
27	472	43.5	465	2	Q6FJB2	Q6fjb2 mus musculus
28	471.5	43.5	472	2	Q6FJA7	Q6fja7 mus musculus
29	467.5	43.1	488	2	Q91WR1	Q91wr1 mus musculus
30	467	43.0	573	2	Q8WU38	Q8wu38 homo sapien
31	466.5	43.0	488	2	Q8K0F2	Q8k0f2 mus musculus

32	465	42.9	480	2	Q8K0Z4	Q8k0z4 mus musculus
33	463	42.7	454	1	MUC_HUMAN	P01871 homo sapien
34	462.5	42.6	593	2	Q6INMS	Q6inms xenopus lae
35	462	42.6	472	2	Q6N089	Q6n089 homo sapien
36	461	42.5	489	2	Q8VCX4	Q8vcx4 mus musculus
37	456	42.0	119	2	Q9UL94	Q9ul94 homo sapien
38	455	41.9	125	2	Q9UL95	Q9ul95 homo sapien
39	451	41.6	244	2	Q6SZC8	Q6szc8 homo sapien
40	451	41.6	481	2	Q91WT3	Q91wt3 mus musculus
41	448.5	41.3	159	2	Q96QSO	Q96qso homo sapien
42	442	40.7	208	2	Q6ZP87	Q6zpb7 homo sapien
43	438.5	40.4	474	2	Q8R3H6	Q8r3h6 mus musculus
44	438	40.4	496	2	Q96DK0	Q96dk0 homo sapien
45	437.5	40.3	464	2	Q6FP95	Q6fp95 mus musculus

ALIGNMENTS

RESULT 1  
Q6GMV2 ID Q6GMV2 PRELIMINARY; PRT; 606 AA.  
AC Q6GMV2;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Small D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
SEQUENCE FROM N.A.  
TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC073758; AAH73758.1; -;  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-sec; 4.  
DR SMART; SM00407; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.



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DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PH0098; PH0098.
DR PIR; PH0120; PH0120.
DR PIR; PH1559; PH1559.
DR PIR; PH1116; PH1116.
DR PIR; PH1119; PH1119.
DR PIR; PH0442; PH0442.
DR HSP; PH1861; IADQ.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F950671E315 CRC64;

Query Match      70.6%; Score 765.5; DB 2; Length 613;
Best Local Similarity 71.8%; Pred. No. 7.6e-58;
Matches 145; Conservative 26; Mismatches 26; Indels 5; Gaps 1;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTGYAQKFGQGRVTWNR 61
DB 32 QPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLWVAIVISDGSNKYVADSVKGRFTISR 91
QY 62 NTSISTAYMELSSLRSDETAIVYCARGGHGGSYFYSGYGMVGMVGQGTITVSSGSASAPT 121
DB 92 DNSKNTLYLQMSLRADTAIVYCARQWSEGVEP-----DIWGQGTWVTVSSGSASAPT 146
QY 122 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKKNNSDISSTRGPPSVLRGKYAA 181
DB 147 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKKNNSDISSTRGPPSVLRGKYAA 206
QY 182 TSQVLLPSKDVNQGTDEHVCK 203
DB 207 TSQVLLPSKDVNQGTDEHVCK 228

RESULT 4
Q8WUX4 PRELIMINARY; PRT; 595 AA.
ID Q8WUX4
AC Q6GMX5; PRELIMINARY; PRT; 597 AA.
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2]
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[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AAH73767.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match 66.7%; Score 724; DB 2; Length 597;
Best Local Similarity 68.9%; Pred. No. 2.9e-54;
Matches 144; Conservative 21; Mismatches 30; Indels 14; Gaps 3;

QY 2 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGNPNSGNTGYAOKFGQGRVTMNR 61
DB 32 KPSETLSITCGVYGSGFSGYWIRQPPGKLEWIGEIN-HSGSTNYPNLSKSRVITSV 90
QY 62 NTSISTAYMELSSLRSEDTAVYYCAR-----GGHGGSYFYSGYGMVDMVQGGTTVTVSS 114
DB 91 DTSKKQLSLKSLSSVNAADTAVYYCARVITRASPGTDG-----RYGMDVMQGGTTVTVSS 144
QY 115 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVL 174
DB 145 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVL 204
QY 175 RGGKYAATSOVLLPSKDVMOGQTDHVVCK 203
DB 205 RGGKYAATSOVLLPSKDVMOGQTDHVVCK 233

RESULT 6
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65274 MW; 2DAPAF8FB7E055851 CRC64;

Query Match 66.7%; Score 724; DB 2; Length 597;
Best Local Similarity 68.9%; Pred. No. 2.9e-54;
Matches 144; Conservative 21; Mismatches 30; Indels 14; Gaps 3;

QY 2 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGNPNSGNTGYAOKFGQGRVTMNR 61
DB 32 KPSETLSITCGVYGSGFSGYWIRQPPGKLEWIGEIN-HSGSTNYPNLSKSRVITSV 90
QY 62 NTSISTAYMELSSLRSEDTAVYYCAR-----GGHGGSYFYSGYGMVDMVQGGTTVTVSS 114
DB 91 DTSKKQLSLKSLSSVNAADTAVYYCARVITRASPGTDG-----RYGMDVMQGGTTVTVSS 144
QY 115 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVL 174
DB 145 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVL 204
QY 175 RGGKYAATSOVLLPSKDVMOGQTDHVVCK 203
DB 205 RGGKYAATSOVLLPSKDVMOGQTDHVVCK 233

RESULT 7
Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.;
RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC011857; AAH1857.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01820; IGT9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 950A1A4A6E8FF27B CRC64;

Query Match 63.4%; Score 687.5; DB 2; Length 620;
Best Local Similarity 67.8%; Pred. No. 4.4e-51;
Matches 137; Conservative 22; Mismatches 38; Indels 5; Gaps 2;

Qy 2 KPGASVKVCKASGYTFTSYDINVRQATGCGLEWGMWNPNSGNTGYAQKFGQGRVTNMR 61
Db 39 KPSETLSTCVSGSISSTYWSWIRQAPAGLEWIGRIY-TSGSTNTPSLKGRVTMSV 97
Qy 62 NTSISTAYMELSLRSEDVAVYCYARGHGSGSYFYSGYGMVDMVGQGTITVTYSSGSASAPT 121
Db 98 DTSKNQPSLKLSSVTAADTAVYCA---SQPWELPTVGLFYWGQGLTAVTSSGSASAPT 153
Qy 122 LFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNSDTSSTGRFPSPVLRGGKYAA 181
Db 154 LFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNSDTSSTGRFPSPVLRGGKYAA 213
Qy 182 TSQVLLPSKDVMOGTDHEHVCK 203
Db 214 TSQVLLPSKDVMOGTDHEHVCK 235

RESULT 10
Q8VCX7 PRELIMINARY; PRT; 613 AA.
ID Q8VCX7
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC018315; AAH18315.1; -.
DR PIR; C30562; C30562.
DR HSSP; P01751; IAGW.
DR MGP; MGI196448; Igh-6.
DR GO; GO:0019815; C:B-cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; P:antigen binding; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016084; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0050871; P:positive regulation of B-cell activation; IDA.
DR GO; GO:0030890; P:positive regulation of B-cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 57.5%; Score 624; DB 2; Length 613;
Best Local Similarity 58.6%; Pred. No. 1.4e-45;
Matches 119; Conservative 36; Mismatches 40; Indels 8; Gaps 3;

Qy 2 KPGASVKVCKASGYTFTSYDINVRQATGCGLEWGMWNPNSGNTGYAQKFGQGRVTNMR 61
Db 32 KPGASVKISKATGYTFTSSYIEWVKQPGHLEWIGBILPGSGSTNYNEFKGKATPTA 91
Qy 62 NTSISTAYMELSLRSEDVAVYCYARGHGSGSYFYSGYGMVDMVGQGTITVTYSSGSASAPT 121
Db 92 DTSNTAYMQLSLTSDSAVYCAR--RLGRWYF-----DVWGAGTIVTVSSSESQSPFN 144
Qy 122 LFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNSD-TSSTGRFPSPVLRGGKYA 180
Db 145 VFPLVSCSPSLSDKNLVAMGCLARDFLPSTISFTYNTQNTVEIQGITFTFTLRTGGKYL 204
Qy 181 ATSQVLLPSKDVMOGTDHEHVCK 203
Db 205 ATSQVLLSPKSLGSDGYLVCK 227

RESULT 11
Q7TWT6 PRELIMINARY; PRT; 614 AA.
ID Q7TWT6
AC Q7TWT6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC60843 protein.
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=23288257; PubMed=1477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.L.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAH53409.1; --
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 614 AA; 67746 MW; 839BAF3BBD124F89 CRC64;

Query Match 56.2%; Score 609.5; DB 2; Length 614;
Best Local Similarity 57.1%; Pred. No. 2.5e-44;
Matches 116; Conservative 38; Mismatches 42; Indels 7; Gaps 3;

QY 2 KPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVTWNR 61
DB |||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
32 KPGASVKISCKASGYAFSSWMNVKQRPKGKLEWIGRVYFGDGTNYNGKFKGKATLTA 91
QY 62 NTSISTAYMELSSLRSEDATVYVCARGHGGSYFYSGMDVMVGQGTVTVTSSGSASAPT 121
DB :|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
92 DKSSSTAWQLSSLTSEDSAVTFCAK-DYGSIRFAY-----WGQGTTLVTVSAESQSPFN 145
QY 122 LPPLVSCNSPDSSTSSAVGCLAQDFLPDSITFSWKYKNNSD-ISTRGFPFSLVLRGGKYA 180
DB |||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
146 VFPLVSCNSPLSDKNLVANGCLARDFLPSTISFTWYQNNAEVIOGIITFTPLRGGKYL 205
QY 181 ATSQVLLSPKSDVMQGTDEHVCK 203
DB |||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
206 ATSQVLLSPKSLGSDYLVC 228
QY 12 RESULT 12
ID Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SMC66 protein.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Pang Y., Dong Q.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1; --
DR HSSP; P01876; 1O00.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 49.5%; Score 537.5; DB 2; Length 497;
Best Local Similarity 52.5%; Pred. No. 3.4e-38;
Matches 107; Conservative 26; Mismatches 62; Indels 9; Gaps 5;

QY 2 KPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVTWNR 61
DB |||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
32 KPGASVKVSKASGYTFIAYDINVRQAPGQGLEWMGMWNPQTGNTFAQKFGQRLTFSR 91
QY 62 NTSISTAYMELSSLRSEDATVYVCARGHGGSYFYSGMDVMVGQGTVTVTSSGSASAPT 121
DB :|||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
92 DTSINTAYMVLSSLSTEDSAIFYCARGNLRGGRGFGYNWFDPMWGHGTLTVTVSSASPTNPK 151
QY 122 LPPLVSCNSPDSSTSSAVGCLAQDFLPDSITFSWKYKNNSDLSSTGFP--SVLRGCK 178
DB |||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
152 VFPLSLCSTQPD--GNVVIACLVGQFPPEPLSLVTWSESGQG--VTARNFPSPQASGDL 207
QY 179 YAATSQVLLSPKSDVMQGTDEHVVC 202
DB |||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
208 YTTSSQLTLPATQCLAG--KSVTC 229

RESULT 13
Q8N030 PRELIMINARY; PRT; 518 AA.
ID Q8N030;
AC Q8N030;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686I15212.
GN Name=DKFZp686I15212;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Foustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; --
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR000005; HTHaraC.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH ARAC FAMILY_1; UNKNOWN 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
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SQ SEQUENCE 518 AA; 57019 MW; 9385F98613BF6382 CRC64;
Query Match 49.4%; Score 535.5; DB 2; Length 518;
Best Local Similarity 54.2%; Pred. No. 5.3e-38; Indels 15; Gaps 6;
Matches 110; Conservative 28; Mismatches 50;
Qy 1 KKPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAQKFGQGRVTMN 60
Dd 31 KKPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAQKFGQGRVTMT 90
Qy 61 RNTSISTAYMELSLRSRSDTAVYICARGHGG---SYFYSYGMDVWGQGTVTTVSSGSAS 117
Dd 91 RDTWTTTAYMDLSLRSRSDTAVYICARDAPOGVTTTF-----DYMGGQGLTVTVSSAST 144
Qy 118 SAPTLFPLVSCNSPSSSSVAVCLAQDFLPDSITFSWKYKNNSDLSSTRGFSVLAR-G 176
Dd 145 KGPSVFPLAPCSRSTSG-GTAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQSS 201
Qy 177 GKYAATSOVLPLPSKDVMOGTDH 199
Dd 202 GLYSLSVVTVPSSSL-GTQTY 222

RESULT 14
Q6N041 PRELIMINARY; PRT; 498 AA.
AC Q6N041
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G016217 (Fragment).
GN Name=DKFZp686G016217;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Foustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640710; CAE45829.1; --
DR HSSP; P01751; 1A6W.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;
Query Match 48.0%; Score 521; DB 2; Length 498;
Best Local Similarity 54.6%; Pred. No. 9.2e-37;
Matches 113; Conservative 25; Mismatches 55; Indels 14; Gaps 7;
Qy 1 KKPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAQKFGQGRVTMN 60
Dd 46 KKPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAQKFGQGRVSMT 105
Qy 61 RNTSISTAYMELSLRSRSDTAVYICARGHGGSYFYSYGMDVWGQGTVTTVSSGSASAP 120
Dd 106 RDTSTTILMELSLRSRSDTAMFPCARAGPGYGTSAAY-FDYWGQGLTVTVSSASPTSP 164
Qy 121 TLFLPLVSCNSPSSSSVAVCLAQDFLPD---SITFSWKYKNNSDISSTRGFP--SVLR 175
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Db 165 KVFFPL-SLDSTPQD-GNVVAVACLVGQFFPQBPPLSVTWSGQN-----VTARNFFPSQDAS 218
Qy 176 GGRYAATSOVLPLPSKDVMOGTDHVVVC 202
Dd 219 GDLYTTSSTQLTLPATQCPDG--KSVTC 243

RESULT 15
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAHS1328.1; --
DR HSSP; P01857; 1HZZ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
Query Match 46.9%; Score 508.5; DB 2; Length 469;
Best Local Similarity 50.2%; Pred. No. 1e-35;
Matches 102; Conservative 34; Mismatches 52; Indels 15; Gaps 6;
Qy 1 KKPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAQKFGQGRVTMN 60
Dd 31 KKPGASVKVSKCTGYNFSSYDILWVRQAPQGLEWGMNPNPNSGNTGYAQKFGQGRVTMT 90
Qy 61 RNTSISTAYMELSLRSRSDTAVYICARGHGG--GSFYFYGMDVWGQGTVTTVSSGSAS 118
Dd 91 TDTSATSYMEFSLRSRSDTALFYCATKSRGQGVDF-----DSWGQGLTVTVSSASTK 143
```



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 94.1163 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-27

Perfect score: 1085

Sequence: 1 KPQASVKVSKASGYFTS.....QVLLPSKDVMOGTDHVVCK 203

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003s.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1085	100.0	203	2 AAY34301	Aay34301 Igm antib
2	985	90.8	199	2 AAY34302	Aay34302 Igm antib
3	894	82.4	627	7 ADE97370	Ad97370 Human imm
4	881.5	81.2	588	2 AAW71880	Aaw71880 Anti-huma
5	881.5	81.2	588	3 AAB12917	Aab12917 Anti-huma
6	867.5	80.0	588	2 AAW71881	Aaw71881 Anti-huma
7	867.5	80.0	588	3 AAB12918	Aab12918 Anti-huma
8	809	74.6	266	8 ADF69305	Adf69305 Human lun
9	783.5	72.2	571	8 ADP84970	Adp84970 ChimERIC
10	781	72.0	228	8 ADL70776	Adl70776 Anti-TNFA
11	775.5	71.5	595	7 ADM05427	Adm05427 Human pro
12	766.5	70.6	596	4 AAM23924	Aam23924 Human EST
13	763.5	70.4	223	2 AAY08598	Aay08598 Anti-huma
14	757.5	69.8	223	8 ADL70773	Adl70773 Anti-TNFA
15	736	67.8	570	8 ADL19329	Adl19329 ChimERIC
16	731.5	67.4	533	7 ADB65070	Adb65070 Human pro
17	728.5	67.1	205	2 AAY34299	Aay34299 Igm antib
18	719.5	66.3	569	8 ADR19330	Adr19330 ChimERIC
19	707.5	65.2	202	2 AAY34303	Aay34303 Igm antib
20	698	64.3	197	2 AAY34300	Aay34300 Igm antib
21	673.5	62.1	190	2 AAY34304	Aay34304 Igm antib
22	645	59.4	590	2 AAW31751	Aaw31751 H chain s
23	645	59.4	590	2 AAW71888	Aaw71888 Anti-huma
24	645	59.0	590	3 AAB12908	Aab12908 Anti-huma
25	638	58.8	476	2 AAW88464	Aaw88464 Monoclonal

26	601	55.4	576	8	ADF69325	Adf69325 Human lun
27	597	55.0	571	8	ADP84967	Adp84967 Murine an
28	596	54.9	470	5	AAU74296	Aau74296 Anti-huma
29	596	54.9	573	8	ADP84968	Adp84968 Murine an
30	592.5	54.6	228	6	ABR01526	Ab01526 Human ant
31	584.5	53.9	230	6	ABR01514	Ab01514 Human ant
32	583	53.7	221	6	ABR01537	Ab01537 Human ant
33	580.5	53.5	471	7	ADE28427	Ad28427 Human ant
34	559.5	51.6	125	7	ADK18814	Adk18814 Anti-huma
35	559.5	51.6	126	7	ADK18864	Adk18864 Anti-huma
36	559.5	51.6	126	7	ADK18595	Adk18595 Anti-huma
37	559.5	51.6	126	7	ADK18777	Adk18777 Anti-huma
38	559.5	51.6	126	8	ADL25408	Adl25408 Human mAb
39	559	51.5	125	7	ADK18614	Adk18614 Anti-huma
40	559	51.5	125	7	ADK18779	Adk18779 Anti-huma
41	559	51.5	125	7	ADK18919	Adk18919 Anti-huma
42	559	51.5	125	7	ADK18816	Adk18816 Anti-huma
43	559	51.5	125	8	ADL25444	Adl25444 Human mAb
44	557	51.3	451	8	ADR23350	Adr23350 Human CD7
45	554	51.1	451	8	ADR23348	Adr23348 Human CD7

ALIGNMENTS

RESULT 1  
AAY34301  
ID AAY34301 standard; protein; 203 AA.  
XX  
AC AAY34301;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE Igm antibody CEM 10.12 F3 heavy chain sequence.  
XX  
KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
OS Homo sapiens.  
XX  
PN WO9945031-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 03-MAR-1999; 99WO-US004583.  
XX  
PR 03-MAR-1998; 98US-00034607.  
XX  
PR 03-FEB-1999; 99US-00244253.  
(ABGE-) ABGENIX INC.  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX  
DR WPI; 1999-540816/45.  
DR N-PSDB; AAZ20402.  
XX  
PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX  
PS Claim 60; Fig 26; 245pp; English.  
XX  
CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (mAb) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the Igm mAb ABX-CBL, providing that the antibody is not CBL1. The mAb  
CC can selectively kill activated T-cells, activated B-cells or treating or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX  
SQ Sequence 203 AA;  
Query Match 100.0%; Score 1085; DB 2; Length 203;  
Best Local Similarity 100.0%; Pred. No. 1.8e-72;  
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KKPASVKVSKASGYTFTSYDINWVRQATCGLEWGMWNPNSGNTGYAQKFGQRTVMN 60  
Db 1 KKPASVKVSKASGYTFTSYDINWVRQATCGLEWGMWNPNSGNTGYAQKFGQRTVMN 60  
Qy 61 RNTSISTAYMELSLRSEDATVYVCARGHGGSFYSYGMDVMGQGTTVTVSSGSASAP 120  
Db 61 RNTSISTAYMELSLRSEDATVYVCARGHGGSFYSYGMDVMGQGTTVTVSSGSASAP 120  
Qy 121 TLFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPFVSLRGKYA 180  
Db 121 TLFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPFVSLRGKYA 180  
Qy 181 ATSQVLLPSKDVMOGTDEHVCK 203  
Db 181 ATSQVLLPSKDVMOGTDEHVCK 203

RESULT 2  
RAY34302  
ID AAY34302 standard; protein; 199 AA.  
XX  
AC AAY34302;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE IgM antibody CEM 10.12 G5 heavy chain sequence.  
XX  
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
OS Homo sapiens.  
XX  
FN WO9945031-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 03-MAR-1999; 99WO-US004583.  
XX  
PR 03-MAR-1998; 98US-00034607.  
XX  
PR 03-FEB-1999; 99US-00244253.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX  
DR WPI; 1999-540816/45.  
DR N-PSDB; AAZ20403.  
XX  
PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX  
PS Claim 60; Fig 27; 245pp; English.  
XX  
CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IgM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.

CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX  
SQ Sequence 199 AA;  
Query Match 90.8%; Score 985; DB 2; Length 199;  
Best Local Similarity 94.0%; Pred. No. 4.3e-65;  
Matches 189; Conservative 1; Mismatches 7; Indels 4; Gaps 1;  
Qy 1 KKPASVKVSKASGYTFTSYDINWVRQATCGLEWGMWNPNSGNTGYAQKFGQRTVMN 60  
Db 3 KKPASVKVSKASGYTFTSYDINWVRQATCGLEWGMWNPNSGNTGYAQKFGQRTVMN 62  
Qy 61 RNTSISTAYMELSLRSEDATVYVCARGHGGSFYSYGMDVMGQGTTVTVSSGSASAP 120  
Db 63 RNTSISTAYMELSLRSEDATVYVCAR----EEWLVRYYGMDVMGQGTTVTVSSGSASAP 118  
Qy 121 TLFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPFVSLRGKYA 180  
Db 119 TLFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPFVSLRGKYA 178  
Qy 181 ATSQVLLPSKDVMOGTDEHV 201  
Db 179 ATSQVLLPSKDVMOGTDEHKV 199

RESULT 3  
ADE97370  
ID ADE97370 standard; protein; 627 AA.  
XX  
AC ADE97370;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human immunoadhesin-related protein - SEQ ID 47.  
XX  
KW immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;  
KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;  
KW intercellular adhesion molecule; ICAM-1, human.  
XX  
OS Homo sapiens.  
XX  
FN WO2003064992-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 25-OCT-2002; 2002WO-US034197.  
XX  
PR 26-OCT-2001; 2001US-00047542.  
XX  
PA (PLAN-) PLANET BIOTECHNOLOGY INC.  
PA (LARR/) LARRICK J W.  
PA (WYCOFF/) WYCOFF K L.  
XX  
PI Larrick JW, Wycoff KL;  
XX  
DR WPI; 2003-636816/60.  
XX  
PT New immunoadhesin, useful for treating anthrax and rhinovirus, comprises  
PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and  
PT J chain and secretory component associated with the chimeric toxin  
PT receptor protein.  
XX  
PS Disclosure; SEQ ID NO 47; 289pp; English.  
XX  
CC The invention relates to a novel immunoadhesin comprising a chimeric  
CC toxin receptor protein consisting of a toxin receptor protein linked to  
CC at least a portion of an immunoglobulin heavy chain with a J (joining)  
CC chain and secretory component (SC) associated with the chimeric toxin  
CC receptor protein. The immunoadhesin comprises a chimeric bacterial or  
CC viral toxin receptor protein and the immunoadhesin has plant-specific  
CC glycosylation. The immunoadhesin of the invention demonstrates virucide



PA (SANY ) SANKYO CO LTD.

PR 18-SEP-1998; 98JP-00264598.



DB 202 ATSQVLLPSKDVWQGTDEHVCK 224

RESULT 7  
AAB12918

ID AAB12918 standard; protein; 588 AA.

XX AAB12918;

XX 16-NOV-2000 (first entry)

XX Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #88.

XX Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
KW immunosuppression; autoimmune disease; treatment; rheumatism;  
KW anti-Fas antibody.  
XX Synthetic.  
OS JP2000154149-A.  
FN 06-JUN-2000.  
XX 17-SEP-1999; 95JP-00263984.  
PF 18-SEP-1998; 95JP-00264598.  
PR (SANY ) SANKYO CO LTD.  
PA WPI, 2000-454476/40.  
DR N-PSDB; AAA78272.  
DR  
XX  
PT Anti-human Fas humanizing antibody-containing antirheumatic agents.  
XX Claim 1; Page 80-81; 109pp; Japanese.  
PS  
XX The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein does not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, especially rheumatism. The IgM molecule used in the invention has human Fas antigen binding properties. Included in the invention are nucleotide sequences of the IgM light and heavy chains (see AAA78267-A78272) and the corresponding protein sequences (see AAB12913-B12918 and AAB12919), and nucleotide sequences of the humanised anti-human Fas Ig CH11 (see AAB12913-B12918) and protein sequences (see AAB12908-B12910). Also included are anti-human Fas antibody CDR peptides (AAB12902-B12907). Primers specific for the anti-human Fas antibody, light, heavy and kappa chains used in the invention are represented by sequences AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the invention are represented by sequences AAA78277-A78318 and AAA78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in the production of the agent of the invention

SQ Sequence 588 AA;

Query Match 80.0%; Score 867.5; DB 3; Length 588;  
Best Local Similarity 81.8%; Pred. No. 6.e-56;  
Matches 166; Conservative 12; Mismatches 16; Indels 9; Gaps 1

Qy 1 KPGASVKVSKCASYTTSYDINVRQTGGLLEWMGHMPNSGNLTGYAQKFQGRVTWN 60  
| | | | | | | | | | | | | | | | | | | | : | | | | | | | | | | | | |  
Db 31 KPGASVKVSKCASYTTDDYNMHVWKVQHGSLEWMGVYIPYNGGTGYNQRFKSKATLT 90  
| | | | | | | | | | | | | | | | | | | | : | | | | | | | | | | | | |  
Qy 61 RNTSIISTAYMELSSLRSEDTAVYYCARCGHGGSYFYFYSYGMDVDWGQGTITTVTVSSGSASAP 120  
: | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | | | | |  
Db 91 VDNASTAYMELSSLRSEDTAVYYCAR -----SYAMDYWGQGTITTVTVSSGSASAP 141  
:  
Qy 121 TLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDI SSTRGFPSPVLGGKYA 180

Db	142	TLFLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVSLRGSKYA	201
Qy	181	ATSQVLLPSKDVMOQTDEHVCK	203
Db	202	ATSQVLLPSKDVMOQTDEHVCK	224
RESULT 8			
AD	AD69305	standard; protein; 266 AA.	
AC	AD69305;		
DT	26-FEB-2004	(first entry)	
XX	Human lung specific protein sequence SEQ ID NO:62.		
XX	human; lung specific nucleic acid; lung specific protein; lung cancer;		
KW	cytostatic; gene therapy.		
KX	Homo sapiens.		
OS			
XX	WO2003102137-A2.		
XX	11-DEC-2003.		
XX	30-MAY-2003; 2003WO-US016810.		
PF	31-MAY-2002; 2002US-0385301P.		
XX	(DIAD-) DIADEXUS INC.		
PA	Chen S, Macina RA, Sun Y, Liu C, Turner LR;		
XX	WPI; 2004-053457/05.		
DR	New human lung specific nucleic acid, useful for preparing a composition		
PT	for diagnosing or treating lung cancer.		
FT	Claim 11; SEQ ID NO 62; 221pp; English.		
XX	The present invention describes a human lung specific nucleic acid		
CC	molecule. Also described: (1) a method for determining the presence of a		
CC	lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising		
CC	the nucleic acid molecule; (3) a host cell comprising the vector; (4) a		
CC	method for producing a polypeptide encoded by the nucleic acid molecule;		
CC	(5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody		
CC	or its fragment that specifically binds to the polypeptide; (7) a method		
CC	for determining the presence of a lung specific protein in a sample; (8)		
CC	a method for diagnosing and monitoring the presence and metastases of		
CC	lung cancer in a patient; (9) a kit for detecting a risk of cancer or		
CC	presence of cancer in a patient comprising a means for determining the		
CC	presence the nucleic acid molecule or polypeptide in a sample of a		
CC	patient; (10) a method of treating a patient with lung cancer; and (11) a		
CC	vaccine comprising the polypeptide or the nucleic acid encoding the		
CC	polypeptide. Human LSNA molecules and related proteins have cytostatic		
CC	activity, and can be used in gene therapy. They are useful for preparing		
CC	a composition for diagnosing or treating lung cancer. The present		
CC	sequence represents a human lung specific protein, which is used in the		
CC	exemplification of the present invention.		
XX	Sequence 266 AA;		
Query Match 74.6%; Score 809; DB 8; Length 266;			
Best Local Similarity 75.4%; Pred. No. 6e-52;			
Matches 156; Conservative 18; Mismatches 21; Indels 12; Gaps 3			
Qy	1	KKPGASVKVSKASGYTFTSYDINWVQATCGGLEWGMNPNNSGNTGYAQKFQGRVTMN	60
XX	23	KKPGESLKIICKSGGYGFTSYWIGWVRQMPQKGLWEMGIIYPGDSITRYSFQGGVTIS	82
Db			
Qy	61	RNTSISTAYMBELSLRSDTAVVYCAR----GGHGSGSYFYSGYGMVDMVQGGTTVTVSSGS	116



XX Example 8; SEQ ID NO 49; 243pp; English.

XX The present invention relates to a library (I) of modified fusion

CC proteins of transferrin (Tf) and therapeutic proteins with increased

CC serum half-life or serum stability. Preferred fusion proteins include

CC those modified so that the Tf moiety exhibits no or reduced

CC glycosylation, iron binding and/or Tf receptor binding. The transferrin

CC fusion proteins are useful for treating, preventing or ameliorating

CC disorders or diseases of endocrine system, nervous system, immune system,

CC respiratory system, cardiovascular system, diseases and/or disorders

CC relating to cell proliferation, and/or diseases or disorders relating to

CC blood. The modified fusion proteins are useful in diagnosis, prognosis,

CC prevention and/or treatment of autoimmune disorders; diseases and

CC disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia

CC and thrombocytopenia); allergic reactions such as allergic asthma,

CC anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and

CC eczema; inflammatory conditions e.g., inflammation associated with

CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,

CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders

CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel

CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders

CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative

CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The

CC fusion protein is also useful as an adjuvant to enhance antibacterial or

CC antifungal immune responses, antiparasitic immune responses, etc. The

CC fusion protein is also useful for treating monoclonal gammopathy of

CC undetermined significance (MGUS), Waldenström's disease, plasmacytomas,

CC adult respiratory distress syndrome, for stimulating wound repair, for

CC preventing or treating infections of joints, bones, skin, etc. The fusion

CC protein is also useful for treating or preventing thrombosis, myocardial

CC infarction, cancers, thrombocytopenia, sickle cell anaemia,

CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,

CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf

CC and a specific example of a SCA that can be fused to Tf is anti-tumour

CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence

CC from an anti-TNFalpha antibody.

XX SQ Sequence 228 AA;

Query Match 72.0%; Score 781; DB 8; Length 228;

Best Local Similarity 71.5%; Pred. No. 6e-50; Indels 12; Gaps 2;

Matches 148; Conservative 27; Mismatches 20;

QY 2 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGMNPNNGTGYAQKFGQRTVWNR 61

DB 13 QPGGSLRLSCAASGFTFTSYVNWVRQAPGKLEWVSGISGGSGTYYADSVKGRFTISR 72

QY 62 NTSISTAWELSLRSEDATVYCYCA-----RGCHGGSFYFYGYMDVWGQGTITVSSGS 116

DB 73 DNSMNTLYLQMSLRSEDATVYCYCAKDLNRLSGGTF-----DIWGQGTITVSSGS 125

QY 117 ASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDLSSTRGPPSVLRG 176

DB 126 ASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDLSSTRGPPSVLRG 185

QY 177 GKYAATSVQLLPKDVWGQGTITVSSGS 203

DB 186 GKYAATSVQLLPKDVWGQGTITVSSGS 212

RESULT 11

ADM05427

ID ADM05427 standard; protein; 595 AA.

XX AC ADM05427;

XX DT 20-MAY-2004 (first entry)

XX DE Human protein of the invention SEQ ID NO:4112.

XX KW human; gene therapy; diagnostic marker; pharmaceutical.

XX

OS Homo sapiens.

XX PN EP1347046-A1.

XX PD 24-SEP-2003.

XX PF 12-APR-2002; 2002EP-00008400.

XX PR 22-MAR-2002; 2002JP-00137785.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

DR WPI; 2003-723558/69.

DR N-PSDB; ADM02984.

XX New polynucleotides and polypeptides are useful in gene therapy, for

PT developing a diagnostic marker or medicines for regulating their

PT expression and activity, or as a target of gene therapy.

PS Claim 1; SEQ ID NO 4112; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded

CC polypeptide. A polynucleotide of the invention may have a use in gene

CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful

CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

CC useful in gene therapy, for developing a diagnostic marker or medicines

CC for regulating their expression and activity, or as a target of gene

CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

CC are useful as pharmaceutical agents. The present sequence represents a

CC protein sequence of the invention.

XX SQ Sequence 595 AA;

Query Match 71.5%; Score 775.5; DB 7; Length 595;

Best Local Similarity 71.8%; Pred. No. 4.3e-49;

Matches 145; Conservative 30; Mismatches 24; Indels 3; Gaps 1;

QY 2 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGMNPNNGTGYAQKFGQRTVWNR 61

DB 33 QPGGSLRLSCAASGFTFTSFAMHVRQAPGKLEWVSTISSNGRQKYGESVKGRFTISR 92

QY 62 NTSISTAWELSLRSEDATVYCYCARGHGSFYFYGYMDVWGQGTITVSSGSASAPT 121

DB 93 DSSKNTLYLQMSLRSEDATVYCYCARGHSIDNY---HYGVDVWGQGTITVSSGSASAPT 149

QY 122 LFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDLSSTRGPPSVLRGKYAA 181

DB 150 LFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDLSSTRGPPSVLRGKYAA 209

QY 182 TSQVLLPSKDVWGQGTITVSSGS 203

DB 210 TSQVLLPSKDVWGQGTITVSSGS 231

RESULT 12

AAW23924

ID AAW23924 standard; protein; 596 AA.

XX AC AAW23924;

XX DT 12-OCT-2001 (first entry)

XX DE Human EST encoded protein SEQ ID NO: 1449.

XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostic; forensic test; gene mapping; genetic disorder; biodiversity;

KW gene therapy; nutrition.

```
XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US002687.
XX PR 25-JAN-2000; 2000US-00491404.
XX FR 17-JUL-2000; 2000US-00617746.
XX PR 03-AUG-2000; 2000US-00631451.
XX PR 15-SEP-2000; 2000US-00663870.
XX XX (HYSE-) HYSEQ INC.
XX XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Aeundi V;
XX PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX DR WPI; 2001-476164/51.
XX DR N-PSDB; AAH98583.
XX XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX PT antibodies and research use.
XX PS Claim 20; Page 1011-1012; 1275pp; English.
XX CC The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,
XX CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX CC from the organism of interest. They can be used in diagnostics,
XX CC forensics, gene mapping, identification of mutations, to assess
XX CC biodiversity and for nutritional purposes. The present sequence is a
XX CC protein of the invention
XX SQ Sequence 596 AA;
Query Match 70.6%; Score 766.5; DB 4; Length 596;
Best Local Similarity 72.3%; Pred. No. 2e-48; Mismatches 1; Gaps 1;
Matches 146; Conservative 25; Indels 30; Indels 1; Gaps 1;
Qy 2 KPGASVKVCKASGYTFTSVDINWVRQATGQGLEWMGMNPNNGNTGYAQKFGQGRVTMNR 61
Db 32 QPGGSLRLSCAASGFTSSYWMHWVRQAPGKGLVWVSRIINTDGSSTSYADSVKGRFTISR 91
Qy 62 NTSISTAYMELSSLRSEDTAVYICARGHGSGSYFYSGMDVWGQGTITVTVSSGSASAPT 121
Db 92 DNAKNTLYLQWNSLRAEDTAVYICARADNCSS-TSCYKCFDYWGQGTITVTVSSGSASAPT 150
Qy 122 LPPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAA 181
Db 151 LPPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAA 210
Qy 182 TSQVLLPSKDVMOGTDHVVCK 203
Db 211 TSQVLLPSKDVMOGTDHVVCK 232
RESULT 13
AAV08598
ID AAV08598 standard; protein; 223 AA.
XX AC AAV08598;
XX XX 05-AUG-1999 (first entry)
XX DT Anti-human TNF-alpha monoclonal antibody H-chain protein.
XX DE Monoclonal antibody; H chain; heavy chain; anti-human; TNF-alpha;
XX KW tumour necrosis factor; light chain; L chain.
XX OS Homo sapiens.
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XX PN JP11127855-A.
XX PD 18-MAY-1999.
XX PF 27-OCT-1997; 97JP-00293994.
XX PP 27-OCT-1997; 97JP-00293994.
XX PR (NTHA ) JAPAN ENERGY CORP.
XX PA WPI; 1999-350318/30.
XX DR N-PSDB; AAX77407.
XX XX Recombinant anti-human TNF-alpha human monoclonal antibody - produced
XX PT stably with a high purity, and in large amounts.
XX PT Claim 3; Page 12-13; 22pp; Japanese.
XX XX This invention describes novel recombinant anti-human TNF-alpha human
XX CC monoclonal antibody consisting of a heavy (H) chain and a light (L)
XX CC chain. The recombinant anti-human TNF-alpha human monoclonal antibody can
XX CC be produced stably in a high purity and in a large amount
XX SQ Sequence 223 AA;
Query Match 70.4%; Score 763.5; DB 2; Length 223;
Best Local Similarity 72.3%; Pred. No. 1.1e-48; Mismatches 24; Indels 2;
Matches 146; Conservative 25; Indels 24; Indels 2; Gaps 2;
Qy 2 KPGASVKVCKASGYTFTSVDINWVRQATGQGLEWMGMNPNNGNTGYAQKFGQGRVTMNR 61
Db 13 QPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLVWVSRIINTDGSSTSYADSVKGRFTISR 72
Qy 62 NTSISTAYMELSSLRSEDTAVYICARGHGSGSYFYSGMDVWGQGTITVTVSSGSASAPT 121
Db 73 DNSKNTLYLQWNSLRAEDTAVYICAKDS-GDLAF-----DINGQGTMTVTSSGSASAPT 125
Qy 122 LPPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAA 181
Db 126 LPPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAA 185
Qy 182 TSQVLLPSKDVMOGTDHVVCK 203
Db 186 TSQVLLPSKDVMOGTDHVVCK 207
RESULT 14
ADL70773
ID ADL70773 standard; protein; 223 AA.
XX AC ADL70773;
XX XX 03-JUN-2004 (first entry)
XX DT Anti-TNFalpha antibody VH region, SEQ ID 46.
XX DE Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;
XX KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;
XX KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulneryary;
XX KW Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antiatherosclerotic;
XX KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
XX KW Tf; transferrin fusion protein; Tf fusion protein; anti-TNFalpha;
XX KW antibody; VH region.
XX OS Unidentified.
XX PN WO2004020588-A2.
XX XX 11-MAR-2004.
XX PD 28-AUG-2003; 2003WO-US026779.
XX PF 28-AUG-2003; 2003WO-US026779.
XX OS
```



Db	13	QPGGMLKSCAASGFTFSDAMDWVRSPEKGLEWAEIRSKANNHATYYAESVKGRFTI	72
Qy	60	NRNTSISTAYMELSSLRSEDTAVYYCARGHGGGSFYFYGYGMDYWGOGTTVTUSSGSASA	119
Db	73	SRDVSKSVYLQMNLRADTGIIYCTRG-----YGFYWGOGTTLTV-SGSASA	122
Qy	120	PTLPPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKY	179
Db	123	PTLPPLVSCENSPSDTSSVAVGCLAQDFLPDSITLSWKYKNSDISSTRGPPSVLRGGKY	182
Qy	180	AATSQVLLPSKDVNQGTDEHVCK	203
Db	183	AATSQVLLPSKDVNQGTDEHVCK	206

Search completed: March 8, 2005, 06:17:09  
Job time : 95.1163 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 107.727 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-27

Perfect score: 1085

Sequence: 1 KPGASVKVSKASGYTFTS.....QVLLPSKDVMTQGDHVVCK 203

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
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- 14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	894	82.4	627	13	US-10-047-542-47 Sequence 47, Appl
2	775.5	71.5	595	15	US-10-108-260A-4112 Sequence 4112, Ap
3	731.5	67.4	533	15	US-10-104-047-3224 Sequence 3224, Ap
4	638	58.8	476	9	US-09-747-669-3 Sequence 3, Appli
5	638	58.8	476	14	US-10-290-703-3 Sequence 3, Appli
6	596	54.9	470	9	US-09-859-053-28 Sequence 28, Appl
7	596	54.9	470	16	US-10-625-105-28 Sequence 28, Appl
8	592.5	54.6	228	16	US-10-128-520-163 Sequence 163, App
9	584.5	53.9	230	16	US-10-128-520-151 Sequence 151, App
10	583	53.7	221	16	US-10-128-520-174 Sequence 174, App
11	580.5	53.5	471	15	US-10-292-088-46 Sequence 46, Appl
12	559.5	51.6	125	14	US-10-041-860-238 Sequence 238, App
13	559.5	51.6	126	14	US-10-041-860-19 Sequence 19, Appl

14	559.5	51.6	126	14	US-10-041-860-201
15	559.5	51.6	126	14	US-10-041-860-288
16	559.5	51.6	126	16	US-10-665-383-18
17	559	51.5	125	14	US-10-041-860-38
18	559	51.5	125	14	US-10-041-860-203
19	559	51.5	125	14	US-10-041-860-240
20	559	51.5	125	14	US-10-041-860-343
21	559	51.5	125	16	US-10-665-383-54
22	543.5	50.1	448	14	US-10-171-452A-42
23	543.5	50.1	448	14	US-10-171-452A-48
24	543.5	50.1	448	14	US-10-171-452A-54
25	543.5	50.1	448	14	US-10-171-452A-60
26	543.5	50.1	448	15	US-10-353-708-42
27	543.5	50.1	448	15	US-10-353-708-48
28	543.5	50.1	448	15	US-10-353-708-54
29	543.5	50.1	448	15	US-10-353-708-60
30	543.5	50.1	448	16	US-10-731-984-8
31	543.5	50.1	448	16	US-10-731-984-16
32	543.5	50.1	448	16	US-10-731-984-34
33	543.5	50.1	448	16	US-10-731-984-42
34	543.5	50.1	467	14	US-10-171-452A-41
35	543.5	50.1	467	14	US-10-171-452A-47
36	543.5	50.1	467	14	US-10-171-452A-53
37	543.5	50.1	467	14	US-10-171-452A-59
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40	543.5	50.1	467	15	US-10-353-708-53
41	543.5	50.1	467	15	US-10-353-708-59
42	543.5	50.1	467	16	US-10-731-984-7
43	543.5	50.1	467	16	US-10-731-984-15
44	543.5	50.1	467	16	US-10-731-984-23
45	543.5	50.1	467	16	US-10-731-984-31

ALIGNMENTS

RESULT 1  
US-10-047-542-47  
; Sequence 47, Application US/10047542  
; Publication No. US20020168367A1  
; GENERAL INFORMATION:  
; APPLICANT: LARRICK, JAMES W.  
; APPLICANT: WYCOFF, KEITH L.  
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
; TITLE OF INVENTION: AND BACTERIAL DISEASES  
; FILE REFERENCE: 030905.0004.CIP1  
; CURRENT APPLICATION NUMBER: US/10/047,542  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: PCT/US01/13932  
; PRIOR FILING DATE: 2001-04-28  
; PRIOR APPLICATION NUMBER: 60/200,298  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 627  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-047-542-47

Query Match	82.4%	Score 894;	DB 13;	Length 627;
Best Local Similarity	83.4%	Pred. No. 4.5e-58;		
Matches 176;	Conservative	7;	Mismatches 20;	Indels 8;
Gaps	1;			
QY	1	KPGASVKVSKASGYTFTS	DTDINVRQATCGLEWGMNPN	SGNTGYAQKFGQRTVW 60
DB	31	KKPGSSVVKVSKASGGTFTS	VAISVVRQAPGQGLEWGMG	GIPIFGTANYAQKFGQRTV 90
QY	61	RNTSISTAMELSSLRSDTAV	YVCARGHGSYF-----	YSYGMVDMVGQGTIVT 112
DB	91	ADESTAINELSSLRSDTAV	YVCARKTGILGPYSSGWP	NSDYFYGMVDMVGQGTIVT 150



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; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001002
; CURRENT APPLICATION NUMBER: US/10/290,703
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/747,669
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/051,945
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-290-703-3

Query Match 58.8%; Score 638; DB 14; Length 476;
Best Local Similarity 62.1%; Pred. No. 2.9e-39;
Matches 126; Conservative 22; Mismatches 47; Indels 8; Gaps 5;

QY 1 KPGASVKVCKASGYTFTSYDINVRQATGCGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 31 KPGASVKVCKASGYTFTSYDINVRQAPGCGLEWGMWNPNSGNTGYAOKFQGRVTMT 90
QY 61 RNTSISTAYMELSLRSRSDTAVYVCARGGHG--GSVFYSYGMVDYVGQGTITVTVSSGAS 118
DB 91 RNTSIRTAYMELSLRSDTAVYFCARADNVEMAIHYHGMVDYVGQGTITVTVSSASTK 150
QY 119 APTLPPLVSCNSPDSSTSSVAVGCLAQPLDPSITFSWKYKKNDSISSTRGPPSVLR 177
DB 151 GSPVFPPLAPSSKSTSG-GTAALGCLVKDYFPEPPTVSM--NSGALTSGVHTTTPPAVLQSSG 207
QY 178 KYAATSOVLPLPSKDVQGTDEHV 200
DB 208 LYSLSVTVTPSSSL--GRTQYI 228

RESULT 6
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match 54.9%; Score 596; DB 9; Length 470;
Best Local Similarity 59.9%; Pred. No. 3.6e-36;
Matches 118; Conservative 26; Mismatches 39; Indels 14; Gaps 6;

QY 1 KPGASVKVCKASGYTFTSYDINVRQATGCGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 31 KPGASVKVCKASGYTFTSYDINVRQAPGCGLEWGMWNPNSGNTGYAOKFQGRVTMT 90
QY 61 RNTSISTAYMELSLRSRSDTAVYVCARGGHG--GSVFYSYGMVDYVGQGTITVTVSSG 115
DB 91 RNTSIRTAYMELSLRSDTAVYFCARADNVEMAIHYHGMVDYVGQGTITVTVSSASTK 145
QY 119 APTLPPLVSCNSPDSSTSSVAVGCLAQPLDPSITFSWKYKKNDSISSTRGPPSVLR 175
DB 151 GSPVFPPLAPSSKSTSG-GTAALGCLVKDYFPEPPTVSM--NSGALTSGVHTTTPPAVLQSSG 207
QY 178 KYAATSOVLPLPSKDVQGTDEHV 200
DB 208 LYSLSVTVTPSSSL--GRTQYI 228

RESULT 7
US-10-625-105-28
; Sequence 28, Application US/10625105
; Publication No. US20040180052A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/10/625,105
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-625-105-28

Query Match 54.9%; Score 596; DB 16; Length 470;
Best Local Similarity 59.9%; Pred. No. 3.6e-36;
Matches 118; Conservative 26; Mismatches 39; Indels 14; Gaps 6;

QY 1 KPGASVKVCKASGYTFTSYDINVRQATGCGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 31 KPGASVKVCKASGYTFTSYDINVRQAPGCGLEWGMWNPNSGNTGYAOKFQGRVTMT 90
QY 61 RNTSISTAYMELSLRSRSDTAVYVCARGGHG--GSVFYSYGMVDYVGQGTITVTVSSG 115
DB 91 RNTSIRTAYMELSLRSDTAVYFCARADNVEMAIHYHGMVDYVGQGTITVTVSSASTK 145
QY 119 APTLPPLVSCNSPDSSTSSVAVGCLAQPLDPSITFSWKYKKNDSISSTRGPPSVLR 175
DB 151 GSPVFPPLAPSSKSTSG-GTAALGCLVKDYFPEPPTVSM--NSGALTSGVHTTTPPAVLQSSG 207
QY 178 KYAATSOVLPLPSKDVQGTDEHV 200
DB 208 LYSLSVTVTPSSSL--GRTQYI 228

RESULT 8
US-10-128-520-163
; Sequence 163, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
```

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; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-163

Query Match      54.6%; Score 592.5; DB 16; Length 228;
Best Local Similarity 58.7%; Pred. No. 3.2e-36;
Matches 121; Conservative 24; Mismatches 44; Indels 17; Gaps 6;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 12 KPGASVKVSKASGYTFTSYDINWVRQAPGQGLEWGMWNPNSGNTGYAOKFQGRVTMT 71
QY 61 RNTSISTAYMELSLRSRSDTAVYYCARGHGGSFYFSGM-----DVMGGTITVTYSSG 115
DB 72 RDTISISTAYMELSLRSRSDTAVYYCAR-----IWMSDYGGQIVKGGDIWGGQTLVTYSSA 125
QY 116 SASAPTLFPLVSCENSPDTSVAVGCLAQDPLPDSITFSWKYKNNDSISSTRGPPSVLR 175
DB 126 STKGPSVFPFLAPSSKSTSG-GTAALGCLVKDYFPEPPTVSW--NSGALTSGVHTFPAVLQ 182
QY 176 -GGKYAATSOVLLPSKDVNQGTDEHV 200
DB 183 SSGLYSLSSVTVTPSSSL--GTQTYI 206

RESULT 9
US-10-128-520-151
; Sequence 151, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-151

Query Match      53.9%; Score 584.5; DB 16; Length 230;
Best Local Similarity 58.7%; Pred. No. 1.3e-35;
Matches 121; Conservative 22; Mismatches 46; Indels 15; Gaps 6;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 12 KPGASVKVSKASGYTFTSYDINWVRQAPGQGLEWGMWNPNSGNTGYAOKFQGRVTMT 71
QY 61 RNTSISTAYMELSLRSRSDTAVYYCAR-----GGHGGSYFYSGYGMVWGGQTTVTYSSG 115
DB 72 RDTISISTAYMELSLRSRSDTAVYYCARLVGIVGKPDLLY----FDVMGGQTLVTYSSA 127
QY 116 SASAPTLFPLVSCENSPDTSVAVGCLAQDPLPDSITFSWKYKNNDSISSTRGPPSVLR 175
DB 128 STKGPSVFPFLAPSSKSTSG-GTAALGCLVKDYFPEPPTVSW--NSGALTSGVHTFPAVLQ 184
QY 176 -GGKYAATSOVLLPSKDVNQGTDEHV 200
DB 185 SSGLYSLSSVTVTPSSSL--GTQTYI 208
```

```
RESULT 10
US-10-128-520-174
; Sequence 174, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-174

Query Match      53.7%; Score 583; DB 16; Length 221;
Best Local Similarity 58.7%; Pred. No. 1.6e-35;
Matches 118; Conservative 24; Mismatches 45; Indels 14; Gaps 5;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 12 KPGSSVKVSKASGGTTFSSYVAISWVRQAPGQGLEWGMWNPNSGGTNYAOKFQGRVTMT 71
QY 61 RNTSISTAYMELSLRSRSDTAVYYCARGHGGSFYFSGYGMVWGGQTTVTYSSGSASAP 120
DB 72 RDTISISTAYMELSLRSRSDTAVYYCAR-----ITYGYDFWGGQGLTVTVSSASTKGP 123
QY 121 TLFPLVSCENSPDTSVAVGCLAQDPLPDSITFSWKYKNNDSISSTRGPPSVLR-GGKY 179
DB 124 SVFPLAPSSKSTSG-GTAALGCLVKDYFPEPPTVSW--NSGALTSGVHTFPAVLQSSGLY 180
QY 180 AATSOVLLPSKDVNQGTDEHV 200
DB 181 SLSSVTVTPSSSL--GTQTYI 199
```

```
RESULT 11
US-10-292-088-46
; Sequence 46, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: AEX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 46
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-46

Query Match      53.5%; Score 580.5; DB 15; Length 471;
Best Local Similarity 59.5%; Pred. No. 5e-35;
Matches 116; Conservative 27; Mismatches 43; Indels 9; Gaps 5;
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```
QY 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 31 KPGASVKVSKASGYTFTGYIMHWVRQAPGQGLEWGMWNPNSGGTNYAOKFQGRVTMT 90
```

```
QY 61 RNTSISTAYMELSSLRSEDYAVYICARG--CHGGSYFYSGYMDVWGQTTVTVSSGSA 117
Db 91 RDTISISTAYMELNRLSRDPTAVYICARDQPLGYCTNGVCYSF--DYWGQGTILVTVSSAST 148
QY 118 SAPTLFPLVSCNSPDSSTSSVAVGCLAODFLDPSITFSWKYKNSDISSTRGFPSPVL-R 176
Db 149 KPSPVFPPLACRSRSE--STAALGCLVKDYFPFPTVSH--NSGALTSGVHTFPAVLQSS 205
QY 177 SKYAATSQVLLPSKD 191
Db 206 GLYSLSSVTVPPSSN 220

RESULT 12
US-10-041-860-238
; Sequence 238, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-238

Query Match 51.6%; Score 559.5; DB 14; Length 125;
Best Local Similarity 92.2%; Pred. No. 4.9e-34;
Matches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

QY 1 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAQKFQGRVTMN 60
Db 11 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAQKFQGRVTMT 70
QY 61 RNTSISTAYMELSSLRSEDYAVYICARG--HGSYFYSGYMDVWGQTTVTVSS 114
Db 71 RNTSISTAYMELSSLRSEDYAVYICAREGIAVAGTYYY-YYGMDVWGQTTVTVSS 125

RESULT 13
US-10-041-860-19
; Sequence 19, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19

QY 61 RNTSISTAYMELSSLRSEDYAVYICARG--HGSYFYSGYMDVWGQTTVTVSS 114
Db 71 RNTSISTAYMELSSLRSEDYAVYICAREGIAVAGTYYY-YYGMDVWGQTTVTVSS 125

RESULT 14
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

Query Match 51.6%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.2%; Pred. No. 4.9e-34;
Matches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

QY 1 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAQKFQGRVTMN 60
Db 12 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAQKFQGRVTMT 71
QY 61 RNTSISTAYMELSSLRSEDYAVYICARG--HGSYFYSGYMDVWGQTTVTVSS 114
Db 72 RNTSISTAYMELSSLRSEDYAVYICAREGIAVAGTYYY-YYGMDVWGQTTVTVSS 126

RESULT 15
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
```

```
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-19

Query Match 51.6%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.2%; Pred. No. 4.9e-34;
Matches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

QY 1 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAQKFQGRVTMN 60
Db 12 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAQKFQGRVTMT 71
QY 61 RNTSISTAYMELSSLRSEDYAVYICARG--HGSYFYSGYMDVWGQTTVTVSS 114
Db 72 RNTSISTAYMELSSLRSEDYAVYICAREGIAVAGTYYY-YYGMDVWGQTTVTVSS 126

RESULT 14
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

Query Match 51.6%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.2%; Pred. No. 4.9e-34;
Matches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

QY 1 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAQKFQGRVTMN 60
Db 12 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAQKFQGRVTMT 71
QY 61 RNTSISTAYMELSSLRSEDYAVYICARG--HGSYFYSGYMDVWGQTTVTVSS 114
Db 72 RNTSISTAYMELSSLRSEDYAVYICAREGIAVAGTYYY-YYGMDVWGQTTVTVSS 126

RESULT 15
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
```

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; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288

Query Match      51.6%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.2%; Pred. No. 4.9e-34;
Matches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

Qy 1 KKPGRASVKVCKASGYTFTSYDINWVRQATGGLEMMGMNPNPNSGNTGYAOKFQGRVTMN 60
Db 12 KKPGRASVKVCKASGYTFTSYDINWVRQATGGLEMMGMNPNPNSGNTGYAOKFQGRVTMT 71

Qy 61 RNTSISTAYMELSSLRSEDYAVYICARGG--HGGSYFYFYGYGMDVWGQGTITVTVSS 114
Db 72 RNTSISTAYMELSSLRSEDYAVYICAREGIAGVAGTYYY-YYGMDVWGQGTITVTVSS 126

Search completed: March 8, 2005, 07:05:50
Job time : 108.727 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 22.3212 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-27

Perfect score: 1085

Sequence: 1 KPGASVKVCKASGYFTS.....QVLPKDVQMGTDHVVCK 203

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Issued Patents AA.\*
- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pap:\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap:\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap:\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap:\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pap:\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	54.9	470	4	US-09-859-053-28
2	527.5	48.6	279	3	US-08-397-411-13
3	519.5	47.9	462	4	US-09-627-896B-24
4	518.5	47.8	467	2	US-07-916-098A-45
5	512	47.2	468	3	US-09-485-737B-67
6	512	47.2	468	4	US-10-071-485-67
7	512	47.2	711	3	US-09-485-737B-90
8	512	47.2	711	4	US-10-071-485-90
9	502.5	46.3	235	3	US-08-444-644-28
10	502.5	46.3	235	3	US-08-232-246A-28
11	502	46.3	222	1	US-08-458-516-22
12	502	46.3	235	1	US-08-458-516-23
13	502	46.3	449	1	US-08-458-516-13
14	497.5	45.9	235	3	US-08-444-644-42
15	497.5	45.9	235	3	US-08-232-246A-42
16	495	45.6	451	4	US-09-472-087-70
17	495	45.6	472	4	US-09-301-593-43
18	489.5	45.1	235	3	US-08-444-644-19
19	489.5	45.1	235	3	US-08-232-246A-19
20	485.5	44.7	120	3	US-09-025-769B-36
21	485.5	44.7	120	3	US-09-025-769B-59
22	485.5	44.7	120	4	US-09-490-070A-36
23	485.5	44.7	120	4	US-09-490-070A-59
24	485.5	44.7	120	4	US-09-490-153-36
25	485.5	44.7	120	4	US-09-490-153-59
26	485.5	44.7	120	4	US-09-490-324-36
27	485.5	44.7	120	4	US-09-490-324-59

ALIGNMENTS

RESULT 1  
US-09-859-053-28

; Sequence 28, Application US/09859053

; Patent No. 6803039

; GENERAL INFORMATION:

; APPLICANT: Tsuji, Takashi

; APPLICANT: Tezuka, Katsumari

; APPLICANT: Hori, No. 6803039uaki

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF

; FILE REFERENCE: 06501-079001

; CURRENT APPLICATION NUMBER: US/09/859,053

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: JP 2001-99508

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: JP 2000-147116

; PRIOR FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 470

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-859-053-28

Query Match 54.9%; Score 596; DB 4; Length 470;

Best Local Similarity 59.9%; Pred. No. 5.6e-45;

Matches 118; Conservative 26; Mismatches 39; Indels 14; Gaps 6;

Qy 1 KPGASVKVCKASGYFTSYDINWVRQATCGGLEWGMGNPNSTGTYAOKFGQRTVMN 60

Db 31 KPGASVKVCKASGYFTGYIMHWVRQAPGQGLEWGMGNPNSTGTYAOKFGQRTVM 90

Qy 61 RNTSISTAYMELSLRSRSDTAVYTCARGHGSYFY---SYV---GMDVWGQGTITVTVSSG 115

Db 91 RDTISITAYMELSLRSRSDTAVYTCAR-----TYYDSGGYHDAFDINGQGTMTVSSA 145

Qy 116 SASAPTLFPLVSCNPSDTSVAVGCLAQDFLPDSITFSWKYKNNSDISTRGPPSVLR 175

Db 146 STKGPSVFPFLAPCSRSTSE--STAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQ 202

Qy 176 -GGKYAATSOVLLPSKD 191

Db 203 SSGLYSLSSVTVTPSSN 219

RESULT 2

US-08-397-411-13

; Sequence 13, Application US/08397411

```

; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: B-spezifc Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/397,411
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 279 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-411-13

```

```

Query Match      48.6%; Score 527.5; DB 3; Length 279;
Best Local Similarity 53.7%; Pred. No. 3.6e-39;
Matches 108; Conservative 27; Mismatches 55; Indels 11; Gaps 5;

Qy      1  KKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMNPNNGTGYAQKFGQGRVTMN 60
Db      12  KKPGASVKVSKASGYTFTSYTHWVRQAPQGQLEWGMVGNPRSGYTHYNQKLDKATLT 71

Qy      61  RNTSISTAYMELSLRSEDATVYTCARGHGGGSFYSYGMDVMVGQGTVTTVSSGSASAP 120
Db      72  ADKASASTAYMELSLRSEDATVYTCAR-----SAYDYDGFAYMGQGTTLTVSSASTKGP 126

Qy      121  TLFPLVSCNSPDSSTSSVAVCLAQDFLPDSITFSWKYKNSDLSSTRGFPVSLR-GGKY 179
Db      127  SVFPLAPSKSTSG-GTAAAGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLY 183

Qy      180  AATSOVLLPSKDVMTGTDH 200
Db      184  SLSSVTVTPSSSL-GTQTYI 202

```

```

RESULT 3
US-09-627-896B-24
; Sequence 24, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ

```

```

; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 462
; TYPE: PRT
; ORGANISM: 3D1 heavy chain
US-09-627-896B-24

Query Match      47.9%; Score 519.5; DB 4; Length 462;
Best Local Similarity 55.7%; Pred. No. 3.5e-38;
Matches 107; Conservative 25; Mismatches 47; Indels 13; Gaps 5;

Qy      1  KKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMNPNNGTGYAQKFGQGRVTMN 60
Db      31  KKPGSSVKVSKASGYTFTDYAIONVRQAPQGQLEWGVINIIYDNTNNGKFKGKATMT 90

Qy      61  RNTSISTAYMELSLRSEDATVYTCARGHGGGSFYSYGMDVMVGQGTVTTVSSGSASAP 120
Db      91  VDKSTSTAYMELSLRSEDATVYTCAR-----AWY-MDYWGQGTTLTVSSASTKGP 141

Qy      121  TLFPLVSCNSPDSSTSSVAVCLAQDFLPDSITFSWKYKNSDLSSTRGFPVSLR-GGKY 179
Db      142  SVFPLAPCSRSTSR-STAAAGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLY 198

Qy      180  AATSOVLLPSKD 191
Db      199  SLSSVTVTPSSN 210

```

```

RESULT 4
US-07-916-098A-45
; Sequence 45, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843

```



RESULT 6  
US-10-07

US-10-071-483-67  
; Sequence 67, Application US/10071485  
; Patent No. 6830752  
; GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange

```

; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-67

```

RESULT 7  
US-09-485-737B-90  
; Sequence 90, Application US/09485737B

```
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90
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Query Match 47.2%; Score 512; DB 3; Length 711;
Best Local Similarity 48.8%; Pred No. 2.7e-37;
Matches 98; Conservative 36; Mismatches 53; Indels 14; Gaps 5;

Qy 1 KPGASVKVCKASGYTFTSYDINNVRQATQGGLEWGMNPNNGTGYAOKFQGRVTMN 60
Db 32 KPGASVKISCKASGYTFTDYGMMWVKQAPGQGLKMWGINTYTGESTYVDDEKGRFVFS 91
Qy 61 RNTSISTAYMELSLRSRSDTAVYYCARGHGGSFYFYGYGMDVWGQGTITVTVSSGSASAP 120
Db 92 LDTSVSAAYLQISLKAEDTATYFCARRG-----FYAMDYWGQGTITVTVSSASTKGP 143
Qy 121 TLPLVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNNSDISSTRGFPSVLR-GGKY 179
Db 144 SVFPLAPSKSTSG-GTAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQSSGLY 200

Qy 180 AATSOVLLPSKDVMOGTDEHV 200
Db 201 SLSSVTVTPSSSL--GTQTYI 219
```

```
RESULT 8
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

Query Match 47.2%; Score 512; DB 4; Length 711;
Best Local Similarity 48.8%; Pred No. 2.7e-37;
Matches 98; Conservative 36; Mismatches 53; Indels 14; Gaps 5;

Qy 1 KPGASVKVCKASGYTFTSYDINNVRQATQGGLEWGMNPNNGTGYAOKFQGRVTMN 60
Db 32 KPGASVKISCKASGYTFTDYGMMWVKQAPGQGLKMWGINTYTGESTYVDDEKGRFVFS 91
Qy 61 RNTSISTAYMELSLRSRSDTAVYYCARGHGGSFYFYGYGMDVWGQGTITVTVSSGSASAP 120
Db 92 LDTSVSAAYLQISLKAEDTATYFCARRG-----FYAMDYWGQGTITVTVSSASTKGP 143
Qy 121 TLPLVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNNSDISSTRGFPSVLR-GGKY 179
Db 144 SVFPLAPSKSTSG-GTAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQSSGLY 200

Qy 180 AATSOVLLPSKDVMOGTDEHV 200
Db 201 SLSSVTVTPSSSL--GTQTYI 219

RESULT 9
US-08-444-644-28
; Sequence 28, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
```



Matches	105;	Conservative	30;	Mismatches	54;	Indels	12;	Gaps	67;
Qy	1	KKPGASVKVSKC	AGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAQKFGQGRVTMN	60					
Db	12	KKPGSSVKVSKC	AGYAFNTYLIIEWVRQAQCGGLEWIGVIYPGSGGTNYNEKFKGRVTLT	71					
Qy	61	RNTSISTAYMELSL	RSRSEDYAVYTCARGGHGGSFYSYGVMDVWGQGTITVTVSSGSASAP	120					
Db	72	VDESTNTAYMELSL	RSRSEDYAVYFCAR--RDGNTGWFPAY---WGQGLFVTVSSASTKGP	125					
Qy	121	TLFPLVSCENSPD	TSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPFSLVR--GGKY	179					
Db	126	SVFPLASRKS	TSG--GTAALGCLVKDYPPEPVTYSW--NSCALTSGVHTFFPAVLQSSGLY	182					
Qy	180	AATSQVLLPSK	VDNMQGTDEHV	200					
Db	183	SLSSWTVTPSS	SL--GTQYI	201					

```

RESULT 12
US-08-458-516-23
; Sequence 23, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIb/IIIa
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Place, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-23

```

```

Db      72  VDESTNAYMELSLRSEDYAVYFCAR--RDNGYWFAY-----WGQGLVTVTVSSASTKGP 125
Qy      121  TLFLPVCSESPDTSYVAVGCLAQDFLPDSITFSWKYKKNSDISSTRGFPFVLK--GGKY 179
Db      126  SVFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSCALTSGVHTFPAVLQSSGLY 182
Qy      180  AATSOVLLPSKDVMOQGTDEHV 200
Db      183  SLGSWTVPPSSL--GTQTYI 201

RESULT 13
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent NO. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-13

```

Query Match	46.3%	Score 502;	DB 1;	Length 235;
Best Local Similarity	52.2%	Pred. NO. 5.4e-37;		
Matches 105;	Conservative 30;	Mismatches 54;	Indels 12;	Gaps 6
Qy	1	KKPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMGMNPNSGNTCYAOKFGQGRVTMN	60	
Db	12	KKPGSSVKVSKASGYAFNTLIEWVRQAPQGGLEWIGVYFPGSGTNYNEKFGKGRVLT	71	
Qy	61	RTNISITAYMELSLRSDTAVYTCARGHGGSVPYSYIGMDVMQGGTIVTVTVSSGASAP	120	

	Query Match	46.3%	Score 502;	DB 1;	Length 449;
	Best Local Similarity	52.2%;	Pred. No. 1.2e-36;		
	Matches 105;	Conservative 30;	Mismatches 54;	Indels 12;	Gaps 6
Qy	1	KKPGASVKVSKASGYFTSDINWVRQATCGGLEWGMWNPNSGNTGYAOKFGQRTVMN	60		
Db	12	KKPGSSVKVSKASGYAFTNLLIEWVRQAPQGLEWIGVIYPGSGGTNYNEKGRVILT	71		
Qy	61	RNTSISTAYMELSLRSIEDTAVVYTCARGHGGSFPYSYIGMDVWGQGTTVTVSSGSASAP	120		
Db	72	VDESTNTAYMELSLRSIEDTAVVFCAR--RDGNYGWPAY----WGQGLTAVTVSSASTKGP	125		
Qy	121	TLFPLVCGENSPDTSVAVGCLAQDFLPDSITTSWKYKNNSDISSTGRFPFSVLR-GGKY	179		
Db	126	SVFFPLAPSSKTSQ-GTAAALGKLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLY	182		

QY 180 AATSOVLLPSKDVMOGTDEHV 200  
Db 183 SLSSVTVTPSSSL--GTQYI 201

## RESULT 14

US-08-444-644-42  
; Sequence 42, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,644  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/232,246  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: N-terminal  
US-08-444-644-42

Query Match 45.9%; Score 497.5; DB 3; Length 235;  
Best Local Similarity 49.5%; Pred. No. 1.3e-36;  
Matches 95; Conservative 36; Mismatches 50; Indels 11; Gaps 4;  
QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGTGYAQKFGQGRVTMNR 61  
Db 32 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGTGYAQKFGQGRVTMNR 91  
QY 62 NTSISTAYMELSLRSEDPAVYICARGHGGSFYFYGMVWGQGTITVTVSSGSASAPT 121  
Db 92 DKSSNTAYMELSLRSEDPAVYICARGHGGSFYFYGMVWGQGTITVTVSSGSASAPT 144  
QY 122 LPPLVSCNSPDSSTSSVAVGCLAQDPLPDSITFSKYNKNSDISSTRGPPSVLR--GGKYA 180

Db 145 VFPLAPCRRRTSE--STAALGCLVKDYFPEPVTWSW--NSGALTSGVHTFPAVLQSSGLYS 201  
QY 181 ATSQVLLPSKDV 192  
Db 202 LSSVTVTPSSSL 213

## RESULT 15

US-08-232-246A-42  
; Sequence 42, Application US/08232246A  
; Patent No. 6329508  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; TITLE OF INVENTION: CONJUGATES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,246A  
; FILING DATE: 04-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: N-terminal  
US-08-232-246A-42

Query Match 45.9%; Score 497.5; DB 3; Length 235;  
Best Local Similarity 49.5%; Pred. No. 1.3e-36;  
Matches 95; Conservative 36; Mismatches 50; Indels 11; Gaps 4;  
QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGTGYAQKFGQGRVTMNR 61  
Db 32 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGTGYAQKFGQGRVTMNR 91  
QY 62 NTSISTAYMELSLRSEDPAVYICARGHGGSFYFYGMVWGQGTITVTVSSGSASAPT 121  
Db 92 DKSSNTAYMELSLRSEDPAVYICARGHGGSFYFYGMVWGQGTITVTVSSGSASAPT 144  
QY 122 LPPLVSCNSPDSSTSSVAVGCLAQDPLPDSITFSKYNKNSDISSTRGPPSVLR--GGKYA 180  
Db 145 VFPLAPCRRRTSE--STAALGCLVKDYFPEPVTWSW--NSGALTSGVHTFPAVLQSSGLYS 201

Qy 181 ATSOVLLPSXDV 192  
:|:|:  
Db 202 LSSVTVFPSSL 213

Search completed: March 8, 2005, 05:54:05  
Job time : 23.3212 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.5893 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-28

Perfect score: 786

Sequence: 1 HSLAVSLGERATINCKSSQS.....VVCLLNFPYPREAKEHQKSP 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	617	78.5	216	2 JEO241	Ig kappa chain Am3
2	590	75.1	240	2 S06084	Ig kappa chain pre
3	566.5	72.1	215	2 JEO242	Ig kappa chain NIG
4	561	71.4	214	2 S68212	Ig kappa chain (Ma
5	553	70.4	220	2 A31790	Ig kappa chain V r
6	544.5	69.3	215	2 JEO244	Ig kappa chain NIG
7	534.5	68.0	215	2 A23746	Ig kappa chain V-I
8	527	67.0	120	2 S51147	antibody light cha
9	522	66.4	114	1 K4HULN	Ig kappa chain V-I
10	520	66.2	113	2 S34002	Ig kappa chain V r
11	515	65.5	134	2 S49531	anti-sm antibody V
12	513.5	65.3	215	2 JEO243	Ig kappa chain NIG
13	512	65.1	129	2 S40347	Ig kappa chain - h
14	504	64.1	134	1 K4HUI7	Ig kappa chain pre
15	502	63.9	113	2 S30520	Ig kappa chain V r
16	502	63.9	113	2 S34003	Ig kappa chain V r
17	498.5	63.4	133	1 K4HUI1	Ig kappa chain pre
18	496.5	63.2	138	2 A53261	Ig kappa chain pre
19	496	63.1	113	2 S30523	Ig kappa chain V r
20	496	63.1	114	2 S44119	Ig kappa chain V-J
21	493	62.7	114	2 S44116	Ig kappa chain V-J
22	485.5	61.8	219	2 PC4203	Ig kappa chain (no
23	480	61.1	124	2 S40364	Ig kappa chain - h
24	479	60.9	132	2 S46373	Ig kappa chain V-J
25	479	60.9	145	2 PL0014	Ig kappa chain pre
26	476.5	60.6	219	2 S52028	Ig kappa chain - m
27	475.5	60.5	225	2 S37484	Ig kappa chain - m
28	474	60.3	121	1 K4HUI	Ig kappa chain pre
29	473.5	60.2	217	2 S42772	Ig kappa chain - m

30	473	60.2	92	2 S37533	Ig kappa chain V r
31	471	59.9	210	2 A56169	Ig kappa chain V r
32	471	59.9	218	2 JC5810	monoclonal antibod
33	470.5	59.9	219	2 S38865	Ig kappa chain - m
34	470	59.8	101	2 PH0869	Ig kappa chain V r
35	468	59.5	92	2 S37532	Ig kappa chain V r
36	468	59.5	92	2 S37534	Ig kappa chain V r
37	468	59.5	218	2 S68241	Ig kappa chain V r
38	467.5	59.5	118	2 PT0356	Ig kappa chain V r
39	467	59.4	92	2 S37535	Ig kappa chain V r
40	467	59.4	92	2 S37529	Ig kappa chain V r
41	467	59.4	230	2 S33161	Ig kappa chain - s
42	465	59.2	92	2 S37530	Ig kappa chain V r
43	464.5	59.1	219	2 S61112	Ig kappa chain V r
44	462	58.8	129	2 S40329	Ig kappa chain V-J
45	459.5	58.5	106	2 A49138	IgA kappa rheumato

ALIGNMENTS

RESULT 1

JE0241

Ig kappa chain Am37 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JE0241

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mult

A:Reference number: JE0241

A:Accession: JE0241

A:Molecule type: protein

A:Residues: 1-216 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 617; DB 2; Length 216;

Best Local Similarity 86.2%; Pred. NO. 4.2e-45;

Matches 125; Conservative 7; Mismatches 9; Indels 4; Gaps 3;

QY	3	LAVSLGERATINCKSSQSVLYSFNNKNVLANVVOOKGQPPKLLIYVASTRESGVDPREGG	62
DB	11	LAVSLGERATINCKSSQSVLY--NSKNFLAVYQQPGQ-PKLLI-WANVRESGVDPDRFG	66
QY	63	SGSGTDFLTITISSLQAEADVAVVYCOQYVSTPRTFGQTKVEIKRTVAAPSVFIFFPSDSQ	122
DB	67	SGVGTDFLTITISNLQAEVLVAVVYCOQYVSTPVSFGQGRLEIKRTVAAPSVFIFFPSDSQ	126
QY	123	LKSGTASVVCLLNFPYPREAKEHQK	147
DB	127	LKSGTASVVCLLNFPYPREAKVQWK	151

RESULT 2

S06084

Ig kappa chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000

C:Accession: S06084

R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.

A:Reference number: S06084; MUID:90016888; PMID:2508067

A:Accession: S06084

A:Molecule type: mRNA

A:Residues: 1-240 <CRO>

A:Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-240/Product: Ig kappa chain #status predicted <MAT>

F:153-222/Domain: immunoglobulin homology <IMM>





```
Db 64 GSGSGTDFLTISLSQSEDFALYYCQYNTWPLTFGGTKVEIKRTVAAPSVFIFFPSD 123
Qy 121 EQLKSGTASVCLLNFFYPRAKEHQK 147
Db 124 EQLKSGTASVCLLNFFYPRAKQVQWK 150

RESULT 7
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 68.0%; Score 534.5; DB 2; Length 215;
Best Local Similarity 74.7%; Pred. No. 3.9e-38;
Matches 109; Conservative 13; Mismatches 19; Indels 5; Gaps 1;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFG 61
Db 10 TLSLSPGERATVLSGASQSV-----SSNYLAWYQKQPPQAPRLLIYDSSRATGIPDRFS 64
Qy 62 GSGSGTDFLTITSSLQAEADVAVYCCQYYSTPRTFGGTKVEIKRTVAAPSVFIFFPSDE 121
Db 65 GSGSGTDFLTITSLRLEPDEFAVYCCQYSGSPLTFGGTKVEIKRTVAAPSVFIFFPSDE 124
Qy 122 QLKSGTASVCLLNFFYPRAKEHQK 147
Db 125 QLKSGTASVCLLNFFYPRAKQVQWK 150

RESULT 8
S51147
antibody light chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S51147
R:de Kruijf, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL data library, January 1995
A:Description: Selection and application of human SCFV antibody fragments from a semi-synthetic library
A:Reference number: S51147
A:Accession: S51147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <DEK>
A:Cross-references: EMBL:X83714; NID:G633227; PIDN:CAA58689.1; PID:G633228
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 67.0%; Score 527; DB 2; Length 120;
Best Local Similarity 93.6%; Pred. No. 9.3e-38;
Matches 102; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFG 61
Db 10 SLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFS 69
Qy 62 GSGSGTDFLTITSSLQAEADVAVYCCQYYSTPRTFGGTKVEIKRTVA 110
Db 70 GSGSGTDFLTITSSLQAEADVAVYCCQYYSTLTWTFGGTKVEIKRAAS 118
```

```
RESULT 9
K4HULN
Ig kappa chain V-IV region (Ien) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
C:Accession: A01903; F61458
R:Schneider, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975
A:Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette der Subgruppe IV von
A:Reference number: A01903; MUID:76004342; PMID:50995
A:Accession: A01903
A:Molecule type: protein
A:Residues: 1-114 <SCH>
A:Note: This is the first completely sequenced V region of a new kappa chain subgroup, d
A:Note: the C region of this chain has the Inv (3) marker
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-asso
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: F61458
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Comment: This is a Bence Jones protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>
F:23-94/Disulfide bonds: #status predicted

Query Match 66.4%; Score 522; DB 1; Length 114;
Best Local Similarity 93.4%; Pred. No. 2.3e-37;
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HSLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRF 60
Db 9 NSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRF 68
Qy 61 GSGSGTDFLTITSSLQAEADVAVYCCQYYSTPRTFGGTKVEIKR 106
Db 69 GSGSGTDFLTITSSLQAEADVAVYCCQYYSTPVSFGQTKLEIKR 114

RESULT 10
S34002
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34002; S30522
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal I
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34002
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z18328
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 66.2%; Score 520; DB 2; Length 113;
Best Local Similarity 95.2%; Pred. No. 3.4e-37;
Matches 99; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFG 61
Db 10 SLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFS 69
Qy 62 GSGSGTDFLTITSSLQAEADVAVYCCQYYSTPRTFGGTKVEIK 105
```

Db 70 GSGSGTDTLTITISLQAEADVAVYYCHQYGIPTFGQGTKVEIK 113

RESULT 11

S49531

anti-Sm antibody VL chain (V kappa 4/J kappa 3) - human

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 21-Jan-2000

C;Accession: S49531

R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994

A;Description: Molecular characterization of natural human anti-Sm autoantibodies.

A;Reference number: S48797

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-134 <MAH>

A;Cross-references: EMBL:Z46347; NID:g560841; PIDN:CAA86466.1; PID:g560842

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;36-116/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 515; DB 2; Length 134;

Best Local Similarity 94.3%; Pred. No. 1.1e-36;

Matches 99; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61

Db 30 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFS 89

Qy 62 GSGSGTDTLTITISLQAEADVAVYYCQYVSTPRTFGQGTKVEIKR 106

Db 90 GSGSGTDTLTITISLQAEADVAVYYCQYVSTPRTFGQGTKVDIKR 134

RESULT 12

JE0243

Ig kappa chain NIG93 precursor - human

C;Species: Homo sapiens (man)

C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C;Accession: JE0243

R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T

submitted to JIPID, November 1998

A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy

A;Reference number: JE0243

A;Accession: JE0243

A;Molecule type: protein

A;Residues: 1-215 <ALI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 65.3%; Score 513.5; DB 2; Length 215;

Best Local Similarity 71.4%; Pred. No. 2.3e-36;

Matches 105; Conservative 14; Mismatches 21; Indels 7; Gaps 2;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61

Db 10 TLVSVPGERATLSCRAQSVAATN-----VVWYQKLGQAPRLIYDASTGATGVPARFS 63

Qy 62 GSGSGTDTLTITISLQAEADVAVYYCQYVSTPRTFGQGTKVEIK-RTVAAPSVEIFPPSD 120

Db 64 GSGSGTEFTLTITISLQSEDAFYCYCHNNAWPPPTFGQGTKVETKRRRTVAAPSVEIFPPSD 123

Qy 121 EQLKSGTASVVCLNNFYPREAKEHOK 147

Db 124 EQLKSGTASVVCLNNFYPREAKVQWK 150

RESULT 13

S40347

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C;Accession: S40347

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40347

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-129 <KLE>

A;Cross-references: EMBL:X72457; NID:g441382; PIDN:CAA51125.1; PID:g441383

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;33-113/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 512; DB 2; Length 129;

Best Local Similarity 93.2%; Pred. No. 1.8e-36;

Matches 96; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61

Db 27 SLTVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPQLLIYWASTRESGVDPDRFS 86

Qy 62 GSGSGTDTLTITISLQAEADVAVYYCQYVSTPRTFGQGTKVEI 104

Db 87 GSGSGTDTLTITISLQAEADVAVYYCQYVSTPRTFGQGTVEI 129

RESULT 14

K4HUL7

Ig kappa chain precursor V-IV region (B17) - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 21-Jan-2000

C;Accession: A01905

R;Marsh, P.; Mills, F.; Gould, H.

Nucleic Acids Res. 13, 6531-6544, 1985

A;Title: Detection of a unique human VkappaIV germline gene by a cloned cDNA probe.

A;Reference number: A01905; MUID:86041854; PMID:2997713

A;Accession: A01905

A;Molecule type: mRNA

A;Residues: 1-134 <MAR>

A;Note: the sequence was determined from the differentiated gene

A;Note: the authors translated the codon IGC for residue 76 as Trp

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-134/Product: Ig kappa chain V-IV region (B17) #status predicted <MAT>

F;21-43/Region: framework 1

F;36-116/Domain: immunoglobulin homology <IMM>

F;44-60/Region: complementarity-determining 1

F;61-75/Region: framework 2

F;76-82/Region: complementarity-determining 2

F;83-114/Region: framework 3

F;115-121/Region: complementarity-determining 3

F;122-134/Region: framework 4

F;43-114/Disulfide bonds: #status predicted

Query Match 64.1%; Score 504; DB 1; Length 134;

Best Local Similarity 92.4%; Pred. No. 9.1e-36;

Matches 97; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61

Db 30 SLAVSLGERATINCKSSQSVLYSDNKNYLAWYQKPGQPPKLLIYCASTRESGVDPDRFS 89

Qy 62 GSGSGTDTLTITISLQAEADVAVYYCQYVSTPRTFGQGTKVEIKR 106

Db 90 GSGSGTDTLTITISLQAEADVAVYYCQYVSTPRTFGQGTKVEIKR 134

RESULT 15

S30520

Ig kappa chain V region - human

C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S30520  
F:Marlette, X.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S30520  
A:Accession: S30520  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-113 <MAR>  
A:Cross-references: EMBL:Z18325  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 63.9%; Score 502; DB 2; Length 113;  
Best Local Similarity 91.3%; Pred. No. 1.1e-35;  
Matches 95; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61  
Db 10 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFS 69

Qy 62 GSGSGTDFTLTISLQAEADVAVYCCQYVSTPTFGQGTKEIK 105  
Db 70 GSGSGTDFTLTISLQAEADVAVYCCQYVSTPTFGQGTKEIK 113

Search completed: March 8, 2005, 06:39:24  
Job time : 11.6393 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 55.644 Seconds  
(without alignment)  
1371.214 Million cell updates/sec

Title: US-09-784-950-28

Perfect score: 786

Sequence: 1 HSLAVSLGERATINCKSSQS.....VCLLNFPYREAKEHQKSP 149

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	558	71.0	236	2	Q6PIT5	Q6pit5 homo sapien
2	558	71.0	240	2	Q6PIH6	Q6pih6 homo sapien
3	557.5	70.9	239	2	Q8NEK0	Q8nek0 homo sapien
4	556.5	70.8	235	2	Q6GMV9	Q6gmw9 homo sapien
5	554	70.5	234	2	Q72473	Q72473 homo sapien
6	550	70.0	236	2	Q6PIL8	Q6pil8 homo sapien
7	545	69.3	236	2	Q6GMW1	Q6gmw1 homo sapien
8	545	69.3	236	2	Q6PIH7	Q6pih7 homo sapien
9	543.5	69.1	239	2	Q6P491	Q6p491 homo sapien
10	543	69.1	235	2	Q6GMX8	Q6gmx8 homo sapien
11	542.5	69.0	235	2	Q6PJF2	Q6pjf2 homo sapien
12	541	68.8	236	2	Q723Y4	Q723y4 homo sapien
13	536	68.2	236	2	Q6P5S8	Q6p5s8 homo sapien
14	534.5	68.0	235	2	Q6GMW0	Q6gmw0 homo sapien
15	534.5	68.0	239	2	Q8TCD0	Q8tcd0 homo sapien
16	533	67.8	236	2	Q6GMX0	Q6gmx0 homo sapien
17	527	67.0	236	2	Q6GMX9	Q6gmx9 homo sapien
18	521	66.3	114	1	KV4A_HUMAN	P01625 homo sapien
19	520	66.2	236	2	Q6PIH4	Q6pih4 homo sapien
20	517	65.8	134	1	KV4C_HUMAN	P06314 homo sapien
21	498.5	63.4	133	1	KV4B_HUMAN	P06313 homo sapien
22	478	60.8	238	2	Q6GJS7	Q6gjs7 mus musculus
23	474	60.3	121	1	KV4O_HUMAN	P06312 homo sapien
24	474	60.3	241	2	Q632X4	Q632x4 mus musculus
25	470.5	59.9	219	2	Q652C0	Q652c0 mus musculus
26	457	58.1	109	1	KV4D_HUMAN	P83593 homo sapien
27	452	57.5	236	2	Q7TS98	Q7te98 mus musculus
28	448.5	57.1	243	2	Q6NTU5	Q6ntu5 xenopus lae
29	446	56.7	237	2	Q7SZ36	Q7sz36 xenopus lae
30	415	52.8	255	2	Q6KB05	Q6kb05 mus musculus
31	391.5	49.8	129	1	KV3L_HUMAN	P18135 homo sapien

32	383.5	48.8	109	1	KV3B_HUMAN	P01620 homo sapien
33	382.5	48.7	109	1	KV3D_HUMAN	P01622 homo sapien
34	380.5	48.4	109	2	Q9UL78	Q9ul78 homo sapien
35	378.5	48.2	109	1	KV3E_HUMAN	P01623 homo sapien
36	378	48.1	108	2	Q9UL70	Q9ul70 homo sapien
37	376	47.8	108	1	KV1M_HUMAN	P01605 homo sapien
38	374	47.6	108	2	Q9UL79	Q9ul79 homo sapien
39	371.5	47.3	109	1	KV3G_HUMAN	P04206 homo sapien
40	371.5	47.3	129	1	KV3H_HUMAN	P04207 homo sapien
41	371.5	47.3	129	1	KV3M_HUMAN	P18136 homo sapien
42	370.5	47.1	109	1	KV3F_HUMAN	P01624 homo sapien
43	368	46.8	99	2	Q9JL74	Q9jl74 mus musculus
44	366	46.6	149	1	KV5A_MOUSE	P01633 mus musculus
45	363.5	46.2	117	1	KV2E_HUMAN	P06309 homo sapien

#### ALIGNMENTS

#### RESULT 1

ID	Q6PITS	PRELIMINARY;	PRT;	236 AA.
AC	Q6PIT5;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=23188257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Stapleton L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schestz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smalusi D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RP	TISSUE=Lung;			
RA	Strausberg R.;			
DR	EMBL; BC029444; AAH29444.1; -			
DR	HSSP; P01607; 1AR2.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig cl.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF07654; C1-set; 1.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 1.			
DR	SMART; SM00406; IGv; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			



DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;  
 Query Match 70.9%; Score 557.5; DB 2; Length 239;  
 Best Local Similarity 75.3%; Pred. No. 7.2e-48;  
 Matches 110; Conservative 12; Mismatches 23; Indels 1; Gaps 1;  
 QY 2 SLAVSLGERATINCKSSQSVLYSFNNKYNLAWYQKQPGPKLLIYWASTRESSGVDPDRFG 61  
 DB 30 SLPTVTPGEPASISCHSSQSLHLS-DGYNLYDWLQKPGSQQLLIYLGNSRASGVDPDRFS 88  
 QY 62 GSGSGTDTFTLTISSLOAEDVAVYYCOQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDE 121  
 DB 89 GSGSGTDTFTLTKISKAEADVGIYCMQGLQTPQTGQGTKEIKRTVAAPSVFIPPPSDE 148  
 QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147  
 DB 149 QKSGTASVVCLLNNFYPREAKVQWK 174

## RESULT 4

Q6GMV9 PRELIMINARY; PRT; 235 AA.  
 ID Q6GMV9  
 AC Q6GMV9  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073793; AAH73793.1; -.  
 DR InterPro; IPR003599; Ig-like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;  
 Query Match 70.8%; Score 556.5; DB 2; Length 235;  
 Best Local Similarity 73.3%; Pred. No. 8.9e-48;  
 Matches 107; Conservative 17; Mismatches 17; Indels 5; Gaps 1;  
 QY 2 SLAVSLGERATINCKSSQSVLYSFNNKYNLAWYQKQPGPKLLIYWASTRESSGVDPDRFG 61  
 DB 30 TLSLSPGFRALUSCRASQSV-----NSKYLAWYQKQPGAPRLMLYASIRATGIPDRFS 84  
 QY 62 GSGSGTDTFTLTISSLOAEDVAVYYCOQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDE 121  
 DB 85 GSGSGTDTFTLTISSLESEDFALYFCQYGTGTPLTGFGGTKEIKRTVAAPSVFIPPPSDE 144  
 QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147  
 DB 145 QKSGTASVVCLLNNFYPREAKVQWK 170

## RESULT 5

Q7Z473 PRELIMINARY; PRT; 234 AA.  
 ID Q7Z473  
 AC Q7Z473  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC056256; AAH56256.1; -.  
 DR HSSP; F01834; IHEZ.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00406; IGV; 1.















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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 69.0805 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-28

Perfect score: 786

Sequence: 1 HSLAVSLGERATINCKSSQS.....VCLLNFFPREAKHOKSP 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	786	100.0	149	2 AAY34311	Aay34311 IgM antib
2	735	93.5	147	2 AAY34314	Aay34314 IgM antib
3	729	92.7	211	5 ABP43134	Abp43134 Human ova
4	715	91.0	179	8 ADK52434	Adk52434 Human ant
5	709	90.2	240	4 AAU00815	Aau00815 Human Imm
6	708	90.1	163	8 ADK52394	Adk52394 Human ant
7	707	89.9	220	8 ADK52314	Adk52314 Human ant
8	706	89.8	159	8 ADK52406	Adk52406 Human ant
9	703	89.4	173	8 ADK52430	Adk52430 Human ant
10	703	89.4	220	8 ADK52386	Adk52386 Human ant
11	702	89.3	171	8 ADK52422	Adk52422 Human ant
12	702	89.3	220	8 ADK52334	Adk52334 Human ant
13	701	89.2	159	8 ADK52382	Adk52382 Human ant
14	701	89.2	163	8 ADK52310	Adk52310 Human ant
15	699	88.9	154	8 ADK52342	Adk52342 Human ant
16	698	88.8	220	8 ADK52362	Adk52362 Human ant
17	696	88.5	163	8 ADK52346	Adk52346 Human ant
18	696	88.5	163	8 ADK52306	Adk52306 Human ant
19	696	88.5	163	8 ADK52326	Adk52326 Human ant
20	696	88.5	173	8 ADK52438	Adk52438 Human ant
21	695	88.4	149	8 ADK52402	Adk52402 Human ant
22	694	88.3	159	8 ADK52302	Adk52302 Human ant
23	694	88.3	264	5 ABP43142	Abp43142 Human ova
24	693	88.2	158	8 ADK52378	Adk52378 Human ant
25	693	88.2	240	2 AAY50161	Aay50161 Human res

ALIGNMENTS

RESULT 1

AAY34311

ID AAY34311 standard; protein; 149 AA.

AC AAY34311;

XX 19-NOV-1999 (first entry)

DE DE IgM antibody CEM 10.12 F3 kappa chain sequence.

KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX N-PSDB; AAZ20412.

XX New monoclonal antibody, used for treating e.g. graft versus host

XX disease, cancers, autoimmune diseases and inflammatory diseases.

XX Claim 61; Fig 26; 245pp; English.

XX This sequence represents the kappa chain of an antibody of the invention.

XX The antibody is a monoclonal antibody (Mab) with an isotype that fixes

XX complement and a variable region that binds to the epitope on CD147 MAb

XX by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab

XX can selectively kill activated T-cells, activated B-cells or treating or

XX activated monocytes. The products and methods can be used for treating

XX diseases involving activated T-cells or B-cells or monocytes, e.g. graft

XX versus host disease (GVHD), organ transplant rejection diseases (e.g.

XX renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
SQ Sequence 149 AA;  
Query Match 100.0%; Score 786; DB 2; Length 149;  
Best Local Similarity 100.0%; Pred. No. 5.2e-56;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HSLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGQPPKLLIYWASTRESGVDPDRF 60  
DB 1 HSLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGQPPKLLIYWASTRESGVDPDRF 60  
QY 61 GSGSGGDTFTLTISLQAEADVAVYCCQYYSYTRTFGQTKVEIKRTVAAPSVFIFFPSD 120  
DB 61 GSGSGGDTFTLTISLQAEADVAVYCCQYYSYTRTFGQTKVEIKRTVAAPSVFIFFPSD 120  
QY 121 EQLKSGTASVVCLLNNFYPREAKEHQSP 149  
DB 121 EQLKSGTASVVCLLNNFYPREAKEHQSP 149  
RESULT 2  
AAY34314  
ID AAY34314 standard; protein; 147 AA.  
AC AAY34314;  
XX AAY34314;  
DT 19-NOV-1999 (first entry)  
DE IgM antibody CEM 13.5 kappa chain sequence.  
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
OS Homo sapiens.  
XX WO9945031-A2.  
XX 10-SEP-1999.  
XX 03-MAR-1999; 99WO-US004583.  
XX 03-MAR-1998; 98US-00034607.  
XX 03-FEB-1999; 99US-00244253.  
XX (ABGE-) ARGENIX INC.  
XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
XX Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX WPI; 1999-540816/45.  
XX N-PSDB; AA220415.  
XX New monoclonal antibody, used for treating e.g. graft versus host  
XX disease, cancers, autoimmune diseases and inflammatory diseases.  
XX Claim 61; Fig 29; 245pp; English.  
XX This sequence represents the kappa chain of an antibody of the invention.  
XX The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
XX complement and a variable region that binds to the epitope on CD147 bound  
XX by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
XX can selectively kill activated T-cells, activated B-cells or resting or  
XX activated monocytes. The products and methods can be used for treating  
XX diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
XX versus host disease (GVHD), organ transplant rejection diseases (e.g.  
XX renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
XX (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
XX (e.g. lupus), and inflammatory diseases (e.g. arthritis)

SQ Sequence 147 AA;  
Query Match 93.5%; Score 735; DB 2; Length 147;  
Best Local Similarity 97.2%; Pred. No. 6.9e-52;  
Matches 141; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGQPPKLLIYWASTRESGVDPDRFG 62  
DB 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGQPPKLLIYWASTRESGVDPDRFG 60  
QY 63 SSGSTDTFTLTISLQAEADVAVYCCQYYSYTRTFGQTKVEIKRTVAAPSVFIFFPSDEQ 122  
DB 61 SSGSTDTFTLTISLQAEADVAVYCCQYYSYTRTFGQTKVEIKRTVAAPSVFIFFPSDEQ 120  
QY 123 LKSGTASVVCLLNNFYPREAKEHQK 147  
DB 121 LKSGTASVVCLLNNFYPREAKEVQWK 145  
RESULT 3  
ABP43134  
ID ABP43134 standard; protein; 211 AA.  
AC ABP43134;  
XX 22-AUG-2002 (first entry)  
XX Human ovarian antigen HVVBK13, SEQ ID NO:4266.  
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;  
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
XX inflammatory condition; immune disorder; blood disorder;  
XX cardiovascular disorder; respiratory disorder; neurological disorder;  
XX gastrointestinal disorder; urinary system disorder; drug screening;  
XX gene therapy; chromosome mapping; forensic analysis;  
XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
XX antiinflammatory; gynaecological; reproductive.  
XX Homo sapiens.  
XX WO200200677-A1.  
XX 03-JAN-2002.  
XX 07-JUN-2001; 2001WO-US018569.  
XX 07-JUN-2000; 2000US-0209467P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Birse CE, Rosen CA;  
XX WPI; 2002-147878/19.  
XX N-PSDB; ABQ56211.  
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
XX cancer), immune disorders, cardiovascular disorders and neurological  
XX diseases.  
XX Claim 11; SEQ ID NO 4266; 2922pp; English.  
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
XX encompasses polypeptides 90% identical and polynucleotides 95% identical  
XX to the sequences of the invention. The invention additionally relates to  
XX recombinant vectors and host cells comprising human ovarian antigen  
XX polynucleotides, antibodies against human ovarian antigens, and the use  
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,  
XX treating, prognosing or preventing various ovary and/or breast-related  
XX disorders. Such conditions include ovarian cancer and breast cancer, and



CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 211 AA;

Query Match 92.7%; Score 729; DB 5; Length 211;  
 Best Local Similarity 95.2%; Pred. No. 3e-51; 4; Indels 0; Gaps 0;  
 Matches 139; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTREGVDPDRFG 61  
 DB 34 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTREGVDPDRFG 93

QY 62 GSGSGTDFLTITSSLAQEDVAVYQCYQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121  
 DB 94 GSGSGTDFLTITSSLAQEDVAVYQCYQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 153

QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147  
 DB 154 QKSGTASVVCLLNNFYPREAKEHOK 179

RESULT 4  
 ADK52434  
 ID ADK52434 standard; protein; 179 AA.  
 AC ADK52434;  
 DT 20-MAY-2004 (first entry)  
 DE Human anti-MCP-1 variable region light chain #35.  
 KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
 KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;  
 KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;  
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
 KW anti-MCP-1; heavy chain; light chain.  
 XX  
 OS Homo sapiens.  
 PN WO2004016769-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 19-AUG-2003; 2003WO-US026232.  
 XX  
 PR 19-AUG-2002; 2002US-0404802P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
 PI Bhakta S;  
 XX  
 DR WPI; 2004-203794/19.  
 DR N-PSDB; ADK52433.

XX New human monoclonal antibody that binds to monocyte chemo-attractant  
 PT protein-1 and is immobilized on an insoluble matrix, useful for  
 PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
 PT rheumatoid arthritis or psoriasis.  
 PS Claim 2; SEQ ID NO 140; 154pp; English.  
 XX  
 CC The present invention relates to a human monoclonal antibody that binds  
 CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
 CC for the preparation of a medicament useful for treating neoplastic or  
 CC inflammatory conditions. The neoplastic disease is selected from breast  
 CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer or prostate cancer. The inflammatory condition is  
 CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
 CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
 CC antibodies are also useful for diagnosing the above diseases. It is also  
 CC useful for the determining the level of MCP-1 and MCP-1 family members in  
 CC patient samples. The present sequence represents a human anti-MCP-1  
 CC variable region light chain sequence.  
 XX  
 SQ Sequence 179 AA;

Query Match 91.0%; Score 715; DB 8; Length 179;  
 Best Local Similarity 93.8%; Pred. No. 3.5e-50;  
 Matches 137; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTREGVDPDRFG 61  
 DB 26 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTREGVDPDRFG 85

QY 62 GSGSGTDFLTITSSLAQEDVAVYQCYQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121  
 DB 86 GSGSGTDFLTITSSLAQEDVAVYQCYQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 145

QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147  
 DB 146 QKSGTASVVCLLNNFYPREAKEHOK 171

RESULT 5  
 AAU00815  
 ID AAU00815 standard; protein; 240 AA.  
 AC AAU00815;  
 DT 01-JUN-2001 (first entry)  
 DE Human Immunoglobulin superfamily, IgsF, protein #1.  
 KW Human; Immunoglobulin superfamily protein; IgsF; Immune response;  
 KW inflammatory response; cell-cell interaction; cell-surface recognition;  
 KW neural disorder; immune system disorder; muscular disorder;  
 KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;  
 KW cardiovascular disorder; renal disorder; proliferative disorder; cancer;  
 KW common variable adhesion deficiency syndrome; AIDS; SCID;  
 KW acquired immunodeficiency syndrome; anaemia; rheumatoid arthritis;  
 KW Alzheimer's disease; Crohn's disease; liver cancer; leukaemia;  
 KW Hodgkin's lymphoma; Parkinson's disease; Huntington's disease;  
 KW arteriosclerosis; stroke; diabetes mellitus; Addison's disease;  
 KW urticaria; severe combined immunodeficiency; antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 52..58 /label= Immunogenic\_epitope  
 FT Region 63..70 /label= Immunogenic\_epitope  
 FT Region 79..90 /label= Immunogenic\_epitope  
 FT Region 118..126 /label= Immunogenic\_epitope

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FT Region /label= Immunogenic_epitope
FT 146..154
FT /label= Immunogenic_epitope
FT Domain 160..240
FT /label= Immunoglobulin_like_domain
FT Region 183..199
FT /label= Immunogenic_epitope
FT Region 209..215
FT /label= Immunogenic_epitope
FT Region 233..240
FT /label= Immunogenic_epitope
XX
XX WO200118176-A1.
XX
XX 15-MAR-2001.
XX
XX 29-AUG-2000; 2000WO-US023662.
XX
XX 03-SEP-1999; 99US-0152248P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (NIJ/) NI J.
XX
XX Young PE, Ruben SM, Shi Y;
XX
XX WPI; 2001-203084/20.
XX N-PSDB; AAS00145.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is used
XX in preventing, treating or ameliorating a medical condition.
XX
XX Claim 11; Page 237; 247pp; English.
XX
XX The sequence is a Human Immunoglobulin superfamily, IgSF, protein, a
XX diverse family of proteins involved in cell-cell interactions, cell-
XX surface recognition, intercellular communication and immune and
XX inflammatory responses. Polypeptides and antibodies directed to
XX polypeptides of the present invention are useful to provide immunological
XX probes for differential identification of tissues. Antibodies can be used
XX to assay levels of polypeptides encoded by polynucleotides of the
XX invention. Polypeptides of the present invention can be used to treat or
XX prevent diseases or conditions such as neural disorders, immune system
XX disorders, muscular disorders, reproductive disorders, gastrointestinal
XX disorders, pulmonary disorders, cardiovascular disorders, renal
XX disorders, proliferative disorders, and/or cancerous diseases and
XX conditions. Polynucleotides of the invention are also useful in treating
XX the above disorders. Examples of the disorders include common variable
XX adhesion deficiency syndrome, acquired immunodeficiency syndrome (AIDS),
XX anaemia, rheumatoid arthritis, Alzheimer's disease, Crohn's disease,
XX liver cancer, leukaemia, Hodgkin's lymphoma, Parkinson's disease,
XX Huntington's disease, dementia, arterosclerosis, stroke, diabetes
XX mellitus, Addison's disease, urticaria, severe combined immunodeficiency
XX (SCID). Many more examples of diseases and disorders are given in the
XX specification
XX
XX SQ Sequence 240 AA;
XX
XX Query Match 90.2%; Score 709; DB 4; Length 240;
XX Best Local Similarity 93.2%; Pred. No. 1.4e-49;
XX Matches 136; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61
XX Db 30 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFS 89
XX
XX QY 62 GSGSGTDFTLTSSLAQEDVAVYCCQYYSYTPRTFGQTKVEIKRTVAAPSVFIPPPSDE 121
XX Db 90 GSGSGTDFTLTSSLAQEDVAVYCCQYYSYTPSPGQTKLEIKRTVAAPSVFIPPPSDE 149
XX
XX QY 122 QKSGTASVWCLLNFFYPREAKEHOK 147
XX Db 150 QKSGTASVWCLLNFFYPREAKVQWK 175
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RESULT 6
ADK52394
ID ADK52394 standard; protein; 163 AA.
XX
XX AC ADK52394;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human anti-MCP-1 variable region light chain #25.
XX
XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
XX Antirheumatic; Nephrotropic; Antiartherosclerotic; Antiporiatic;
XX Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
XX inflammatory condition; cancer; arthritis; multiple sclerosis;
XX anti-MCP-1; heavy chain; light chain.
XX
XX OS Homo sapiens.
XX
XX PN WO2004016769-A2.
XX
XX PD 26-FEB-2004.
XX
XX PF 19-AUG-2003; 2003WO-US026232.
XX
XX PR 19-AUG-2002; 2002US-0404802P.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
XX Bhakta S;
XX
XX DR WPI; 2004-203794/19.
XX N-PSDB; ADK52393.
XX
XX New human monoclonal antibody that binds to monocyte chemo-attractant
XX protein-1 and is immobilized on an insoluble matrix, useful for
XX diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
XX rheumatoid arthritis or psoriasis.
XX
XX Claim 2; SEQ ID NO 100; 154pp; English.
XX
XX The present invention relates to a human monoclonal antibody that binds
XX to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
XX for the preparation of a medicament useful for treating neoplastic or
XX inflammatory conditions. The neoplastic disease is selected from breast
XX cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
XX stomach cancer, endometrial cancer, kidney cancer, colon cancer,
XX pancreatic cancer or prostate cancer. The inflammatory condition is
XX selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
XX psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
XX antibodies are also useful for diagnosing the above diseases. It is also
XX useful for the determining the level of MCP-1 and MCP-1 family members in
XX patient samples. The present sequence represents a human anti-MCP-1
XX variable region light chain sequence.
XX
XX SQ Sequence 163 AA;
XX
XX Query Match 90.1%; Score 708; DB 8; Length 163;
XX Best Local Similarity 93.2%; Pred. No. 1.2e-49;
XX Matches 136; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61
XX Db 10 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFS 69
XX
XX QY 62 GSGSGTDFTLTSSLAQEDVAVYCCQYYSYTPRTFGQTKVEIKRTVAAPSVFIPPPSDE 121
XX Db 70 GSGSGTDFTLTSSLAQEDVAVYCCQYYSYTPWTFGQTKVEIKRTVAAPSVFIPPPSDE 129
XX
XX QY 122 QKSGTASVWCLLNFFYPREAKEHOK 147
XX Db 130 QKSGTASVWCLLNFFYPREAKVQWK 155
```

RESULT 7  
ADK52314  
ID ADK52314 standard; protein; 220 AA.  
XX AC ADK52314;  
XX AC ADK52314;  
DT 20-MAY-2004 (first entry)  
XX DE Human anti-MCP-1 variable region light chain #5.  
XX DE monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;  
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.  
XX OS Homo sapiens.  
XX PN WO2004016769-A2.  
XX PD 26-FEB-2004.  
XX PF 19-AUG-2003; 2003WO-US026232.  
XX PR 19-AUG-2002; 2002US-0404802P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;  
XX DR WPI; 2004-203794/19.  
XX DR N-PSDB; ADK52313.  
XX PT New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.  
XX PS Claim 2; SEQ ID NO 20; 154pp; English.  
XX CC The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.  
XX SQ Sequence 220 AA;  
Query Match 89.9%; Score 707; DB 8; Length 220;  
Best Local Similarity 93.8%; Pred. No. 1.9e-49;  
Matches 137; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFG 61  
DB 10 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFS 69  
QY 62 GSGSGTDFLTITSSLAQEDVAVYQCYYSTPRFTFGQGTKEIKRTVAAPSFIIPPSPDE 121  
DB 70 GSGSGTDFLTITSSLAQEDVAVYQCYYSTPRFTFGQGTKEIKRTVAAPSFIIPPSPDE 129  
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147

Db 130 QLKSGTASVVCLLNNFYPREAKEHOK 155  
RESULT 8  
ADK52406  
ID ADK52406 standard; protein; 159 AA.  
XX AC ADK52406;  
XX AC ADK52406;  
DT 20-MAY-2004 (first entry)  
XX DE Human anti-MCP-1 variable region light chain #28.  
XX DE monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;  
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.  
XX OS Homo sapiens.  
XX PN WO2004016769-A2.  
XX PD 26-FEB-2004.  
XX PF 19-AUG-2003; 2003WO-US026232.  
XX PR 19-AUG-2002; 2002US-0404802P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;  
XX DR WPI; 2004-203794/19.  
XX DR N-PSDB; ADK52405.  
XX PT New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.  
XX PS Claim 2; SEQ ID NO 112; 154pp; English.  
XX CC The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.  
XX SQ Sequence 159 AA;  
Query Match 89.8%; Score 706; DB 8; Length 159;  
Best Local Similarity 93.8%; Pred. No. 1.7e-49;  
Matches 137; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFG 61  
DB 10 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFS 69  
QY 62 GSGSGTDFLTITSSLAQEDVAVYQCYYSTPRFTFGQGTKEIKRTVAAPSFIIPPSPDE 121  
DB 70 GSGSGTDFLTITSSLAQEDVAVYQCYYSTPRFTFGQGTKEIKRTVAAPSFIIPPSPDE 129  
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147

Db 130 QLKSGTASVCLNNFYPREAKVQWK 155  
|||||

RESULT 9  
ADK52430  
ID ADK52430 standard; protein; 173 AA.  
XX AC ADK52430;  
XX DT 20-MAY-2004 (first entry)  
XX DE Human anti-MCP-1 variable region light chain #34.  
XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antiporiatic;  
KW Vasotropic; Immunosuppressive; Neuroprotective; Neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.  
XX OS Homo sapiens.  
XX FN WO2004016769-A2.  
XX PD 26-FEB-2004.  
XX PF 19-AUG-2003; 2003WO-US026232.  
XX PR 19-AUG-2002; 2002US-0404802P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;  
XX DR WPI; 2004-203794/19.  
XX DR N-PSDB; ADK52429.  
XX PT New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.  
XX PS Claim 2; SEQ ID NO 136; 154pp; English.  
XX CC The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.  
XX SQ Sequence 173 AA;

Query Match 89.4%; Score 703; DB 8; Length 173;  
Best Local Similarity 92.5%; Pred. No. 3.2e-49;  
Matches 135; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 61  
Db 25 SLAVSLGERAAINCKSSQTVLYSSNNKNLYVMYQKPGQPKLLIYWASTRESGVDPDRFS 84  
QY 62 GSGSGTDTLTLSLQAEADVAVYCOQYYSPTFTGQTKVEIKETVAAPSFIIPPSDE 121  
Db 85 GSGSGTDTLTLSLQAEADVAVYCOQYYSPTFTGQTKVEIKETVAAPSFIIPPSDE 144

QY 122 QLKSGTASVCLNNFYPREAKEHQK 147  
Db 145 QLKSGTASVCLNNFYPREAKVQWK 170  
|||||

RESULT 10  
ADK52386  
ID ADK52386 standard; protein; 220 AA.  
XX AC ADK52386;  
XX DT 20-MAY-2004 (first entry)  
XX DE Human anti-MCP-1 variable region light chain #23.  
XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antiporiatic;  
KW Vasotropic; Immunosuppressive; Neuroprotective; Neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.  
XX OS Homo sapiens.  
XX FN WO2004016769-A2.  
XX PD 26-FEB-2004.  
XX PF 19-AUG-2003; 2003WO-US026232.  
XX PR 19-AUG-2002; 2002US-0404802P.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;  
XX DR WPI; 2004-203794/19.  
XX DR N-PSDB; ADK52385.  
XX PT New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.  
XX PS Claim 2; SEQ ID NO 92; 154pp; English.  
XX CC The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.  
XX SQ Sequence 220 AA;

Query Match 89.4%; Score 703; DB 8; Length 220;  
Best Local Similarity 92.5%; Pred. No. 4e-49;  
Matches 135; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 61  
Db 10 SLAVSLGERATINCKSSQSVLYSSNNKNLYVMYQKPGQPKLLIYWASTRESGVDPDRFS 69  
QY 62 GSGSGTDTLTLSLQAEADVAVYCOQYYSPTFTGQTKVEIKETVAAPSFIIPPSDE 121  
Db 70 GSGSGTDTLTLSLQAEADVAVYCOQYYSPTFTGQTKVEIKETVAAPSFIIPPSDE 129

QY 122 QLKSGTASVCLNNFYPREAKEHOK 147  
 DB 130 QLKSGTASVCLNNFYPREAKVQWK 155

RESULT 11  
 ADKS2422  
 ID ADKS2422 standard; protein; 171 AA.  
 AC ADKS2422;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human anti-MCP-1 variable region light chain #32.  
 XX  
 KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
 KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antiporiatic;  
 KW Vasotrophic; Immunosuppressive; Neuroprotective; Neoplastic;  
 KW Inflammatory condition; cancer; arthritis; multiple sclerosis;  
 KW anti-MCP-1; heavy chain; light chain.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004016769-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 19-AUG-2003; 2003WO-US026232.  
 XX  
 PR 19-AUG-2002; 2002US-0404802P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
 PI Bhakta S;  
 XX  
 DR WPI; 2004-203794/19.  
 DR N-PSDB; ADKS2421.  
 XX  
 PT New human monoclonal antibody that binds to monocyte chemo-attractant  
 PT protein-1 and is immobilized on an insoluble matrix, useful for  
 PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
 PT rheumatoid arthritis or psoriasis.  
 XX  
 PS Claim 2; SEQ ID NO 128; 154pp; English.  
 XX  
 CC The present invention relates to a human monoclonal antibody that binds  
 CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
 CC for the preparation of a medicament useful for treating neoplastic or  
 CC inflammatory conditions. The neoplastic disease is selected from breast  
 CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer or prostate cancer. The inflammatory condition is  
 CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
 CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
 CC antibodies are also useful for diagnosing the above diseases. It is also  
 CC useful for the determining the level of MCP-1 and MCP-1 family members in  
 CC patient samples. The present sequence represents a human anti-MCP-1  
 CC variable region light chain sequence.  
 XX  
 SQ Sequence 171 AA;

Query Match 89.3%; Score 702; DB 8; Length 171;  
 Best Local Similarity 91.8%; Pred. No. 3.8e-49;  
 Matches 134; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQVLYSFNNKNLAWYQKQPPKLLIYWASTRESGVDPFRG 61  
 DB 24 SLAVSLGERATINCKSSQVLYSFNNKNLAWYQKQPPKLLIYWASTRESGVDPFRS 83  
 QY 62 GSGSGTDFLTITSSLOAEDVAVYCCQYYSPTFTGQTKVEIKRTVAAPSVFIFFPSDE 121

QY 84 GSGSGTDFLTITSSLOAEDVAVYCCQYYSPTFTGQTKVEIKRTVAAPSVFIFFPSDE 143

QY 122 QLKSGTASVCLNNFYPREAKEHOK 147  
 DB 144 QLKSGTASVCLNNFYPREAKVQWK 169

RESULT 12  
 ADKS2334  
 ID ADKS2334 standard; protein; 220 AA.  
 AC ADKS2334;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human anti-MCP-1 variable region light chain #10.  
 XX  
 KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
 KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antiporiatic;  
 KW Vasotrophic; Immunosuppressive; Neuroprotective; Neoplastic;  
 KW Inflammatory condition; cancer; arthritis; multiple sclerosis;  
 KW anti-MCP-1; heavy chain; light chain.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004016769-A2.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 19-AUG-2003; 2003WO-US026232.  
 XX  
 PR 19-AUG-2002; 2002US-0404802P.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
 PI Bhakta S;  
 XX  
 DR WPI; 2004-203794/19.  
 DR N-PSDB; ADKS2333.  
 XX  
 PT New human monoclonal antibody that binds to monocyte chemo-attractant  
 PT protein-1 and is immobilized on an insoluble matrix, useful for  
 PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
 PT rheumatoid arthritis or psoriasis.  
 XX  
 PS Claim 2; SEQ ID NO 40; 154pp; English.  
 XX  
 CC The present invention relates to a human monoclonal antibody that binds  
 CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
 CC for the preparation of a medicament useful for treating neoplastic or  
 CC inflammatory conditions. The neoplastic disease is selected from breast  
 CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer or prostate cancer. The inflammatory condition is  
 CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
 CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
 CC antibodies are also useful for diagnosing the above diseases. It is also  
 CC useful for the determining the level of MCP-1 and MCP-1 family members in  
 CC patient samples. The present sequence represents a human anti-MCP-1  
 CC variable region light chain sequence.  
 XX  
 SQ Sequence 220 AA;

Query Match 89.3%; Score 702; DB 8; Length 220;  
 Best Local Similarity 92.5%; Pred. No. 4.8e-49;  
 Matches 135; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQVLYSFNNKNLAWYQKQPPKLLIYWASTRESGVDPFRG 61  
 DB 10 SLAVSLGERATINCKSSQVLYSFNNKNLAWYQKQPPKLLIYWASTRESGVDPFRS 69  
 QY 62 GSGSGTDFLTITSSLOAEDVAVYCCQYYSPTFTGQTKVEIKRTVAAPSVFIFFPSDE 121

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Db      70  GSGSGTDFLTIISSLAQEDVAVYVYCOQYFYSPWTFGGTKVEIKRTVAAPSVFIFPPSDE 129
Qy      122  QLKSGTASVVCILNNFYPREAKEHOK 147
Db      130  QLKSGTASVVCILNNFYPREAKVOMK 155

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RESULT 13	
ADK52382	
ID	ADK52382 standard; protein; 159 AA.
XX	
AC	ADK52382;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	Human anti-MCP-1 variable region light chain #22.
XX	
KW	monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW	Antiheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW	Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;
KW	Inflammatory condition; cancer; arthritis; multiple sclerosis;
KW	anti-MCP-1; heavy chain; light chain.
XX	
OS	Homo sapiens.
XX	
PN	WO2004016769-A2.
XX	
PD	26-FEB-2004.
XX	
PF	19-AUG-2003; 2003WO-US026232.
XX	
PR	19-AUG-2002; 2002US-0404802P.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI	Bhakta S;
XX	
DR	WPI; 2004-203794/19.
DR	N-PSDB; ADK52381.
XX	
PT	New human monoclonal antibody that binds to monocyte chemo-attractant
PT	protein-1 and is immobilized on an insoluble matrix, useful for
PT	diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT	rheumatoid arthritis or psoriasis.
XX	
PS	Claim 2; SEQ ID NO 88; 154pp; English.
XX	
CC	The present invention relates to a human monoclonal antibody that binds
CC	to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC	for the preparation of a medicament useful for treating neoplastic or
CC	inflammatory conditions. The neoplastic disease is selected from breast
CC	cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC	stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC	pancreatic cancer or prostate cancer. The inflammatory condition is
CC	selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC	psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC	antibodies are also useful for diagnosing the above diseases. It is also
CC	useful for determining the level of MCP-1 and MCP-1 family members in
CC	patient samples. The present sequence represents a human anti-MCP-1
CC	variable region light chain sequence.
XX	
SQ	Sequence 159 AA;

[illegible]

RESULT 14	
ADK52310	
ID	ADK52310 standard; protein; 163 AA.
XX	
AC	ADK52310;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	Human anti-MCP-1 variable region light chain #4.
XX	
KW	monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW	Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;
KW	Vasotrophic; Immunosuppressive; Neuroprotective; Neoplastic;
KW	inflammatory condition; cancer; arthritis; multiple sclerosis;
KW	anti-MCP-1; heavy chain; light chain.
XX	
OS	Homo sapiens.
XX	
PN	WO2004016769-A2.
XX	
PD	26-FEB-2004.
XX	
PF	19-AUG-2003; 2003WO-US026232.
XX	
PR	19-AUG-2002; 2002US-0404802P.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI	Bhakta S;
XX	
DR	WPI; 2004-203794/19.
DR	N-PSDB; ADK52309.
XX	
PT	New human monoclonal antibody that binds to monocyte chemo-attractant
PT	protein-1 and is immobilized on an insoluble matrix, useful for
PT	diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT	rheumatoid arthritis or psoriasis.
XX	
PS	Claim 2; SEQ ID NO 16; 154pp; English.
XX	
CC	The present invention relates to a human monoclonal antibody that binds
CC	to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC	for the preparation of a medicament useful for treating neoplastic or
CC	inflammatory conditions. The neoplastic disease is selected from breast
CC	cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC	stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC	pancreatic cancer or prostate cancer. The inflammatory condition is
CC	selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC	psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC	antibodies are also useful for diagnosing the above diseases. It is also
CC	useful for the determining the level of MCP-1 and MCP-1 family members in
CC	patient samples. The present sequence represents a human anti-MCP-1
CC	variable region light chain sequence.



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 79.0704 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-28

Perfect score: 786

Sequence: 1 HSLAVSLGERATINCKSSQS.....VCLLNFFPREAKHQKSP 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	729	92.7	211	15	US-10-264-049-4266
2	709	90.2	240	9	US-09-799-514-8
3	694	88.3	264	15	US-10-264-049-4274
4	693	88.2	240	9	US-09-301-593-36
5	693	88.2	240	14	US-10-159-006-26
6	668.5	85.1	165	15	US-10-364-743-26
7	661	84.1	153	9	US-09-187-693-62
8	660	84.0	240	16	US-10-630-406-8
9	649.5	82.6	239	9	US-09-249-011A-22
10	646	82.2	239	9	US-09-825-012-9
11	646	82.2	242	10	US-09-819-266-26
12	640	81.4	220	9	US-09-995-693-1
13	640	81.4	220	14	US-10-232-408-1

14	629	80.0	220	9	US-09-301-593-17	Sequence 17, Appl
15	629	80.0	220	14	US-10-159-006-17	Sequence 17, Appl
16	629	80.0	240	9	US-09-301-593-28	Sequence 28, Appl
17	629	80.0	240	14	US-10-159-006-28	Sequence 28, Appl
18	624	79.4	220	9	US-09-917-410-5	Sequence 5, Appl
19	617	78.5	218	15	US-10-449-566-102	Sequence 102, App
20	613	78.0	218	15	US-10-449-566-119	Sequence 119, App
21	610	77.6	218	14	US-10-171-452A-39	Sequence 39, Appl
22	610	77.6	218	14	US-10-171-452A-57	Sequence 57, Appl
23	610	77.6	218	15	US-10-353-708-39	Sequence 39, Appl
24	610	77.6	218	15	US-10-353-708-57	Sequence 57, Appl
25	610	77.6	218	16	US-10-731-984-4	Sequence 4, Appl
26	610	77.6	218	16	US-10-731-984-28	Sequence 28, Appl
27	610	77.6	238	14	US-10-171-452A-38	Sequence 38, Appl
28	610	77.6	238	14	US-10-171-452A-56	Sequence 56, Appl
29	610	77.6	238	15	US-10-353-708-38	Sequence 38, Appl
30	610	77.6	238	15	US-10-353-708-56	Sequence 56, Appl
31	610	77.6	238	16	US-10-731-984-3	Sequence 3, Appl
32	610	77.6	238	16	US-10-731-984-27	Sequence 27, Appl
33	609	77.5	218	15	US-10-449-566-98	Sequence 98, Appl
34	600	76.3	218	14	US-10-171-452A-45	Sequence 45, Appl
35	600	76.3	218	14	US-10-171-452A-51	Sequence 51, Appl
36	600	76.3	218	15	US-10-353-708-45	Sequence 45, Appl
37	600	76.3	218	15	US-10-353-708-51	Sequence 51, Appl
38	600	76.3	218	16	US-10-731-984-12	Sequence 12, Appl
39	600	76.3	218	16	US-10-731-984-20	Sequence 20, Appl
40	600	76.3	238	14	US-10-171-452A-44	Sequence 44, Appl
41	600	76.3	238	14	US-10-171-452A-50	Sequence 50, Appl
42	600	76.3	238	15	US-10-353-708-44	Sequence 44, Appl
43	600	76.3	238	15	US-10-353-708-50	Sequence 50, Appl
44	600	76.3	238	16	US-10-731-984-11	Sequence 11, Appl
45	600	76.3	238	16	US-10-731-984-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1  
US-10-264-049-4266  
; Sequence 4266, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PAL33P1  
; CURRENT APPLICATION NUMBER: US/10/264,049  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/18569  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 4266  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (5)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-10-264-049-4266

Query Match	92.7%	Score 729;	DB 15;	Length 211;
Best Local Similarity	95.2%	Pred. No. 4e-49;		
Matches 139;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	2	SLAVSLGERATINCKSSQSVLYSFNNKYLAWYQQPGPKLLIYWASTRESGVDPDRG	61	
Db	34	SLAVSLGERATINCKSSQSVLYSPDNKYLAWYQQPGHPKLLIYWASTRESGVDPDRG	93	
Qy	62	CGSGTDTLTISSLOAEDVAVYCOQYSPRTTGGTQKVEIKETVAAPSFIIPPSDE	121	



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; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-36

Query Match      88.2%; Score 693; DB 9; Length 240;
Best Local Similarity 91.8%; Pred. No. 2.8e-46;
Matches 134; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFG 61
Db 30 SLAVSLGERATINCKSSOSVLYSRNQKNYLAWYQKPGOPPKLLIFWASTRESGVDPDRFS 89
QY 62 GSGGTDFTLTISLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121
Db 90 GSGGTDFTLTISLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 149
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147
Db 150 QLKSGTASVVCLLNNFYPREAKEVQWK 175

RESULT 5
US-10-159-006-36
; Sequence 36, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John B.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-36

Query Match      88.2%; Score 693; DB 14; Length 240;
Best Local Similarity 91.8%; Pred. No. 2.8e-46;
Matches 134; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFG 61
Db 30 SLAVSLGERATINCKSSOSVLYSRNQKNYLAWYQKPGOPPKLLIFWASTRESGVDPDRFS 89
QY 62 GSGGTDFTLTISLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121
Db 90 GSGGTDFTLTISLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 149
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147
Db 150 QLKSGTASVVCLLNNFYPREAKEVQWK 175

RESULT 6
US-10-364-743-26
; Sequence 26, Application US/10364743
; Publication No. US20040009178A1
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; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 26
; LENGTH: 165
; TYPE: PRT
; ORGANISM: human
US-10-364-743-26

Query Match      85.1%; Score 668.5; DB 15; Length 165;
Best Local Similarity 88.4%; Pred. No. 1.6e-44;
Matches 129; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFG 61
Db 12 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFS 70
QY 62 GSGGTDFTLTISLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121
Db 71 GSGGTDFTLTISLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 130
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147
Db 131 QLKSGTASVVCLLNNFYPREAKEVQWK 156

RESULT 7
US-09-187-693-62
; Sequence 62, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(153)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-187-693-62

Query Match      84.1%; Score 661; DB 9; Length 153;
Best Local Similarity 90.3%; Pred. No. 5.7e-44;
Matches 130; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFG 61
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Db 6 SLAVSLGERATINCKSSQSVLYSGKNQNYLAWYQKQGPCKLLIYWASTRESGVDPDRF 65
Qy 62 GSGSGTDFLTLSLQADVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 121
Db 66 GSGSGTDFLTLSLQADVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 125
Qy 122 QKSGGTASVCLLNFFY--PREAK 143
Db 126 QKSGGTASVCLLNLYRKPRTRK 149

RESULT 8
US-10-630-406-8
; Sequence 8, Application US/10630406
; Publication No. US20040105855A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Ganguly, Subinay
; APPLICANT: Abraham, Ralph
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Rillema, Jill
; APPLICANT: Thorne, Barbara
; APPLICANT: Shuford, Walter W.
; APPLICANT: Mittler, Robert S.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: D0288 NP
; CURRENT APPLICATION NUMBER: US/10/630,406
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/399,646
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-630-406-8

Query Match 84.0%; Score 660; DB 16; Length 240;
Best Local Similarity 89.0%; Pred. No. 1e-43;
Matches 130; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPCKLLIYWASTRESGVDPDRFG 61
Db 30 SLAVSLGERATINCKSSQSVLYSGKNQNYLAWYQKQGPCKLLIYASTRQSGVDPDRFS 89
Qy 62 GSGSGTDFLTLSLQADVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 121
Db 90 GSGSGTDFLTLSLQADVAVYCLQYDRYPTFTFGQGTKEIKRTVAAPSVFI PPPSDE 149
Qy 122 QKSGGTASVCLLNFFYPREAKEHOK 147
Db 150 QKSGGTASVCLLNFFYPREAKVQWK 175

RESULT 9
US-09-249-011A-22
; Sequence 22, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.

Db 6 SLAVSLGERATINCKSSQSVLYSGKNQNYLAWYQKQGPCKLLIYWASTRESGVDPDRF 65
Qy 62 GSGSGTDFLTLSLQADVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 121
Db 66 GSGSGTDFLTLSLQADVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 125
Qy 122 QKSGGTASVCLLNFFY--PREAK 143
Db 126 QKSGGTASVCLLNLYRKPRTRK 149

RESULT 10
US-09-825-012-9
; Sequence 9, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFg-1 light chain
US-09-825-012-9

Query Match 82.2%; Score 646; DB 9; Length 239;
Best Local Similarity 84.2%; Pred. No. 1.3e-42;
Matches 123; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPCKLLIYWASTRESGVDPDRFG 61
Db 29 SLSASVGDVRVTICKSSQSVLYSGKNQNYLAWYQKQGPCKLLIYWASTRESGVPSRFS 88
Qy 62 GSGSGTDFLTLSLQADVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 121
Db 89 GSGSGTDFLTLSLQADVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 148
Qy 122 QKSGGTASVCLLNFFYPREAKEHOK 147
Db 149 QKSGGTASVCLLNFFYPREAKVQWK 174

RESULT 11
US-09-819-266-26
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; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-249-011A-22

Query Match 82.6%; Score 649.5; DB 9; Length 239;
Best Local Similarity 88.4%; Pred. No. 6.8e-43;
Matches 129; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPCKLLIYWASTRESGVDPDRFG 61
Db 30 SLAVSLGERATISCKSSQSVLYSGKNQNYLAWYQKQGPCKLLIYWASTRESGVDPDRFS 89
Qy 62 GSGSGTDFLTLSLQADVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 121
Db 90 GSGSGTDFLTLSLQADVAVYCSQSVLYSGKNQNYLAWYQKQGPCKLLIYWASTRESGVDPDRFS 148
Qy 122 QKSGGTASVCLLNFFYPREAKEHOK 147
Db 149 QKSGGTASVCLLNFFYPREAKVQWK 174

RESULT 10
US-09-825-012-9
; Sequence 9, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFg-1 light chain
US-09-825-012-9

Query Match 82.2%; Score 646; DB 9; Length 239;
Best Local Similarity 84.2%; Pred. No. 1.3e-42;
Matches 123; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPCKLLIYWASTRESGVDPDRFG 61
Db 29 SLSASVGDVRVTICKSSQSVLYSGKNQNYLAWYQKQGPCKLLIYWASTRESGVPSRFS 88
Qy 62 GSGSGTDFLTLSLQADVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 121
Db 89 GSGSGTDFLTLSLQADVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 148
Qy 122 QKSGGTASVCLLNFFYPREAKEHOK 147
Db 149 QKSGGTASVCLLNFFYPREAKVQWK 174

RESULT 11
US-09-819-266-26
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; Sequence 26, Application US/09819266
; Publication No. US20030017163A1
; GENERAL INFORMATION:
; APPLICANT: Antisoma Research limited
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: JG-EPC-4955/500563.20013
; CURRENT APPLICATION NUMBER: US/09/819,266
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/193,156
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Seqwin99
; SEQ ID NO 26
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HMPG1 Fab/Caspase-3 fusion protein light chain
US-09-819-266-26

Query Match      82.2%; Score 646; DB 10; Length 242;
Best Local Similarity 84.2%; Pred. No. 1.3e-42;
Matches 123; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFG 61
Db 32 SLASVGRVTRITCKSSQSVLYSSNQKIYLAWYQKPGKAPKLLIYWASTRESGVPSRFS 91
QY 62 GSGSGTDFTLTISLSQAEDVAVYQCYVSTPRFTGGQTKVEIKRTVAAPSFIIPPSPDE 121
Db 92 GSGSGTDFTLTISLSQPEDIAIYQCYVSTPRFTGGQTKVEIKRTVAAPSFIIPPSPDE 151
QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
Db 152 QKSGTASVVCLLNNFYPREAKVQWK 177

RESULT 12
US-09-995-693-1
; Sequence 1, Application US/09995693
; Patent No. US20020136721A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,693
; FILING DATE: 29-Nov-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/952,235
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881

; Sequence 26, Application US/09819266
; Publication No. US20030017163A1
; GENERAL INFORMATION:
; APPLICANT: Antisoma Research limited
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: JG-EPC-4955/500563.20013
; CURRENT APPLICATION NUMBER: US/09/819,266
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/193,156
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Seqwin99
; SEQ ID NO 26
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HMPG1 Fab/Caspase-3 fusion protein light chain
US-09-819-266-26

Query Match      81.4%; Score 640; DB 9; Length 220;
Best Local Similarity 82.2%; Pred. No. 3.4e-42;
Matches 120; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFG 61
Db 10 SLTVSVGEKVTVSCSSQSVLYSSQKLYLAWYQKPGQSPKLLIYWASTRESGVDPDRFT 69
QY 62 GSGSGTDFTLTISLSQAEDVAVYQCYVSTPRFTGGQTKVEIKRTVAAPSFIIPPSPDE 121
Db 70 GSGSGTDFTLTISLSVKADDLAVYQCYVSTPRFTGGQTKVEIKRTVAAPSFIIPPSPDE 129
QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
Db 130 QKSGTASVVCLLNNFYPREAKVQWK 155

RESULT 13
US-10-232-408-1
; Sequence 1, Application US/10232408
; Publication No. US20030118587A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,408
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/669,971
; FILING DATE: 05-Jul-2001
; APPLICATION NUMBER: US/08/952,235
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/460368
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-232-408-1
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.3835 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-28

Perfect score: 786

Sequence: 1 HSLAVSLGERATINCKSSQS.....VVCLLNFFPREAKEHQKSP 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	693	88.2	240	4	US-09-301-593-36
2	683.5	87.0	241	2	US-07-916-098A-56
3	649.5	82.6	239	4	US-09-627-898B-22
4	640	81.4	220	3	US-08-952-235-1
5	640	81.4	220	4	US-09-669-971-1
6	629	80.0	220	4	US-09-301-593-17
7	629	80.0	240	4	US-09-301-593-28
8	607	77.2	239	3	US-08-812-586-29
9	607	77.2	239	4	US-09-535-832A-30
10	581	73.9	120	1	US-08-026-320A-4
11	573	72.9	214	4	US-09-472-087-71
12	572	72.8	139	4	US-09-472-087-22
13	572	72.8	139	4	US-09-472-087-96
14	567.5	72.2	235	4	US-09-472-087-14
15	567.5	72.2	235	4	US-09-472-087-65
16	566.5	72.1	141	4	US-09-472-087-88
17	566	72.0	226	4	US-09-456-090A-74
18	566	72.0	226	4	US-09-453-234-74
19	565	71.9	226	4	US-09-456-090A-86
20	565	71.9	226	4	US-09-453-234-86
21	564	71.8	224	4	US-09-456-090A-82
22	564	71.8	224	4	US-09-456-090A-88
23	564	71.8	224	4	US-09-456-090A-90
24	564	71.8	224	4	US-09-453-234-82
25	564	71.8	224	4	US-09-453-234-88
26	564	71.8	224	4	US-09-453-234-90
27	564	71.8	226	4	US-09-456-090A-50

28	564	71.8	226	4	US-09-456-090A-80	Sequence 80, Appl
29	564	71.8	226	4	US-09-453-234-50	Sequence 50, Appl
30	564	71.8	226	4	US-09-453-234-80	Sequence 80, Appl
31	562	71.5	146	4	US-09-472-087-21	Sequence 21, Appl
32	562	71.5	146	4	US-09-472-087-93	Sequence 93, Appl
33	561	71.4	139	4	US-09-472-087-16	Sequence 16, Appl
34	561	71.4	139	4	US-09-472-087-90	Sequence 90, Appl
35	560	71.2	218	2	US-08-887-352B-13	Sequence 13, Appl
36	560	71.2	218	3	US-08-466-151-9	Sequence 9, Appl
37	560	71.2	218	3	US-09-109-207C-13	Sequence 13, Appl
38	560	71.2	218	3	US-09-296-005-13	Sequence 13, Appl
39	560	71.2	218	3	US-08-466-163B-9	Sequence 9, Appl
40	560	71.2	218	4	US-09-920-171-13	Sequence 13, Appl
41	560	71.2	218	4	US-09-802-096-9	Sequence 9, Appl
42	560	71.2	218	4	US-09-802-077-9	Sequence 9, Appl
43	560	71.2	218	4	US-09-716-028-13	Sequence 13, Appl
44	560	71.2	218	4	US-10-113-996-13	Sequence 13, Appl
45	560	71.2	224	4	US-09-456-090A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-09-301-593-36

; Sequence 36, Application US/09301593A

; Patent No. 6455677

; GENERAL INFORMATION:

; APPLICANT: Park, John B.

; APPLICANT: Garin-Chesa, Pilar

; APPLICANT: Bamberger, Uwe

; APPLICANT: Leger, Olivier

; APPLICANT: Saldanha, Jose W.

; APPLICANT: Rettig, Wolfgang J.

; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility

; FILE REFERENCE: 0652.1890001

; CURRENT APPLICATION NUMBER: US/09/301,593A

; CURRENT FILING DATE: 1999-04-29

; EARLIER APPLICATION NUMBER: EP 98107925.4

; EARLIER FILING DATE: 1998-04-30

; EARLIER APPLICATION NUMBER: US 60/086,049

; EARLIER FILING DATE: 1998-05-18

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-301-593-36

Query Match 88.2%; Score 693; DB 4; Length 240;

Best Local Similarity 91.8%; Pred. NO. 7.9e-62;

Matches 134; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQS...VLFNNKYLAWYQKQPPKLLIYWA...TRESGVDPDRG 61

DB 30 SLAVSLGERATINCKSSQS...VLFNNKYLAWYQKQPPKLLIYWA...TRESGVDPDRFS 89

QY 62 GSGGTDTFTLTISSLOAEDVAVYQYQYVSTPTFGQGTKEIKTVAAPS...VFI... 121

DB 90 GSGGTDTFTLTISSLOAEDVAVYQYQYVSTPTFGQGTKEIKTVAAPS...VFI... 149

QY 122 QKSGTASVCLLNFFPREAKEHQK 147

DB 150 QKSGTASVCLLNFFPREAKEVQWK 175

RESULT 2

US-07-916-098A-56

; Sequence 56, Application US/07916098A

; Patent No. 5871732

; GENERAL INFORMATION:

; APPLICANT: BURKDY, LINDA C.

APPLICANT: CHISHOLM, PATRICIA L.  
APPLICANT: THOMAS, DAVID W.  
APPLICANT: ROSA, MARGARET D.  
APPLICANT: ROSA, JOSEPH J.  
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
STREET: 10 SOUTH WACKER DRIVE  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: U.S.A.  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/916.098A  
FILING DATE: July 24, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/08843  
FILING DATE: No. 5871732ember 27, 1991  
CLASSIFICATION: 424  
APPLICATION NUMBER: 07/618,542  
FILING DATE: No. 5871732ember 27, 1990  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: JOHN J. MC DONNELL  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,310-G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 715-1000  
TELEFAX: (312) 715-1234  
TELEX: 910/221-5317  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-916-098A-56

Query Match 87.0%; Score 683.5; DB 2; Length 241;  
Best Local Similarity 91.8%; Pred. No. 7.1e-61;  
Matches 134; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAUWYQKPGQPKLLIYWASTRESGVDPDRFG 61  
Db 32 SLAVSLGERATINCKSSQSVLYSFNNKNYLAUWYQKPGQPKLLIYWASTRESGVDPDRFS 91

QY 62 GSGSGTDTFTLTISLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIFPPSDE 121  
Db 92 GSGSGTDTFTLTISLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIFPPSDE 150

QY 122 QKSGTASVCLNNFYPREAKEHQK 147  
Db 151 QKSGTASVCLNNFYPREAKEVQWK 176

RESULT 3  
US-09-627-896B-22  
Sequence 22, Application US/09627896B  
Patent No. 6827934  
GENERAL INFORMATION:  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
APPLICANT: CARENNO, BEATRIZ  
APPLICANT: CELNIKER, ABBIE CHERYL  
APPLICANT: COLLINS, MARY

APPLICANT: GOLDMAN, SAMUEL  
APPLICANT: GRAY, GARY S.  
APPLICANT: KNIGHT, ANDREA  
APPLICANT: O'HARA, DENISE  
APPLICANT: RUP, BONITA  
APPLICANT: VEJDMAN, GEBTRUIDA M.  
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
TITLE OF INVENTION: OF TREATMENT THEREWITH  
FILE REFERENCE: 08702.0081-01000  
CURRENT APPLICATION NUMBER: US/09/627,896B  
CURRENT FILING DATE: 2000-07-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Mus sp.  
FEATURE:  
OTHER INFORMATION: 3d1 light chain  
US-09-627-896B-22

Query Match 82.6%; Score 649.5; DB 4; Length 239;  
Best Local Similarity 88.4%; Pred. No. 1.8e-57;  
Matches 129; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAUWYQKPGQPKLLIYWASTRESGVDPDRFG 61  
Db 30 SLAVSLGERATISCKSSQSVLYSFNNKNYLAUWYQKPGQPKLLIYWASTRESGVDPDRFS 89

QY 62 GSGSGTDTFTLTISLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIFPPSDE 121  
Db 90 GSGSGTDTFTLTISLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIFPPSDE 148

QY 122 QKSGTASVCLNNFYPREAKEHQK 147  
Db 149 QKSGTASVCLNNFYPREAKEVQWK 174

RESULT 4  
US-08-952-235-1  
Sequence 1, Application US/08952235  
Patent No. 6207152  
GENERAL INFORMATION:  
APPLICANT: Schwall, Ralph H.  
APPLICANT: Tabor, Kelly H.  
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
TITLE OF INVENTION: Antagonists and Uses Thereof  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/952,235  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/460368  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P0938P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416





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; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-28

Query Match      80.0%; Score 629; DB 4; Length 240;
Best Local Similarity 82.2%; Pred. No. 2.1e-55;
Matches 120; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy  2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPQPKLLIYWASTRESGVDPDRFG 61
Db  30 SLAVSVGEKVTMSCKSSQSVLYSRNQKNYLAWFQKQSPKLLIFWASTRESGVDPDRFT 89
Qy  62 GSGSGTDTLTITISSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDE 121
Db  90 GSGGTFDNLTITISSVQAEADLAVYCCQYVSTPRTFGAGTKLELKRRTVAAPSVFIPPPSDE 149
Qy  122 QLKSGTASVCLLNFPYPRAKEHOK 147
Db  150 QLKSGTASVCLLNFPYPRAKEVQWK 175

RESULT 8
US-08-812-586-29
; Sequence 29, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-29
; Query Match      77.2%; Score 607; DB 3; Length 239;

; BEST LOCAL SIMILARITY 83.6%; Pred. No. 3.4e-53;
; MATCHES 122; CONSERVATIVE 6; MISMATCHES 18; INDELS 0; GAPS 0;

Qy  2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPQPKLLIYWASTRESGVDPDRFG 61
Db  29 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPQPKLLIYWASTRESGVDPDRFS 88
Qy  62 GSGSGTDTLTITISSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDE 121
Db  89 GSGSGTDTLTITISRLPEDFAVYCCQYVSTPRTFGGSKVETVAAPSVFIPPPSDE 148
Qy  122 QLKSGTASVCLLNFPYPRAKEHOK 147
Db  149 QLKBITASVGLLNFPYPRAKEVQWK 174

RESULT 9
US-09-535-832A-30
; Sequence 30, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535,832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-30

Query Match      77.2%; Score 607; DB 4; Length 239;
Best Local Similarity 83.6%; Pred. No. 3.4e-53;
Matches 122; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy  2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPQPKLLIYWASTRESGVDPDRFG 61
Db  29 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPQPKLLIYWASTRESGVDPDRFS 88
Qy  62 GSGSGTDTLTITISSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDE 121
Db  89 GSGSGTDTLTITISRLPEDFAVYCCQYVSTPRTFGGSKVETVAAPSVFIPPPSDE 148
Qy  122 QLKSGTASVCLLNFPYPRAKEHOK 147
Db  149 QLKBITASVGLLNFPYPRAKEVQWK 174

RESULT 10
US-08-026-320A-4
; Sequence 4, Application US/08026320A
; Patent No. 5419904
; GENERAL INFORMATION:
; APPLICANT: Irie, Reiko F
; TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
; TITLE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pons, Smith, Lande & Rose
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States of America
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 14.1428 Seconds  
(without alignment)  
1353.842 Million cell updates/sec

Title: US-09-784-950-29

Perfect score: 1054

Sequence: 1 EVKPGASVKVCKASGYTF.....TSQVLLPSKDVMOGTDEHKV 199

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	82.5	627	2	S14683
2	663.5	63.0	231	2	B23746
3	590	56.0	288	2	S29690
4	526.5	50.0	136	2	S31600
5	524	49.7	127	2	S34014
6	506.5	48.1	110	2	PH1670
7	500	47.4	160	2	PL0105
8	497.5	47.2	132	2	S31596
9	495.5	47.0	246	2	S38950
10	495.5	47.0	446	2	S40295
11	492	46.7	469	2	S37483
12	491	46.6	171	2	PH1666
13	476.5	45.2	118	2	PH1666
14	476	45.2	98	2	S26918
15	474	45.0	142	2	A32483
16	473	44.9	129	2	S46393
17	470.5	44.6	241	2	S69131
18	467.5	44.4	118	2	S36265
19	466.5	44.3	568	2	A34891
20	466	44.2	592	2	S25705
21	463.5	44.0	114	2	PH1667
22	462.5	43.9	135	2	S49530
23	458	43.5	129	2	S36260
24	458	43.5	475	2	S01321
25	454	43.1	109	2	PH1668
26	454	43.1	123	2	D33548
27	451.5	42.8	474	1	G2MS11
28	451	42.8	214	2	PC4202
29	447.5	42.5	110	2	PH1669

30 443 42.0 452 1 MEHU  
31 443 42.0 453 2 S37768  
32 443 42.0 473 1 MHUM  
33 443 42.0 474 2 S15590  
34 442.5 42.0 549 2 S04845  
35 438.5 41.6 104 2 PH1665  
36 438.5 41.6 124 2 S19665  
37 436 41.4 119 2 PH0961  
38 434 41.2 126 2 I41151  
39 433 41.1 131 2 S26792  
40 429.5 40.7 132 2 PH0954  
41 429.5 40.7 136 2 PH0960  
42 427 40.5 133 2 C33548  
43 426.5 40.5 120 2 C33548  
44 425.5 40.4 143 1 EIHUND  
45 425 40.3 122 2 S36271

## ALIGNMENTS

### RESULT 1

S14683

Ig mu chain precursor, membrane-bound (clone 201) - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999

C/Accession: S14683; S08047

R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.

Nucleic Acids Res. 18, 4278, 1990

A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.

A:Reference number: S14683; MUID:90332450; PMID:2115996

A/Accession: S14683

A/Molecule type: mRNA

A/Residues: 1-627 <PRI>

A/Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin; membrane protein

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-627/Product: Ig mu chain #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match	82.5%	Score 870;	DB 2;	Length 627;
Best Local Similarity	82.0%	Pred. No. 7.5e-62;		
Matches 173;	Conservative	7;	Mismatches 19;	Indels 12; Gaps 2;
Qy	1	EVKPGASVKVCKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTGYAQKFGQGRVT	60	
Db	29	EVKPGSSVKVCKASGTFSSYAIISWVRQAPGGGLEWGGIIPIFGTANYAQKFGQGRVT	88	
Qy	61	MTRNTSISTAYMELSSLRSEDTAVYYCAR-----EEWLVR-----YGMVMDVMOGQTTV	108	
Db	89	ITADESTSTAYMELSSLRSEDTAVYYCAKTGILGFSYSGWYPNSDYYYYGMDVMOGQTTV	148	
Qy	109	TVSSGSASAPTLFPLVSCNSPSTSSVAVCCLAQDFLPDSITFSWKYKNNSDISSTRGF	168	
Db	149	TVSSGSASAPTLFPLVSCNSPSTSSVAVCCLAQDFLPDSITFSWKYKNNSDISSTRGF	208	
Qy	169	PSVLRGKGYAATSOVLLPSKDVMOGTDEHKV	199	
Db	209	PSVLRGKGYAATSOVLLPSKDVMOGTDEHVV	239	

### RESULT 2

B23746

Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000

C/Accession: B23746

R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.

J. Biol. Chem. 266, 2836-2842, 1991

A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin

A:Reference number: A23746; MUID:91131575; PMID:1993660

A/Accession: B23746

```
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-231 <LBO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:140-209/Domain: immunoglobulin homology <IMM>

Query Match      63.0%; Score 663.5; DB 2; Length 231;
Best Local Similarity 67.3%; Pred. No. 7.4e-46;
Matches 132; Conservative 24; Mismatches 39; Indels 1; Gaps 1;

Qy      4  KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVTWTR 63
Db      12  KPSSTLSLTGAVYGGSDYDYNWIRPPGKGLWIGGIN-HSGSTYNPLKSRVTSV 70

Qy      64  NTSISTAYMELSSLRSEDTAVYVCAREEWLVRYGMDVWGQGTVTTVSSGSASAPTLFPL 123
Db      71  DTSKNQPSLKLSSVTAADTAVYCARPPHDTSGHYWVWGQTLTVTVSSGSASAPTLFPL 130

Qy      124  VSCNSPDSSTSSVAVGCLAQDFLPSDITFSWKYKKNNSDISSTRGFPSPVLRGGKYAATSQV 183
Db      131  VSCNSPDSSTSSVAVGCLAQDFLPSDITFSWKYKKNNSDISSTRGFPSPVLRGGKYAATSQV 190

Qy      184  LLPSKDVMOGTDDEHKV 199
Db      191  LLPSKDVMOGTDDEHV 206

RESULT 3
S29690
Ig heavy chain VDJ region - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000
C:Accession: S29690
R:Dammer, P.M.; Bos, N.A.; Kroese, F.G.M.
submitted to the EMBL Data Library, October 1992
A:Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.
A:Reference number: S29690
A:Accession: S29690
A:Molecule type: mRNA
A:Residues: 1-288 <DMA>
A:Cross-references: EMBL:X68782; NID:g56442; PID:g1334294
A:Experimental source: strain D2B
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:12-95/Domain: immunoglobulin homology <IMM>

Query Match      56.0%; Score 590; DB 2; Length 288;
Best Local Similarity 56.5%; Pred. No. 6.9e-40;
Matches 113; Conservative 38; Mismatches 45; Indels 4; Gaps 2;

Qy      1  EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVT 60
Db      7  ELVRGSSVKISKASGYTFTDYNMHVQKRPQGLWIGRINPANGNTEYAEKPKSRAT 66

Qy      61  MTRNTSISTAYMELSSLRSEDTAVYVCAREEWLVRYGMDVWGQGTVTTVSSGSASAPTL 120
Db      67  LTADKSSNAYVQLSSLTSEDTATFTCTGTGTVVFPF---DYWGQGVYVTVSSSESQSPTV 123

Qy      121  PLVSCNSPDSSTSSVAVGCLAQDFLPSDITFSWKYKKNNSDI-SSTRGFPSPVLRGGKYAA 179
Db      124  LPLVSCSPSLDENLVAMGLARDFLPSSISFSWYQNNTEVWQGVRFPTLTGDKYTA 183

Qy      180  TSQVLLPSKDVMOGTDDEHKV 199
Db      184  TSQVLLSAKNVLEGSDEYLV 203

RESULT 4
S31600
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31600

R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31600
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <CUI>
A:Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      50.0%; Score 526.5; DB 2; Length 136;
Best Local Similarity 89.4%; Pred. No. 3.5e-35;
Matches 101; Conservative 3; Mismatches 4; Indels 5; Gaps 2;

Qy      1  EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVT 60
Db      29  EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVT 88

Qy      61  MTRNTSISTAYMELSSLRSEDTAVYVCAREEWLVRYGMDVWGQGTVTTVSSG 113
Db      89  MTRNTSISTAYMELSSLRSEDTAVYVCAR--WRDAF---DIWGQGTWTVTVSSG 136

RESULT 5
S34014
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C:Accession: S34014; S30535
R:Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34014
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-127 <MAR>
A:Cross-references: EMBL:Z18321
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      49.7%; Score 524; DB 2; Length 127;
Best Local Similarity 85.6%; Pred. No. 5.2e-35;
Matches 101; Conservative 7; Mismatches 4; Indels 6; Gaps 2;

Qy      1  EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVT 60
Db      10  EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVT 69

Qy      61  MTRNTSISTAYMELSSLRSEDTAVYVCARE---EWLVR---YGMVMDVWGQGTVTTVSS 112
Db      70  MTRNTSISTAYMELSSLRSEDTAVYFCARLSIGVAVIRGYVYALDVMWGQGTVTTVSSV 127

RESULT 6
PH1670
Ig heavy chain V region (clone 2A12) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1670
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1670
A:Molecule type: mRNA
A:Residues: 1-110 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```

S40295  
Ig gamma-2a chain (mAb735) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C:Accession: S40295  
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisg  
submitted to the EMBL data library, January 1993  
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb  
A:Reference number: S40295  
A:Accession: S40295  
A:Molecule type: protein  
A:Residues: 1-446 <LE>  
A:Cross-references: UNIPROT:Q99L25  
C:Genetics:  
A:Map position: 12  
C:Superfamily: immunoglobulin C region: immunoglobulin homology

C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid  
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>  
F:1-117/Domain: V-D-J region <VDJ>  
F:118-446/Domain: C region <CHR>  
F:118-214/Domain: C1 region <CH1>  
F:215-230/Region: hinge  
F:231-340/Domain: C2 region <CH2>  
F:341-446/Domain: C3 region <CH3>  
F:360-427/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:22-96,144-199,261-367-425/Disulfide bonds: #status predicted  
F:132/Disulfide bonds: interchain (to light chain) #status predicted  
F:224,227,229/Disulfide bonds: interchain #status predicted  
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 47.0%; Score 495.5; DB 2; Length 446;  
Best Local Similarity 51.8%; Pred. No. 3.8e-32;  
Matches 99; Conservative 34; Mismatches 43; Indels 15; Gaps 6;  
QY 1 EVKKEGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60  
Db 10 ELVRFGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGKAT 69  
QY 61 MTRNTSISTAYMELSLRSEDVAVYCAEEWLVRYGMDVWGQGTFTVTVSSGSASAPTL 120  
Db 70 LTVDTSSSTAYMQLSLSLTSSEDSAVYFCARG---GKFAMDYWGQGTFTVTVSSAKTTAPSV 125  
QY 121 PFLVS-CENSPDPT--SSVAVGCLAQDFLPDSITFSWKYKNSDILSS-TRGPPSVLRGK 176  
Db 126 YPLAPVC---GDTTSSVTLGCLVKGYFPEPVTLTW---NSGSLSSGWHVTFPAVLQSDL 178  
QY 177 YAATSOVLPLS 187  
Db 179 YTLSSSVTVTS 189

RESULT 11  
S37483  
Ig gamma-2a chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S37483  
R:Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S37483  
A:Accession: S37483  
A:Status: preliminary  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-469 <DUC>  
A:Cross-references: EMBL:X70423; NID:G406252; PIDN:CAA49868.1; PID:G406253  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:276-345/Domain: immunoglobulin homology <IMM>  
Query Match 46.7%; Score 492; DB 2; Length 469;  
Best Local Similarity 52.4%; Pred. No. 7.6e-32;  
Matches 100; Conservative 31; Mismatches 48; Indels 12; Gaps 6;  
QY 1 EVKKEGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60  
Db 29 ELVKEGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGKAT 88  
QY 61 MTRNTSISTAYMELSLRSEDVAVYCAEEWLVRYGMDVWGQGTFTVTVSSGSASAPTL 120  
Db 89 LTVDTSSSTAYMQLSLSLTSSEDAVYFCARGMATL-LDYWGQGTFTVTVSSAKTTAPSV 147  
QY 121 PFLVS-CENSPDPT--SSVAVGCLAQDFLPDSITFSWKYKNSDILSS-TRGPPSVLRGK 176  
Db 148 YPLAPVC---GDTTSSVTLGCLVKGYFPEPVTLTW---NSGSLSSGWHVTFPAVLQSDL 200  
QY 177 YAATSOVLPLS 187  
Db 201 YTLSSSVTVTS 211

RESULT 12  
S23623

Ig heavy chain V region precursor - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S23623  
R:Olee, T.; Lu, E.W.; Huang, D.P.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992  
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv  
A:Reference number: S23623; MUID:92156804; PMID:1740665  
A:Accession: S23623  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-171 <OLE>  
A:Cross-references: EMBL:X59702; NID:G32010; PIDN:CAA42223.1; PID:G32011  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 46.6%; Score 491; DB 2; Length 171;  
Best Local Similarity 66.0%; Pred. No. 3.1e-32;  
Matches 97; Conservative 13; Mismatches 25; Indels 12; Gaps 3;  
QY 1 EVKKEGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60  
Db 29 EVKKEGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 88  
QY 61 MTRNTSISTAYMELSLRSEDVAVYCAEEWLVRYG-----MDVWGQGTFTVTVSS 112  
Db 89 LTRDTSISTAYMELSLRSDVAVYCAIEYF---YDGSCLKPSDFVIGQGTTVTVSS 145  
QY 113 GSASAPTLFPLVSCENSPDPTSSVAVG 139  
Db 146 ASTKGPVSFPLAPSSKTSKG-GTAALG 171

RESULT 13  
PH1666

Ig heavy chain V region (clone 6C9) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C:Accession: PH1666  
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc  
A:Reference number: PH1642; MUID:93301610; PMID:8315388  
A:Accession: PH1666  
A:Molecule type: mRNA  
A:Residues: 1-118 <HIL>  
A:Experimental source: B cell  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 45.2%; Score 476.5; DB 2; Length 118;  
Best Local Similarity 79.5%; Pred. No. 2.9e-31;  
Matches 93; Conservative 6; Mismatches 13; Indels 5; Gaps 1;  
QY 1 EVKKEGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60  
Db 2 EVKKEGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 61  
QY 61 MTRNTSISTAYMELSLRSEDVAVYCAEEW-----LVRYGMDVWGQGTFTVTVSS 112  
Db 62 ITRDTSASTAYMELSLRSEDVAVYCAEEW-----LVRYGMDVWGQGTFTVTVSS 118

RESULT 14  
S26918

Ig heavy chain V region (DP-15) - human (fragment)  
C:Species: Homo sapiens (man)



```
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26918
R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26918
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <IOM>
A:Cross-references: EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID:g32858
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 45.2%; Score 476; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.6e-31;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTGYAQKFGQRTV 60
Db 10 EVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTGYAQKFGQRTV 69
QY 61 MTRNTSISTAYMELSLRSEDYAVYYCAR 89
Db 70 MTRNTSISTAYMELSLRSEDYAVYYCAR 98

RESULT 15
A32483
IG heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C:Accession: A32483
R:Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A:Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usi
A:Reference number: A32483; MUID:89273586; PMID:2499327
A:Accession: A32483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-142 <LAR>
A:Cross-references: GB:M26463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-108/Domain: immunoglobulin homology <IMM>

Query Match 45.0%; Score 474; DB 2; Length 142;
Best Local Similarity 75.6%; Pred. No. 5.7e-31;
Matches 93; Conservative 9; Mismatches 15; Indels 6; Gaps 1;

QY 1 EVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTGYAQKFGQRTV 60
Db 20 EVKKPGASVKVSKASGYTFTSYDINWVRQATQGQLEWGMWNPNSGNTGYAQKFGQRTV 79
QY 61 MTRNTSISTAYMELSLRSEDYAVYYCAR 117
Db 80 MTRDTSTVYMEELSLRSEDYAVYYCAR 139
QY 115 ASA 117
Db 140 ASA 142

Search completed: March 8, 2005, 06:39:24
Job time: 14.1928 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 74.3165 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-29

Perfect score: 1054

Sequence: 1 EVKPKASVKVSKASGYTF.....TSQVLLPSKDVMOGTDEHKV 199

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	778.5	73.9	606	Q6GMV2	Q6gmv2 homo sapien
2	754.5	71.6	613	Q8WUK1	Q8wuk1 homo sapien
3	749	71.1	597	Q96BB9	Q96bb9 homo sapien
4	702	66.6	595	Q8WUX4	Q8wux4 homo sapien
5	702	66.6	597	Q6GMX5	Q6gmx5 homo sapien
6	702	66.6	597	Q9BU10	Q9bu10 homo sapien
7	702	66.6	625	Q96A6	Q96a6 homo sapien
8	698	66.2	597	Q9BQB8	Q9bqb8 homo sapien
9	692.5	65.7	620	Q96EY0	Q96ey0 homo sapien
10	625	59.3	613	Q8VCX7	Q8vcx7 mus musculus
11	586.5	55.6	614	Q7TWT6	Q7twt6 mus musculus
12	544.5	51.7	518	Q6N030	Q6n030 homo sapien
13	518.5	49.2	497	Q8WZ24	Q8wz24 homo sapien
14	512.5	48.6	469	Q7Z7P5	Q7z7p5 homo sapien
15	511	48.5	500	Q9BRV0	Q9brv0 homo sapien
16	508.5	48.2	475	Q6N095	Q6n095 homo sapien
17	505	47.9	498	Q6N041	Q6n041 homo sapien
18	503.5	47.8	470	Q7TMK1	Q7tmk1 mus musculus
19	497.5	47.2	500	Q6N091	Q6n091 homo sapien
20	484.5	46.0	480	Q6P089	Q6p089 homo sapien
21	484	45.9	480	Q6PJF1	Q6pjf1 homo sapien
22	481	45.6	481	Q91WT1	Q91wt1 mus musculus
23	480.5	45.6	482	Q8K172	Q8k172 mus musculus
24	480	45.5	483	Q991C4	Q991c4 mus musculus
25	478	45.4	484	Q991A6	Q991a6 mus musculus
26	475	45.1	465	Q6PJB2	Q6pjb2 mus musculus
27	474.5	45.0	473	Q9D814	Q9d814 mus musculus
28	468.5	44.4	472	Q6PJA7	Q6pia7 mus musculus
29	465	44.1	480	Q8K0Z4	Q8k0z4 mus musculus
30	462	43.8	244	Q65ZC8	Q65zc8 homo sapien
31	461	43.7	489	Q8VCX4	Q8vcx4 mus musculus

32	460.5	43.7	593	2	Q6INN5
33	457.5	43.4	488	2	Q8K0F2
34	456.5	43.3	488	2	Q91WR1
35	456	43.3	208	2	Q6ZP87
36	455	43.2	125	2	Q9UL95
37	454.5	43.1	159	2	Q9GQ80
38	450	42.7	472	2	Q6N089
39	448.5	42.6	464	2	Q6PF95
40	448	42.5	573	2	Q8WU38
41	446.5	42.4	145	2	Q924Q6
42	445	42.2	119	2	Q9UL94
43	444.5	42.2	145	2	Q924Q9
44	444	42.1	142	2	Q924Q1
45	443.5	42.1	124	2	Q9UL92

## ALIGNMENTS

RESULT 1  
Q6GMV2 PRELIMINARY; PRT; 606 AA.

AC Q6GMV2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzywinski M.I., Skaleka U., Schmutz D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR ENBL; BC073758; AAH73758.1; -;  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; Cl-set; 4.  
DR SMART; SM00407; IG; 4.  
DR SMART; SM00409; IGcl; 4.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.



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RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC015760; AAH15760.1; -.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65039 MW; 4FC3AD8ECE263D9 CRC64;

Query Match 71.1%; Score 749; DB 2; Length 597;
Best Local Similarity 70.9%; Pred. No. 4.4e-59;
Matches 144; Conservative 25; Mismatches 24; Indels 10; Gaps 2;

QY 4 KPGASVKVSKASGYTFTSYDINWVRQATGGGLEWMGMNPNNGTGYAQKFGQRTVWTR 63
Db 32 QFGGSLRLSCAASGFSFSSYAMNWRQAPGKLEWVSAISGGSTYYADSVKGRFTISR 91
QY 64 NTSISTAYMELSSLRSEDYAVYCARBEWLYVYCM-----DYWGQGTFTVYSSGSAS 116
Db 92 DNSRDLYLQNSLRSEDYAVYCARBEWLYVYCM-----DYWGQGTFTVYSSGSAS 148
QY 117 APTLFPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLRGK 176
Db 149 APTLFPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLRGK 208
QY 177 YAATSQVLLPSKDVNQGTDEHKV 199
Db 209 YAATSQVLLPSKDVNQGTDEHV 231

RESULT 4
Q8WUX4 PRELIMINARY; PRT; 595 AA.
ID Q8WUX4 AC Q8WUX4 Q6GMX5 PRELIMINARY; PRT; 597 AA.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

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RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Lymph;
RA  Strausberg R.;
RL  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC073767; AAH73767.1; -.
DR  InterPro; IPR003599; IG.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG cl.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF07654; Cl-set; 4.
DR  Pfam; PF00047; Ig; 4.
DR  SMART; SM00409; IG; 2.
DR  SMART; SM00407; IGcl; 4.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS0835; IG LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW  Hypothetical protein.
SQ  SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match 66.6%; Score 702; DB 2; Length 597;
Best Local Similarity 69.0%; Pred. No. 7.7e-55;
Matches 140; Conservative 22; Mismatches 31; Indels 10; Gaps 3;

Qy  4 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVTWTR 63
Db  || : : || : : || : : || : : || : : || : : || : : || : : || : :
32 KPSETLSITCGVYGGSGFYWMIQPPGKGLEWIGEIN-HSGSTNYPNLSKSRVTISV 90
Qy  64 NTSISTAYMELSSLRSEDTAVVYCAREEWLVR-----YGMVDVWGQTTVTVSSGSAS 116
Db  || : : || : : || : : || : : || : : || : : || : : || : : || : :
91 DTSKKQLSLKSLSSNAADTAVVYCARV--ITRASPGTDGRYGMVDVWGQTTVTVSSGSAS 148
Qy  117 APTLFPVLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPSVLRGCK 176
Db  || : : || : : || : : || : : || : : || : : || : : || : : || : :
149 APTLFPVLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPSVLRGCK 208
Qy  177 YAATSQVLLPSKDVWQGTDEHKV 199
Db  || : : || : : || : : || : : || : : || : : || : : || : : || : :
209 YAATSQVLLPSKDVWQGTDEHVV 231

RESULT 6
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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RA Krzywinski M.I., Skalska U., Smailus D.B., Schnertch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC002963; AAH02963.1; -.
DR  HSSP; P01861; 1ADQ.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG cl.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF07654; Cl-set; 4.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS0835; IG LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ  SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 66.6%; Score 702; DB 2; Length 597;
Best Local Similarity 69.0%; Pred. No. 7.7e-55;
Matches 140; Conservative 22; Mismatches 31; Indels 10; Gaps 3;

Qy  4 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVTWTR 63
Db  || : : || : : || : : || : : || : : || : : || : : || : : || : :
32 KPSETLSITCGVYGGSGFYWMIQPPGKGLEWIGEIN-HSGSTNYPNLSKSRVTISV 90
Qy  64 NTSISTAYMELSSLRSEDTAVVYCAREEWLVR-----YGMVDVWGQTTVTVSSGSAS 116
Db  || : : || : : || : : || : : || : : || : : || : : || : : || : :
91 DTSKKQLSLKSLSSNAADTAVVYCARV--ITRASPGTDGRYGMVDVWGQTTVTVSSGSAS 148
Qy  117 APTLFPVLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPSVLRGCK 176
Db  || : : || : : || : : || : : || : : || : : || : : || : : || : :
149 APTLFPVLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPSVLRGCK 208
Qy  177 YAATSQVLLPSKDVWQGTDEHKV 199
Db  || : : || : : || : : || : : || : : || : : || : : || : : || : :
209 YAATSQVLLPSKDVWQGTDEHVV 231

RESULT 7
Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC017356; AAH17356.2; -  
DR PIR; S15590; S15590.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBFE CRC64;

Query Match 66.6%; Score 702; DB 2; Length 625;  
Best Local Similarity 69.0%; Pred. No. 8.2e-55;  
Matches 140; Conservative 22; Mismatches 31; Indels 10; Gaps 3;  
Qy 4 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGNPNNGTGYAQKFGRTVWTR 63  
Db 39 KPESTLSLTCTGVYGGSGFYWSWIRQPPGKLEWIGIN-HSGSTNPNLSKSRVTISV 97  
Qy 64 NTSISTAYMELSSLRSEDTAVVYCARBEWLVYR-----YIGMDVWGQGTITVTVSSGSGS 116  
Db 98 DTSKKQLSLKSSVNAADTAVVYCARV--ITRASPGTDGRYGMVWGQGTITVTVSSGSGS 155  
Qy 117 APTLPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGPPSVLRGK 176  
Db 156 APTLPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGPPSVLRGK 215  
Qy 177 YAATSQVLLPSKDVWQGTDEHKV 199  
Db 216 YAATSQVLLPSKDVWQGTDEHV 238

RESULT 8  
Q9BQ88 PRELIMINARY; PRT; 597 AA.  
AC Q9BQ88  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE IGHM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richarde S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
FAhey J., Helton E., Kettman M., Madao A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC006180; AAH06180.1; -  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;  
Query Match 66.2%; Score 698; DB 2; Length 597;  
Best Local Similarity 69.0%; Pred. No. 1.8e-54;  
Matches 140; Conservative 21; Mismatches 32; Indels 10; Gaps 3;  
Qy 4 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGNPNNGTGYAQKFGRTVWTR 63  
Db 32 KPESTLSLTCTGVYGGSGFYWSWIRQPPGKLEWIGIN-HSGITNPNLSKSRVTISV 90  
Qy 64 NTSISTAYMELSSLRSEDTAVVYCARBEWLVYR-----YIGMDVWGQGTITVTVSSGSGS 116  
Db 91 DTSKKQLSLKSSVNAADTAVVYCARV--ITRASPGTDGRYGMVWGQGTITVTVSSGSGS 148  
Qy 117 APTLPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGPPSVLRGK 176  
Db 149 APTLPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGPPSVLRGK 208  
Qy 177 YAATSQVLLPSKDVWQGTDEHKV 199  
Db 209 YAATSQVLLPSKDVWQGTDEHV 231  
RESULT 9  
Q96EY0 PRELIMINARY; PRT; 620 AA.  
AC Q96EY0  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE IGHM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAHL1857.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS0290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 65.7%; Score 692.5; DB 2; Length 620;
Best Local Similarity 68.9%; Pred. No. 5.9e-54;
Matches 135; Conservative 23; Mismatches 37; Indels 1; Gaps 1;

Qy 4 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNGTGYAQKFGQRTVMT 63
Db 39 KPSETLSITCTVSGGSISSYYWMIQAPAGGLEWIGRIY-TSGSTNYPNLSKSRVMTSV 97

Qy 64 NTSISTAYMELSLRSEDTAVVYCARBWLVRYYGMDVMVGQGTVTTVSSGASAPTLFPL 123
Db 98 DTSKNQFSLKLSVTAADTAVVYCASQWELPTVGLFYWGQGLTVTVSSGASAPTLFPL 157

Qy 124 VSCNSPSSDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGGKYAATSOV 183
Db 158 VSCNSPSSDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGGKYAATSOV 217

Qy 184 LLPSKDVMQGTDEHKV 199
Db 218 LLPSKDVMQGTDEHV 233

RESULT 10
Q8VCX7 PRELIMINARY; PRT; 613 AA.
ID Q8VCX7;
AC Q8VCX7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=23386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usadin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAHL18315.1; -.
DR PIR; C30562; C30562.
DR HSSP; P01751; 1A6W.
DR MGD; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B-cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0050871; P:positive regulation of B-cell activation; IDA.
DR GO; GO:0030890; P:positive regulation of B-cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS0290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 59.3%; Score 625; DB 2; Length 613;
Best Local Similarity 60.5%; Pred. No. 7.2e-48;
Matches 121; Conservative 34; Mismatches 41; Indels 4; Gaps 3;

Qy 1 EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNGTGYAQKFGQRTV 60
Db 29 ELMKPGASVKISCKATGYTFTSSYWIWVKQRPQHGLEWIGILPGSGSTNYNEKFKGRAT 88

Qy 61 MTRNTSISTAYMELSLRSEDTAVVYCARBWLVRYYGMDVMVGQGTVTTVSSGSAPTL 120
Db 89 FTADTSNTAYMQLSLTSEDSAVYICARR--LGRWY-FDVMGAGITTVTSSESQSFPNV 145

Qy 121 PPLVSCNSPSSDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGGKYAA 179
Db 146 PPLVSCNSPSSDLSDKNLVAMGCLARDFLPSTISFTWYQNNTVEIQGIRTFPLRTGGKYLA 205

Qy 180 TSQVLLPSKDVVMQGTDEHKV 199
Db 206 TSQVLLPSKLSILEGSDVYL 225

RESULT 11
Q7TWT6 PRELIMINARY; PRT; 614 AA.
ID Q7TWT6;
AC Q7TWT6;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE MGC60843 protein.
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusan K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.K., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC033409; AAH33409.1; -;  
DR HSSP; P01820; 1G7J.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
SQ SEQUENCE 614 AA; 67746 MW; 835BAF3B8D124F89 CRC64;  
  
Query Match 55.6%; Score 586.5; DB 2; Length 614;  
Best Local Similarity 55.9%; Pred. No. 2.2e-44;  
Matches 114; Conservative 36; Mismatches 43; Indels 11; Gaps 3;  
  
QY 1 EVKKGASVKVSKASGYFTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 60  
Db ELVKGASVKVSKASGYAFSSWMNVYKQRPKGLEWIGRVYPGDGTNYNGKFKGKAT 88  
  
QY 61 MTRNTSISTAYMELSSLRSEDTAVYVCAREEVLRYGMD---VWGQGTITVTVSSGSAS 116  
Db LTADKSSSTAYMQLSSLSRSEDAVVFCAED-----YGSYRFPATWGQGTITVTVSSASQS 142  
  
QY 117 APTLPLVSCENSPSDTSVAVGCLAQDPLPDSITFSWKYKNNSD-ISTRGFPVSLRG 175  
Db FNVFPLVSCSPSLSDKNLVAMGCLARDPLPDSITFSWKYKNNAEVIQIRTFPTLRGG 202  
  
QY 176 KYAATSOVLPLSKDVMOGTDEHKV 199  
Db KYLATSOVLPLSKDSILEGSDYLIV 226  
  
RESULT 12  
Q6N030 PRELIMINARY; PRT; 518 AA.  
AC Q6N030;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686i15212.

GN Name=DKFZp686i15212;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640724; CAE45841.1; -;  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR000005; HTHARAC.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00409; IGV; 3.  
DR SMART; SM00407; IGV; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00041; HTH ARAC FAMILY\_1; UNKNOWN\_1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;  
  
Query Match 51.7%; Score 544.5; DB 2; Length 518;  
Best Local Similarity 55.5%; Pred. No. 1.1e-40;  
Matches 111; Conservative 30; Mismatches 50; Indels 9; Gaps 6;  
  
QY 1 EVKKGASVKVSKASGYFTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 60  
Db EVKKGASVKVSKASGYFTFHFNWVRQAPGQSGLEWGMWNTGNTKYSQKFGQRTV 88  
  
QY 61 MTRNTSISTAYMELSSLRSEDTAVYVCARE--EMLVRYGMDVWGQGTITVTVSSGSASAP 118  
Db ITRDTWTTTAYMDLSSLRSEDTAVVWCARDAPQGVTTTY-FDYWGQGTITVTVSSASTKGP 147  
  
QY 119 TFLPLVSCENSPSDTSVAVGCLAQDPLPDSITFSWKYKNNSDISSTGFSPVLR-GGKY 177  
Db SVFPLAPCSRSTSG-GTAALGCLVKDYPPETVTSW--NSGALTSGVHTFPAVLQSSGLY 204  
  
QY 178 AATSOVLPLSKDVMOGTDEH 197  
Db SLSSVTVTPSSSL--GTQTY 222  
  
RESULT 13  
Q8WY24 PRELIMINARY; PRT; 497 AA.  
AC Q8WY24;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE SNG66 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF283666; AAL36987.1; -;  
DR HSSP; P01876; 1OWO.  
DR Pfam; PF07654; CI-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.



```
DR SMART: SM00406; IGv: 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 500 AA; 54154 MW; 0A3BF43F2A3CC6D9 CRC64;

Query Match      48.5%; Score 511; DB 2; Length 500;
Best Local Similarity 51.2%; Pred. No. 1,1e-37;
Matches 104; Conservative 25; Mismatches 60; Indels 14; Gaps 5;

Qy 1 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGMNPNNGNTGYAOKFQGRVT 60
Db |||||:||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
29 EVMSPGASVRVSKTSGYAFHTYSIIWVRQAPGQGLEWMGWI SPSSDNTREFAKKFQGRVT 88
Qy 61 MTRNTSISTAYWELSLRSEDYAVYICAREEWLVR-----YIGMDYWGQGTITVTVSSG 113
Db :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
89 LTDTSTSTVYMELSRLSRDDTAVYICARYCSYSSCQNDYIIYYTMDYWGKGTITVTVSSA 148
Qy 114 SASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLP--DSITFSWKYKNNSDISSTRGFP--S 170
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
149 SPTSPKVPFLSLCSTQPD--GNVVIACLIVQGFPPQEPPLSVTWSESGQG--VTARNFPFPSQ 204
Qy 171 VLRGKYAATSQVLLPSKDVMOG 193
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
205 DASGDLTTSSQLTLPATQCLAG 227
```

Search completed: March 8, 2005, 06:35:50  
Job time : 75.3165 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 92.2618 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-29

Perfect score: 1054

Sequence: 1 EVKPGASVKVSCRASGYTF.....TSQVLLPSKDVQGTDEHKV 199

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A: Geneseq 16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1054	100.0	199	2	AAY34302 IgM antib
2	985	93.5	203	2	AAY34301 IgM antib
3	873.5	82.9	588	2	Aaw71880 Anti-huma
4	873.5	82.9	588	3	AAB12917 Anti-huma
5	870	82.5	627	7	ADP84970 Chimeric
6	859.5	81.5	588	2	Aaw71881 Anti-huma
7	859.5	81.5	588	3	AAB12918 Anti-huma
8	803	76.2	266	8	ADP69305 Human lun
9	766.5	72.7	571	8	ADL70776 Anti-TNFA
10	755	71.6	228	8	ADL70776 Anti-TNFA
11	750.5	71.2	223	2	AAY08598 Anti-huma
12	749.5	71.1	595	7	ADM05427 Human pro
13	744.5	70.6	223	8	ADL70773 Anti-TNFA
14	742.5	70.4	596	4	AAM23324 Human EST
15	707.5	67.1	205	2	AAY34299 IgM antib
16	707.5	67.1	533	7	ADB65070 Human pro
17	702	66.6	570	8	ADR19329 Chimeric
18	701.5	66.6	569	8	ADR19330 Chimeric
19	698	66.2	197	2	AAY34300 IgM antib
20	682.5	64.8	202	2	AAY34303 IgM antib
21	673.5	63.9	190	2	AAY34304 IgM antib
22	643	61.0	476	2	AAW88464 Monoclonal
23	635	60.2	590	2	Aaw31751 H chain s
24	635	60.2	590	2	Aaw71888 Anti-huma
25	635	60.2	590	3	AAB12908 Anti-huma

25	609.5	57.8	228	6	ABR01526 Human ant
26	602.5	57.2	430	6	ABR01514 Human ant
28	600	56.9	470	5	AAU74296 Anti-huma
29	598	56.7	221	6	ABR01537 Human ant
30	594.5	56.4	471	7	ADP84967 Murine an
31	592	56.2	576	8	ADP69325 Murine lun
32	586	55.6	571	8	ADP84967 Murine an
33	582	55.2	573	8	ADP84968 Murine an
34	574	54.5	451	8	ADR23348 Human CD7
35	571	54.2	451	8	ADR23350 Human CD7
36	559.5	53.1	125	7	ADK18814 Anti-huma
37	559.5	53.1	126	7	ADK18864 Anti-huma
38	559.5	53.1	126	7	ADK18595 Anti-huma
39	559.5	53.1	126	7	ADK18777 Anti-huma
40	559.5	53.1	126	8	ADL25408 Human mAb
41	553.5	52.5	126	7	ADK18597 Anti-huma
42	553.5	52.5	126	7	ADK18870 Anti-huma
43	553.5	52.5	126	7	ADK18812 Anti-huma
44	553.5	52.5	126	7	ADK18775 Anti-huma
45	553.5	52.5	126	8	ADL25412 Human mAb

## ALIGNMENTS

RESULT 1  
AAY34302  
ID AAY34302 standard; protein; 199 AA.  
XX  
AC AAY34302;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE IgM antibody CEM 10.12 G5 heavy chain sequence.

KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

PN WO9945031-A2.

XX  
PD 10-SEP-1999.

XX  
PF 03-MAR-1999; 99WO-US004583.

PR 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX  
(ABGE-) ABGENIX INC.

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX  
WPI; 1999-540816/45.

XX  
N-PSDB; AA220403.

XX  
New monoclonal antibody, used for treating e.g. graft versus host

XX  
disease, cancers, autoimmune diseases and inflammatory diseases.

XX  
Claim 60; Fig 27; 245pp; English.

CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (mAb) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IgM mAb ABX-CBL, providing that the antibody is not CBL1. The mAb  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood



XX WPI: 1998-482965/42.  
 DR N-PSDB; AAV61363.  
 XX  
 PT Production of anti-Fas protein humanised antibodies - for use in inducing  
 PT apoptosis on Fas expressing cells in the treatment of auto:immune  
 PT diseases, especially rheumatoid arthritis.  
 XX  
 PS Claim 21; Page 105-107; 187pp; English.  
 XX  
 CC This is the amino acid sequence of a humanised anti-Fas antibody CH11  
 CC heavy chain, designated HmuH. HmuH is based on the heavy chain (see  
 CC AAW71889) of murine anti-human Fas monoclonal antibody CH11. The  
 CC humanised sequence was designed following selection of donor residues  
 CC from CH11 to be grafted onto acceptor molecule 21.28'Cb. 2 Heavy chain  
 CC sequences (see AAW71880-81) have been designed, and each can be used in  
 CC combination with any of 4 light chain sequences (see AAW71876-79) to  
 CC provide novel, claimed humanised CH11 IgM antibodies that lack a J chain.  
 CC These humanised anti-human Fas antibodies are capable of inducing  
 CC apoptosis in cells expressing Fas (e.g. synoviocytes) and are useful in  
 CC the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA  
 CC sequences encoding the humanised antibodies are claimed, as are vectors  
 CC such as pMuH5-1 including the HmuH nucleotide sequence (see AAV61363),  
 CC and host cells such as Escherichia coli pMuH5-1 (PERM BP-5863)  
 XX  
 XX Sequence 588 AA;  
 SQ  
 Query Match 82.9%; Score 873.5; DB 2; Length 588;  
 Best Local Similarity 84.4%; Pred. No. 6.2e-55;  
 Matches 168; Conservative 10; Mismatches 16; Indels 5; Gaps 1;  
 QY 1 EVKPGASVKVSKAGSYFTTSDINWVRQATGQGLEWGWGMPNSGNTGYAQKQGRVT 60  
 DB 29 EVKPGASVKVSKAGSYFTTSDINWVRQATGQGLEWGWGMPNSGNTGYAQKQGRVT 88  
 QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEWLVRYGMDVWGQGTITVTVSSGSASAPTL 120  
 DB 89 LTVDSASTAYMELSLRSEDVAVYCARAEWLVRYGMDVWGQGTITVTVSSGSASAPTL 143  
 QY 121 PFLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAAT 180  
 DB 144 PFLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAAT 203  
 QY 181 SQVLLPSKDVMOGTDEHKV 199  
 DB 204 SQVLLPSKDVMOGTDEHVV 222  
 RESULT 4  
 AAB12917  
 ID AAB12917 standard; protein; 588 AA.  
 XX  
 AC AAB12917;  
 XX  
 DT 16-NOV-2000 (first entry)  
 XX  
 DE Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #86.  
 DE  
 KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
 KW immunosuppression; autoimmune disease; treatment; rheumatism;  
 KW anti-Fas antibody.  
 XX  
 OS Synthetic.  
 OS  
 XX JP2000154149-A.  
 PN  
 XX 06-JUN-2000.  
 PD  
 PF 17-SEP-1999; 99JP-00263984.  
 XX  
 PR 18-SEP-1998; 98JP-00264598.  
 XX  
 PA (SANY ) SANKYO CO LTD.

XX WPI: 2000-454476/40.  
 DR N-PSDB; AAA78271.  
 XX  
 PT Anti-human Fas humanizing antibody-containing antirheumatic agents.  
 PT  
 PS Claim 1; Page 75-77; 109pp; Japanese.  
 XX  
 CC The present invention relates to antirheumatic agents which comprise as  
 CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
 CC does not include a J segment, has apoptosis inducing activity, and  
 CC consists of a light and heavy chain polypeptide produced synthetically.  
 CC The agents of the invention exhibit antirheumatic and immunosuppressive  
 CC activity and can be used to treat autoimmune diseases, especially  
 CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
 CC binding properties. Included in the invention are nucleotide sequences of  
 CC the IgM light and heavy chains (see AAA78267-A78272) and the  
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
 CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also  
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
 CC chains used in the invention are represented by sequences AAA78213-  
 CC A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AAA78277-A78318 and AAA78335-  
 CC A78337, while humanised anti-Fas Ig DNA sequencing primers are  
 CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer  
 CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in  
 CC the production of the agent of the invention  
 XX  
 XX Sequence 588 AA;  
 SQ  
 Query Match 82.9%; Score 873.5; DB 3; Length 588;  
 Best Local Similarity 84.4%; Pred. No. 6.2e-55;  
 Matches 168; Conservative 10; Mismatches 16; Indels 5; Gaps 1;  
 QY 1 EVKPGASVKVSKAGSYFTTSDINWVRQATGQGLEWGWGMPNSGNTGYAQKQGRVT 60  
 DB 29 EVKPGASVKVSKAGSYFTTSDINWVRQATGQGLEWGWGMPNSGNTGYAQKQGRVT 88  
 QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEWLVRYGMDVWGQGTITVTVSSGSASAPTL 120  
 DB 89 LTVDSASTAYMELSLRSEDVAVYCARAEWLVRYGMDVWGQGTITVTVSSGSASAPTL 143  
 QY 121 PFLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAAT 180  
 DB 144 PFLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAAT 203  
 QY 181 SQVLLPSKDVMOGTDEHKV 199  
 DB 204 SQVLLPSKDVMOGTDEHVV 222  
 RESULT 5  
 ADE97370  
 ID ADE97370 standard; protein; 627 AA.  
 XX  
 AC ADE97370;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human immunoadhesin-related protein - SEQ ID 47.  
 DE  
 KW immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;  
 KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;  
 KW intercellular adhesion molecule; ICAM-1; human.  
 XX  
 OS Homo sapiens.  
 OS  
 XX WO2003064992-A2.  
 PN  
 XX 07-AUG-2003.  
 PD  
 XX





```
Db      204 SQVLLPSKDVMOGTDHVV 222
RESULT 7
ID      AAB12918
AA      AAB12918 standard; protein; 588 AA.
XX
XX      AAB12918;
AC
DT      16-NOV-2000 (first entry)
DE
DE      Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #89.
XX
XX      Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
KW      immunosuppression; autoimmune disease; treatment; rheumatism;
KW      anti-Fas antibody.
XX
XX      Synthetic.
OS
XX      JP2000154149-A.
FN
PD
PD      06-JUN-2000.
XX
XX      17-SEP-1999; 99JP-00263984.
PF
XX
XX      18-SEP-1998; 98JP-00264598.
PR
XX
XX      (SANY ) SANKYO CO LTD.
PA
XX
XX      WPI; 2000-454476/40.
DR
DR      N-PSDB; AAB78272.
XX
PT      Anti-human Fas humanizing antibody-containing antirheumatic agents.
XX
PS      Claim 1; Page 80-81; 109pp; Japanese.
XX
CC      The present invention relates to antirheumatic agents which comprise as
CC      active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC      does not include a J segment, has apoptosis inducing activity, and
CC      consists of a light and heavy chain polypeptide produced synthetically.
CC      The agents of the invention exhibit antirheumatic and immunosuppressive
CC      activity and can be used to treat autoimmune diseases, especially
CC      rheumatism. The IgM molecule used in the invention has human Fas-antigen
CC      binding properties. Included in the invention are nucleotide sequences of
CC      the IgM light and heavy chains (see AAB78267-A78272) and the
CC      corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
CC      nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
CC      AAB78202-A78206) and protein sequences (see AAB12908-B12910). Also
CC      included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
CC      Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC      chains used in the invention are represented by sequences AAB78213-
CC      A78266. Primers used for sequencing the human Ig DNA used in the
CC      invention are represented by sequences AAB78277-A78318 and AAB78335-
CC      A78337, while humanised anti-Fas Ig DNA sequencing primers are
CC      represented by sequences AAB78321-A78334 and AAB78338-A78367. Primer
CC      sequences AAB78207-A78212 are specific for murine Ig DNA, and are used in
CC      the production of the agent of the invention
XX
SQ      Sequence 588 AA;
Query Match      81.5%; Score 859.5; DB 3; Length 588;
Best Local Similarity 82.9%; Pred. No. 6.4e-54;
Matches 165; Conservative 12; Mismatches 17; Indels 5; Gaps 1;
QY      1 EVKPGASVKYCKASGYTFTSYDINWVROATGCGLEWGMWNPNSGNTGYAQKFGQRYT 60
DB      29 EVKPGASVKYCKASGYTFTSYDINWVROATGCGLEWGMWNPNSGNTGYAQKFGKAT 88
QY      61 MTRNTSISTAYMELSLRSEDTAVYICAREEVLRYGYMDVMOGQTTTVTSSGSASAPTL 120
DB      89 LTVDSASTAYMELSLRSEDTAVYICARS-----YYANDYMGQQTTLTVSSGSASAPTL 143
QY      121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLRGGKYAAT 180

Db      144 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLRGGKYAAT 203
QY      181 SQVLLPSKDVMOGTDHVKV 199
DB      204 SQVLLPSKDVMOGTDHVV 222
RESULT 8
ID      ADF69305
AA      ADF69305 standard; protein; 266 AA.
XX
XX      ADF69305;
AC
DT      26-FEB-2004 (first entry)
DE
DE      Human lung specific protein sequence SEQ ID NO:62.
XX
XX      human; lung specific nucleic acid; lung specific protein; lung cancer;
KW      cytostatic; gene therapy.
XX
XX      Homo sapiens.
OS
XX      WO2003102137-A2.
FN
PD
PD      11-DEC-2003.
XX
XX      30-MAY-2003; 2003WO-US016810.
PF
XX
XX      31-MAY-2002; 2002US-0385301P.
PR
XX
XX      (DIAD-) DIADEXUS INC.
PA
XX
XX      Chen S, Macina RA, Sun Y, Liu C, Turner LR;
PI
XX      WPI; 2004-053457/05.
DR
XX
XX      New human lung specific nucleic acid, useful for preparing a composition
XX      for diagnosing or treating lung cancer.
PS      Claim 11; SEQ ID NO 62; 221pp; English.
XX
CC      The present invention describes a human lung specific nucleic acid
CC      molecule. Also described: (1) a method for determining the presence of a
CC      lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising
CC      the nucleic acid molecule; (3) a host cell comprising the vector; (4) a
CC      method for producing a polypeptide encoded by the nucleic acid molecule;
CC      (5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody
CC      or its fragment that specifically binds to the polypeptide; (7) a method
CC      for determining the presence of a lung specific protein in a sample; (8)
CC      a method for diagnosing and monitoring the presence and metastases of
CC      lung cancer in a patient; (9) a kit for detecting a risk of cancer or
CC      presence of cancer in a patient comprising a means for determining the
CC      presence the nucleic acid molecule or polypeptide in a sample of a
CC      patient; (10) a method of treating a patient with lung cancer; and (11) a
CC      vaccine comprising the polypeptide or the nucleic acid encoding the
CC      polypeptide. Human LSNA molecules and related proteins have cytostatic
CC      activity, and can be used in gene therapy. They are useful for preparing
CC      a composition for diagnosing or treating lung cancer. The present
CC      sequence represents a human lung specific protein, which is used in the
XX      exemplification of the present invention.
XX
SQ      Sequence 266 AA;
Query Match      76.2%; Score 803; DB 8; Length 266;
Best Local Similarity 76.9%; Pred. No. 3.4e-50;
Matches 153; Conservative 18; Mismatches 28; Indels 0; Gaps 0;
QY      1 EVKPGASVKYCKASGYTFTSYDINWVROATGCGLEWGMWNPNSGNTGYAQKFGQRYT 60
DB      21 EVKPGESLKISCKSGSYFTSYWIGWRQMPGKLEWNGIYPGDSIDTRYSPFSGQQT 80
QY      61 MTRNTSISTAYMELSLRSEDTAVYICAREEVLRYGYMDVMOGQTTTVTSSGSASAPTL 120
```

Db 81 ISADKISTAVLQWSSLSKASDTAMTCARPIAVAGHYFYVWGQTLTVTVSSGSASAPTL 140  
Qy 121 FPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSRGPSPVLRGGKYAAT 180  
Db 141 FPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSRGPSPVLRGGKYAAT 200  
Qy 181 SQVLLPSKDVMOGTDDEHKV 199  
Db 201 SQVLLPSKDVMOGTDDEHV 219

RESULT 9  
ADP84970  
ID ADP84970 standard; protein; 571 AA.  
XX ADP84970;  
XX 09-SEP-2004 (first entry)  
XX Chimeric antibody c1gM-kar04.  
XX antibody; Core-1 antigen; framework region; immunoglobulin superfamily;  
KW protease inhibitor; lectin; helix-bundle protein; lipocalin;  
KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;  
KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;  
KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;  
KW metastasis.  
XX Mus musculus.  
XX WO2004050707-A2.  
XX 17-JUN-2004.  
XX 01-DEC-2003; 2003WO-DE003994.  
XX 29-NOV-2002; 2002DE-01056900.  
XX (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.  
XX Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;  
PI Christensen PA;  
XX WPI; 2004-461095/43.  
XX New recognition molecules, e.g. antibodies (and nucleic acids) that bind  
PT specifically to Core-1 antigens, useful for diagnosis, treatment and  
PT prevention of tumors and metastases.  
XX Claim 26; SEQ ID NO 112; 136pp; German.

XX This invention describes novel recognition molecules, especially  
CC antibodies that bind specifically to the Core-1 antigen. The recognition  
CC molecules are used to make constructs containing the framework regions  
CC that separate, include and/or flank the specified sequences, especially  
CC where the framework regions are from the immunoglobulin (Ig) superfamily,  
CC protease inhibitors, lectins, helix-bundle proteins and/or lipocalins.  
CC Most especially the framework regions are from antibodies, particularly  
CC the variable heavy chain (VH) and the variable light chain (VL) of human  
CC and/or murine origin. The constructs may also include a His or myc tag, a  
CC lysine-rich region and/or a multimerisation domain, most particularly it  
CC is a single-chain antibody fragment, multibody, Fab fragment, fusion  
CC protein of an antibody fragment with peptide or protein, and/or an Ig of  
CC types G, M, A, E or D and/or their subclasses. It may be human,  
CC humanised, murine or chimeric, e.g. IgM without the J chain. The  
CC additional sequences/structures in the constructs are Ig domains of  
CC various species, interacting or stabilising domains, signal sequences,  
CC fluorescent dyes, toxins, antibodies with catalytic activity or other  
CC specificities, cytolytic agents, enzymes, immuno-modulators or -  
CC effectors, MHC molecules, antigens, chelators for radioactive labels,  
CC liposomes, transmembrane domains, viruses and/or cells, specifically  
CC macrophages. The antibodies, also constructs containing them, nucleic

CC acid encoding them, and related vectors and host cells, are useful for  
CC prevention (e.g. as vaccine), diagnosis, alleviation, treatment,  
CC monitoring and/or secondary treatment of tumours (specifically of breast,  
CC colon, stomach, pancreas, large/small intestine, ovary, cervix, lung,  
CC prostate, kidney and/or liver) and/or metastases (particularly to liver),  
CC specifically where these are positive for the CI antigen. The products of  
CC the invention provide simple, reliable and efficient detection of  
CC tumours. They are specific for carcinoma and show almost no binding to  
CC healthy tissue.

XX Sequence 571 AA;

Query Match 72.7%; Score 766.5; DB 8; Length 571;  
Best Local Similarity 74.0%; Pred. No. 3.2e-47;  
Matches 151; Conservative 16; Mismatches 24; Indels 13; Gaps 3;  
Qy 1 EVKPKGASVKYCKASGYTFTSYDINWVROATGQGLEWMMWNPNSGNTGYAQKFGQRTV 60  
Db 10 ELVRPGTSVKISCKASGYTFYTNWLGWVKQRPQGHLEWIGDIYPGGGTYNNEKFKGKAT 69  
Qy 61 MTRNTSISTAYMELSSLRSEDTAVVYCAREEMLVRYG-----MDVMGQGITTVTVSSGSA 115  
Db 70 LTADTSSSTAMQSLTSEDSANVFCA-----YYDAAGPWFAYWGQTTTVTVSSGA 121  
Qy 116 SAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSRGPSPVLRGG 175  
Db 122 SAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITLSWKYKNNSDISSRGPSPVLRGG 181  
Qy 176 KYAATSQVLLPSKDVMOGTDDEHKV 199  
Db 182 KYAATSQVLLPSKDVMOGTDDEHV 205

RESULT 10  
ADL70776  
ID ADL70776 standard; protein; 228 AA.  
XX ADL70776;  
XX 03-JUN-2004 (first entry)  
XX Anti-TNFalpha antibody VH region, SEQ ID 49.  
XX Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;  
KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;  
KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnerary;  
KW Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antiatherosclerotic;  
KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;  
KW Tf; transferrin fusion protein; Tf fusion protein; anti-TNFalpha;  
KW antibody; VH region.  
XX Unidentified.  
XX WO2004020588-A2.  
XX 11-MAR-2004.  
XX 28-AUG-2003; 2003WO-US026779.  
XX 30-AUG-2002; 2002US-0406977P.  
PR 10-MAR-2003; 2003US-00384060.  
PR 09-JUL-2003; 2003US-0485404P.  
XX (BIOR-) BIOREXIS PHARM CORP.  
XX Prior CP, Turner AJ, Sadeghi H;  
XX WPI; 2004-239175/22.  
XX Novel library containing several fusion proteins each of which comprises  
PT first transferrin polypeptide fused to at least one second peptide,  
PT useful for screening for transferrin fusion protein having the particular  
PT activity.





```
RESULT 14
AAM23924
ID AAM23924 standard; protein; 596 AA.
XX
AC AAM23924;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1449.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX
Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
WPI: 2001-476164/51.
DR N-PSDB; AAM98583.
XX
Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
Claim 20; Page 1011-1012; 1275pp; English.
XX
The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
Sequence 596 AA;
Query Match 70.4%; Score 742.5; DB 4; Length 596;
Best Local Similarity 71.4%; Pred. No. 1.8e-45;
Matches 142; Conservative 25; Mismatches 29; Indels 3; Gaps 1;
QY 4 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTVMT 63
DB 32 QPGSURLSCASGFTSSYWMHWVQAPQKGLVWVSRINTDGSSTSYADSVKGRFTISR 91
QY 64 NTSISTAYMELSLRSEDYAVYCAR--YYGMDVMGQGTITVTVSSGSASAPTL 120
DB 92 DNAKNTLYLQMSLRAEDYAVYCARADNCSSYSCYKCFDYMGQGLTVTVSSGSASAPTL 151
QY 121 PFLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFFSVLGGKYAT 180
DB 152 PFLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFFSVLGGKYAT 211
QY 181 SQVLLPSKDVMOGTDEHKV 199
DB 212 SQVLLPSKDVMOGTDEHV 230
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```
RESULT 15
AAY34299
ID AAY34299 standard; protein; 205 AA.
XX
AC AAY34299;
XX
DT 19-NOV-1999 (first entry)
XX
DE IgM antibody CEM 10.1 C3 heavy chain sequence.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 150
FT /label= unknown
FT /note= "encoded by TYC"
XX
WO9945031-A2.
XX
10-SEP-1999.
XX
03-MAR-1999; 99WO-US004583.
XX
03-MAR-1998; 98US-00034607.
XX
03-FEB-1999; 99US-0024253.
XX
(ABGE-) ABGENIX INC.
XX
Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
WPI: 1999-540816/45.
DR N-PSDB; AAZ20400.
XX
New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
Claim 60; Fig 24; 245pp; English.
XX
This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
Sequence 205 AA;
Query Match 67.1%; Score 707.5; DB 2; Length 205;
Best Local Similarity 70.7%; Pred. No. 2e-43;
Matches 140; Conservative 23; Mismatches 32; Indels 3; Gaps 2;
QY 4 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTVMT 63
DB 4 KSETLSLTCVYGGSGFYYSWIRQPPKGLWIGBIN-HSGSTNYNPSPSKSRVTISV 62
QY 64 NTSISTAYMELSLRSEDYAVYCAR--BEWLVRYYGMDVMGQGTITVTVSSGSASAPTL 121
DB 63 DTSKNQPSLKLSSVTAADYAVYCARGTTEYYYYYGMVDMVGQGTITVTVSSGSASAPTL 122
QY 122 PFLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFFSVLGGKYAATS 181
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Db 123 PLVSCENSPDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVLRGGKYAATS 182  
Qy 182 QVLLPSKDVMOGTDEHKV 199  
Db 183 QVLLPSKDVMOGTDEHV 200

Search completed: March 8, 2005, 06:17:12  
Job time : 93.2618 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 105.604 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-29  
Perfect score: 1054  
Sequence: 1 EVKPGASVKVSKASGYTF.....TSQVLLPSKDVNQGTDEHKV 199

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCT05\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	870	82.5	627	13	US-10-047-542-47 Sequence 47, Appl
2	749.5	71.1	595	15	US-10-108-260A-4112 Sequence 4112, Ap
3	707.5	67.1	533	15	US-10-104-047-3224 Sequence 3224, Ap
4	643	61.0	476	9	US-09-747-669-3 Sequence 3, Appli
5	643	61.0	476	14	US-10-290-703-3 Sequence 3, Appli
6	609.5	57.8	228	16	US-10-128-520-163 Sequence 163, App
7	602.5	57.2	230	16	US-10-128-520-151 Sequence 151, App
8	600	56.9	470	9	US-09-859-053-28 Sequence 28, Appl
9	600	56.9	470	16	US-10-625-105-28 Sequence 28, Appl
10	598	56.7	221	16	US-10-128-520-174 Sequence 174, Appl
11	594.5	56.4	471	15	US-10-292-088-45 Sequence 46, Appl
12	559.5	53.1	125	14	US-10-041-860-238 Sequence 238, App
13	559.5	53.1	126	14	US-10-041-860-19 Sequence 19, Appl

14	559.5	53.1	126	14	US-10-041-860-201 Sequence 201, App
15	559.5	53.1	126	14	US-10-041-860-288 Sequence 288, App
16	559.5	53.1	126	16	US-10-665-383-18 Sequence 18, Appl
17	559	53.0	448	9	US-09-917-410-6 Sequence 6, Appli
18	553.5	52.5	126	14	US-10-041-860-21 Sequence 21, Appl
19	553.5	52.5	126	14	US-10-041-860-199 Sequence 199, App
20	553.5	52.5	126	14	US-10-041-860-236 Sequence 236, App
21	553.5	52.5	126	14	US-10-041-860-294 Sequence 294, App
22	553.5	52.5	126	16	US-10-665-383-22 Sequence 22, Appl
23	549.5	52.1	126	14	US-10-041-860-40 Sequence 40, Appl
24	549.5	52.1	126	14	US-10-041-860-204 Sequence 204, App
25	549.5	52.1	126	14	US-10-041-860-241 Sequence 241, App
26	549.5	52.1	126	14	US-10-041-860-349 Sequence 349, App
27	549.5	52.1	126	16	US-10-665-383-58 Sequence 58, Appl
28	549	52.1	125	14	US-10-041-860-38 Sequence 38, Appl
29	549	52.1	125	14	US-10-041-860-203 Sequence 203, App
30	549	52.1	125	14	US-10-041-860-240 Sequence 240, App
31	549	52.1	125	14	US-10-041-860-343 Sequence 343, App
32	549	52.1	125	16	US-10-665-383-54 Sequence 54, Appl
33	546.5	51.9	122	14	US-10-289-805-61 Sequence 61, Appl
34	545.5	51.8	230	10	US-09-791-153A-53 Sequence 53, Appl
35	545.5	51.8	230	10	US-09-791-153A-55 Sequence 55, Appl
36	545	51.7	470	14	US-10-216-484-157 Sequence 157, App
37	545	51.7	470	14	US-10-384-933-157 Sequence 157, App
38	544.5	51.7	461	9	US-09-249-011A-24 Sequence 24, Appl
39	544.5	51.7	1052	17	US-10-856-272-21 Sequence 21, Appl
40	544.5	51.7	1342	17	US-10-856-272-14 Sequence 14, Appl
41	543.5	51.6	126	14	US-10-041-860-37 Sequence 37, Appl
42	543.5	51.6	126	14	US-10-041-860-202 Sequence 202, App
43	543.5	51.6	126	14	US-10-041-860-239 Sequence 239, App
44	543.5	51.6	126	16	US-10-665-383-74 Sequence 74, Appl
45	543.5	51.6	220	16	US-10-128-520-175 Sequence 175, App

ALIGNMENTS

RESULT 1

US-10-047-542-47  
; Sequence 47, Application US/10047542  
; Publication No. US20020168367A1  
; GENERAL INFORMATION:  
; APPLICANT: LARRICK, JAMES W.  
; APPLICANT: WYCOFF, KEITH L.  
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
; TITLE OF INVENTION: AND BACTERIAL DISEASES  
; FILE REFERENCE: 030905.0004.CIPI  
; CURRENT APPLICATION NUMBER: US/10/047,542  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: PCT/US01/13932  
; PRIOR FILING DATE: 2001-04-28  
; PRIOR APPLICATION NUMBER: 60/200,298  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 627  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-047-542-47

Query Match	82.5%	Score	870	DB	13	Length	627
Best Local Similarity	82.0%	Pred. No.	3.6e-56				
Mismatches	173	Conservative	7	Mismatches	19	Indels	12
Gaps	2						
Qy	1	EVKPGASVKVSKASGYTFSTYDINWRQATCGGLEWGNWNPNSGVTGYAQKFGQRTV	60				
Db	29	EVKPGSSVKVSKASGCTPSSVAISWVRQAPGQLEWMGGIPIFGTANYAQKFGQRTV	88				
Qy	61	MTRNTSISTAYMELSSLRSEDATVAVYCAR-----BEWLV-----YGMVDVWGQTTV	108				
Db	89	ITADESTAYMELSSLRSEDATVAVYCAR-----BEWLV-----YGMVDVWGQTTV	148				

QY 109 TVSSGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGF 168  
Db 149 TVSSGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGF 208  
QY 169 PSVLGGKYAATSOVLLPSKDVMOGTDEHKV 199  
Db 209 PSVLGGKYAATSOVLLPSKDVMOGTDEHV 239

RESULT 2  
US-10-108-260A-4112  
; Sequence 4112, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1el full length cdna  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4112  
; LENGTH: 595  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-108-260A-4112

Query Match 71.1%; Score 749.5; DB 15; Length 595;  
Best Local Similarity 71.6%; Pred. No. 2.6e-47;  
Matches 141; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

QY 4 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTVWTR 63  
Db 33 QPGSLRLSCAASGTFPSFAHWVRQAPGKGLVYSIISNGRQKYIGESVKGRFTISR 92  
QY 64 NTSISTAYMELSLRSEDPAVYICAREEWLRY-YGMVDVWGQTTTVTSSGSASAPTLFP 122  
Db 93 DSSKNTLPQMGSLREDTPAVYICARGHSIDNHYGVGVWGQTTTVTSSGSASAPTLFP 152  
QY 123 LVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQ 182  
Db 153 LVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQ 212  
QY 183 VLLPSKDVMOGTDEHKV 199  
Db 213 VLLPSKDVMOGTDEHV 229

RESULT 3  
US-10-104-047-3224  
; Sequence 3224, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cdna  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3224  
; LENGTH: 533  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3224

Query Match 67.1%; Score 707.5; DB 15; Length 533;  
Best Local Similarity 70.3%; Pred. No. 2.9e-44;  
Matches 142; Conservative 21; Mismatches 28; Indels 11; Gaps 4;  
QY 4 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTVWTR 63

Db 32 QPGSLRLSCAASGTFPSNTYMSWRQSPGKPEWATMY-GGGNTYYAESVKGRFTYSR 90  
QY 64 NTSISTAYMELSLRSEDPAVYICAREEWLRYVYGMVDV-----WGQGTTVTVSSGSASA 117  
Db 91 DGSQNTLYLEMSLRPDDTAVYICVRDH---RNVA-DTSPYGRKWGQGTTLTVSSGSASA 146  
QY 118 PTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKY 177  
Db 147 PTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKY 206  
QY 178 AATSOVLLPSKDVMOGTDEHKV 199  
Db 207 AATSOVLLPSKDVMOGTDEHV 228

RESULT 4  
US-09-747-669-3  
; Sequence 3, Application US/09747669  
; Patent No. US20020122807A1  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Saleh, Mansoor  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED  
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES  
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS  
; TITLE OF INVENTION: AND DETECTION OF CANCERS  
; FILE REFERENCE: 316082001001  
; CURRENT APPLICATION NUMBER: US/09/747,669  
; CURRENT FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: US 09/111,286  
; PRIOR FILING DATE: 1998-07-07  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 476  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-747-669-3

Query Match 61.0%; Score 643; DB 9; Length 476;  
Best Local Similarity 62.7%; Pred. No. 1.5e-39;  
Matches 128; Conservative 21; Mismatches 43; Indels 12; Gaps 5;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 60  
Db 29 EVKPGASVKVSKASGYTFTSFDLNWVRQAPGQGLEWGMWNPNSGKTGYAQKFGQRTV 88  
QY 61 MTRNTSISTAYMELSLRSEDPAVYICARE-----EWLVRYGMVDVWGQGTTVTVSSGS 114  
Db 89 MTRNTSISTAYMELSGLRSEDPAVYFCARNADNVEMAAIHYHYGMVDVWGQGTTVTVSSAS 148  
QY 115 ASAPTFLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR- 173  
Db 149 TKGPSVFFPLAPSCKSTSG-GTAAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQS 205  
QY 174 GGYKAATSOVLLPSKDVMOGTDEH 197  
Db 206 SGLYSLSVTVTVPPSSSL--GTQTY 227

RESULT 5  
US-10-290-703-3  
; Sequence 3, Application US/10290703  
; Publication No. US20030118593A1  
; GENERAL INFORMATION:  
; APPLICANT: Dan, Michael D.  
; APPLICANT: Saleh, Mansoor  
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED  
; TITLE OF INVENTION: 4B5, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES  
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS



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; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001002
; CURRENT APPLICATION NUMBER: US/10/290,703
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/747,669
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/051,945
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-290-703-3

Query Match      61.0%; Score 643; DB 14; Length 476;
Best Local Similarity 62.7%; Pred. No. 1.5e-39;
Matches 128; Conservative 21; Mismatches 43; Indels 12; Gaps 5;

QY 1 EVKXPGASVKVSKASGYFTSYDINWVRQATGQGLEWGNWNPNSGNTGYAQQKQGRVT 60
DB 29 EVKXPGASVKVSKASGYFTSYDINWVRQATGQGLEWGNWNPNSGNTGYAQQKQGRVT 88
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARLGVGKPDDELYFDVWGQGLTVTVSSGS 114
DB 89 MTRNTSISTAYMELSLRSEDVAVYCARLGVGKPDDELYFDVWGQGLTVTVSSGS 148
QY 115 ASAPTLPFLVSCENSPDTSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVL-R 173
DB 149 TKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQSS 205
QY 174 GKYAATSQVLLPSKDVMOGTDEH 197
DB 206 SGLYSLSSVTVTPSSSL--GTQTY 227

RESULT 6
US-10-128-520-163
; Sequence 163, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-163

Query Match      57.8%; Score 609.5; DB 16; Length 228;
Best Local Similarity 61.6%; Pred. No. 2.2e-37;
Matches 125; Conservative 23; Mismatches 42; Indels 13; Gaps 6;

QY 1 EVKXPGASVKVSKASGYFTSYDINWVRQATGQGLEWGNWNPNSGNTGYAQQKQGRVT 60
DB 10 EVKXPGASVKVSKASGYFTSYDINWVRQATGQGLEWGNWNPNSGNTGYAQQKQGRVT 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARLGVGKPDDELYFDVWGQGLTVTVSSGS 115
DB 70 MTRNTSISTAYMELSLRSEDVAVYCARLGVGKPDDELYFDVWGQGLTVTVSSAST 127

; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001002
; CURRENT APPLICATION NUMBER: US/10/290,703
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/747,669
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/051,945
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-290-703-3

Query Match      61.0%; Score 643; DB 14; Length 476;
Best Local Similarity 62.7%; Pred. No. 1.5e-39;
Matches 128; Conservative 21; Mismatches 43; Indels 12; Gaps 5;

QY 1 EVKXPGASVKVSKASGYFTSYDINWVRQATGQGLEWGNWNPNSGNTGYAQQKQGRVT 60
DB 29 EVKXPGASVKVSKASGYFTSYDINWVRQATGQGLEWGNWNPNSGNTGYAQQKQGRVT 88
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARLGVGKPDDELYFDVWGQGLTVTVSSGS 114
DB 89 MTRNTSISTAYMELSLRSEDVAVYCARLGVGKPDDELYFDVWGQGLTVTVSSGS 148
QY 115 ASAPTLPFLVSCENSPDTSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVL-R 173
DB 149 TKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQSS 205
QY 174 GKYAATSQVLLPSKDVMOGTDEH 197
DB 206 SGLYSLSSVTVTPSSSL--GTQTY 227

RESULT 6
US-10-128-520-163
; Sequence 163, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-163

Query Match      57.8%; Score 609.5; DB 16; Length 228;
Best Local Similarity 61.6%; Pred. No. 2.2e-37;
Matches 125; Conservative 23; Mismatches 42; Indels 13; Gaps 6;

QY 1 EVKXPGASVKVSKASGYFTSYDINWVRQATGQGLEWGNWNPNSGNTGYAQQKQGRVT 60
DB 10 EVKXPGASVKVSKASGYFTSYDINWVRQATGQGLEWGNWNPNSGNTGYAQQKQGRVT 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARLGVGKPDDELYFDVWGQGLTVTVSSGS 115
DB 70 MTRNTSISTAYMELSLRSEDVAVYCARLGVGKPDDELYFDVWGQGLTVTVSSAST 127

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
```

```

; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match      56.9%; Score 600; DB 9; Length 470;
Best Local Similarity 58.9%; Pred. No. 2.2e-36;
Matches 123; Conservative 26; Mismatches 44; Indels 16; Gaps 7;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60
DB 29 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 88
QY 61 MTRNTSISTAYMELSLRSEDATVAYYCAREEWL--VRY--GMDVWGQGTWTVTVSSGAS 116
DB 89 MTRDTSISTAYMELSLRSDATVAYYCARTYYDSSGYHDAFDIWGQGTWTVTVSSASTK 148
QY 117 APTLPFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR-GG 175
DB 149 GPSVFLAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSG 205
QY 176 KYAATSOVLPLPSKDYVMQGT-----EHK 198
DB 206 LYSLSVVTVPPSNF--GTQTYTCNVDHK 232

RESULT 9
US-10-625-105-28
; Sequence 28, Application US/10625105
; Publication No. US20040180052A1
; GENERAL INFORMATION:
; APPLICANT: Teuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/10/625,105
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-625-105-28

Query Match      56.9%; Score 600; DB 16; Length 470;
Best Local Similarity 58.9%; Pred. No. 2.2e-36;
Matches 123; Conservative 26; Mismatches 44; Indels 16; Gaps 7;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60
DB 29 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 88
QY 61 MTRNTSISTAYMELSLRSEDATVAYYCAREEWL--VRY--GMDVWGQGTWTVTVSSGAS 116
DB 89 MTRDTSISTAYMELSLRSDATVAYYCARTYYDSSGYHDAFDIWGQGTWTVTVSSASTK 148
QY 117 APTLPFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR-GG 175
DB 149 GPSVFLAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSG 205
QY 176 KYAATSOVLPLPSKDYVMQGT-----EHK 198
DB 206 LYSLSVVTVPPSNF--GTQTYTCNVDHK 232
```

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RESULT 10
US-10-128-520-174
; Sequence 174, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-174

Query Match      56.7%; Score 598; DB 16; Length 221;
Best Local Similarity 61.1%; Pred. No. 1.5e-36;
Matches 121; Conservative 23; Mismatches 44; Indels 10; Gaps 5;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60
DB 10 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 69
QY 61 MTRNTSISTAYMELSLRSEDATVAYYCAREEWLRYRYGMDVWGQGTWTVTVSSGASAPTL 120
DB 70 MTRDTSISTAYMELSLRSEDATVAYYCAREEWLRYRYGMDVWGQGTWTVTVSSASTKGPVS 125
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR-CGKYAA 179
DB 126 PFLAPSSKSTSG-GTAAAGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLISL 182
QY 180 TSQVLLPSKDYVMQGTDEH 197
DB 183 SSVTVTPSSSL--GTQTY 198

RESULT 11
US-10-292-088-46
; Sequence 46, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-46

Query Match      56.4%; Score 594.5; DB 15; Length 471;
Best Local Similarity 57.5%; Pred. No. 5.6e-36;
Matches 122; Conservative 28; Mismatches 41; Indels 21; Gaps 7;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60
DB 29 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 88
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QY 61 MTRNTSISTAYMELSSLRSEDVAVYCCAREWL-----VRYGMDVWGQTTVTVSSG 113
Db 89 MTRNTSISTAYMELNLRSDDTAVYCCARDQLGCTGNCVCSYF--DYWGQGLTLVTVSSA 146
QY 114 SASAPTLPLVSCSPSTSSVAVGCLAQDFLPDSITPSWKYKNNSDISSRGRFPVLR 173
Db 147 STKGPSVRPLAFCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTFAVLQ 203
QY 174 -CGKYAATSQVLLPSKDVWQGT-----EHK 198
Db 204 SSGLYSLSSVVTVPSSNF--GTQYTCNVYDHK 233

RESULT 12
US-10-041-860-238
; Sequence 238, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-238

Query Match 53.1%; Score 559.5; DB 14; Length 125;
Best Local Similarity 92.3%; Pred. No. 5.9e-34;
Matches 108; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
Db 9 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 68
QY 61 MTRNTSISTAYMELSSLRSEDVAVYCCAREWLVR-----YVGMDVWGQTTVTVSS 112
Db 69 MTRNTSISTAYMELSSLRSEDVAVYCCAREGLAVAGTYYYYYGMVWGQTTVTVSS 125

RESULT 13
US-10-041-860-19
; Sequence 19, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19

Query Match 53.1%; Score 559.5; DB 14; Length 125;
Best Local Similarity 92.3%; Pred. No. 5.9e-34;
Matches 108; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
Db 9 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 68
QY 61 MTRNTSISTAYMELSSLRSEDVAVYCCAREWLVR-----YVGMDVWGQTTVTVSS 112
Db 69 MTRNTSISTAYMELSSLRSEDVAVYCCAREGLAVAGTYYYYYGMVWGQTTVTVSS 125

RESULT 14
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

Query Match 53.1%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.3%; Pred. No. 5.9e-34;
Matches 108; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
Db 10 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 69
QY 61 MTRNTSISTAYMELSSLRSEDVAVYCCAREWLVR-----YVGMDVWGQTTVTVSS 112
Db 70 MTRNTSISTAYMELSSLRSEDVAVYCCAREGLAVAGTYYYYYGMVWGQTTVTVSS 126

RESULT 15
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
```

```
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-19

Query Match 53.1%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.3%; Pred. No. 5.9e-34;
Matches 108; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
Db 10 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 69
QY 61 MTRNTSISTAYMELSSLRSEDVAVYCCAREWLVR-----YVGMDVWGQTTVTVSS 112
Db 70 MTRNTSISTAYMELSSLRSEDVAVYCCAREGLAVAGTYYYYYGMVWGQTTVTVSS 126

RESULT 14
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

Query Match 53.1%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.3%; Pred. No. 5.9e-34;
Matches 108; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
Db 10 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 69
QY 61 MTRNTSISTAYMELSSLRSEDVAVYCCAREWLVR-----YVGMDVWGQTTVTVSS 112
Db 70 MTRNTSISTAYMELSSLRSEDVAVYCCAREGLAVAGTYYYYYGMVWGQTTVTVSS 126

RESULT 15
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
```

```
; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288

Query Match      53.1%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.3%; Pred. No. 5.9e-34;
Matches 108; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

Qy      1 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWMMNPNNGNTGYAQKFGQGRVT 60
      |||
Db      10 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWMMNPNNGNTGYAQKFGQGRVT 69
      |||

Qy      61 MTRNTSISTAYMELSSLRSEDTAVYYCAREEWLYR-----YYGMDVMQGQTTVTVSS 112
      |||
Db      70 MTRNTSISTAYMELSSLRSEDTAVYYCAREGIAGTAVYYGYGMDVMQGQTTVTVSS 126
      |||
```

Search completed: March 8, 2005, 07:05:52  
Job time : 107.604 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 21.8813 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-29

Perfect score: 1054

Sequence: 1 EVKPGASVKVSKASGYTF.....TSQVLLPSKDVNQGTDEHKV 199

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/iaa/PCUTS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	600	56.9	470	4	US-09-859-053-28
2	544.5	51.7	462	4	US-09-627-896B-24
3	537.5	51.0	467	2	US-07-916-098A-45
4	526.5	50.0	279	3	US-08-397-411-13
5	511	48.5	468	3	US-09-485-737B-67
6	511	48.5	468	4	US-10-071-485-67
7	511	48.5	711	3	US-09-485-737B-90
8	511	48.5	711	4	US-10-071-485-90
9	510	48.4	472	4	US-09-301-593-43
10	509	48.3	222	1	US-08-458-516-22
11	509	48.3	235	1	US-08-458-516-23
12	509	48.3	449	1	US-08-458-516-13
13	501.5	47.6	235	3	US-08-444-644-28
14	501.5	47.6	235	3	US-08-444-644-28
15	496.5	47.1	235	3	US-08-444-644-42
16	496.5	47.1	235	3	US-08-444-644-42
17	487	46.2	476	2	US-08-332-246A-42
18	485.5	46.1	120	3	US-08-378-939-10
19	485.5	46.1	120	3	US-09-025-769B-36
20	485.5	46.1	120	3	US-09-025-769B-59
21	485.5	46.1	120	4	US-09-490-070A-36
22	485.5	46.1	120	4	US-09-490-070A-59
23	485.5	46.1	120	4	US-09-490-153-36
24	485.5	46.1	120	4	US-09-490-324-36
25	485.5	46.1	120	4	US-09-490-324-59
26	484.5	46.0	235	3	US-08-444-644-19
27	484.5	46.0	235	3	US-08-232-246A-19

28	484.5	46.0	468	2	US-08-116-247-7	Sequence 7, Appli
29	484.5	46.0	468	4	US-09-348-224-7	Sequence 7, Appli
30	483.5	45.9	453	4	US-09-301-593-18	Sequence 18, Appl
31	481	45.6	117	3	US-09-025-769B-22	Sequence 22, Appl
32	481	45.6	117	4	US-09-490-070A-22	Sequence 22, Appl
33	481	45.6	117	4	US-09-490-153-22	Sequence 22, Appl
34	481	45.6	117	4	US-09-490-324-22	Sequence 22, Appl
35	479.5	45.5	233	3	US-08-444-644-33	Sequence 33, Appl
36	479.5	45.5	233	3	US-08-232-246A-33	Sequence 33, Appl
37	479.5	45.5	468	2	US-08-303-569B-7	Sequence 7, Appli
38	479.5	45.5	468	4	US-09-795-515-7	Sequence 33, Appl
39	478.5	45.4	445	1	US-08-353-400-33	Sequence 36, Appl
40	478.5	45.4	464	1	US-08-353-400-36	Sequence 36, Appl
41	477.5	45.3	253	3	US-09-027-449-52	Sequence 52, Appl
42	477.5	45.3	253	3	US-08-804-444A-52	Sequence 52, Appl
43	477.5	45.3	253	3	US-09-026-985-52	Sequence 52, Appl
44	477.5	45.3	253	4	US-09-121-952A-52	Sequence 52, Appl
45	477.5	45.3	253	4	US-09-234-340A-52	Sequence 52, Appl

## ALIGNMENTS

## RESULT 1

US-09-859-053-28

; Sequence 28, Application US/09859053

; Patent No. 6803039

; GENERAL INFORMATION:

; APPLICANT: Tezuka, Katsunari

; APPLICANT: Hori, No. 6803039uaki

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

; FILE REFERENCE: 06501-079001

; CURRENT APPLICATION NUMBER: US/09/859,053

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: JP 2001-99508

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: JP 2000-147116

; PRIOR FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 470

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-859-053-28

Query Match

Best Local Similarity 56.9%; Score 600; DB 4; Length 470;

Matches 123; Conservative 26; Mismatches 44; Indels 16; Gaps 7;

QY	1	EVKPGASVKVSKASGYTF	TSYDINWYRQATCGGLEWGMWNPNSGNTGYAQKFGQRTV	60
DB	29	EVKPGASVKVSKASGYTF	GYHWWVRQAPGQGLEWGMWNPNSGNTGYAQKFGQRTV	88
QY	61	MTNRTSISTAYNELSLRSED	TAIVYICAREEVL--VRYV--GMDVMGQGTITVTVSSGSAS	116
DB	89	MTNRTSISTAYNELSLRSED	TAIVYICARTYDSSGYHDAFDINGQGTWTVSSASTK	148
QY	117	APTLPLVSCENSPDTS	SVAVGCLAQDPLPDSITFWMKYKNNSDISTRGPFVLR--GG	175
DB	149	GSVFPFLAPCSRSTSE	--STAALGCLVKDYFPEPVTVSM--NSGALTSGVHTFPAVLQSSG	205
QY	176	KYAATSQVLLPSKDVNQGT	D-----EHK	198
DB	206	LYSLSSVTVPSNPF--	GTQTYTCNVDHK	232

## RESULT 2

US-09-627-896B-24

; Sequence 24, Application US/09627896B

```
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ CHERYL
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 462
; TYPE: PRT
; ORGANISM: 3D1 heavy chain
US-09-627-896B-24

Query Match          51.7%; Score 544.5; DB 4; Length 462;
Best Local Similarity 55.6%; Pred. No. 7.1e-41;
Matches 114; Conservative 24; Mismatches 50; Indels 17; Gaps 6;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGYAQKPGQGRVT 60
Db 29 EVKPGSSVKVSKASGYTFTDYAIQWVRQAPGQGLEWMIGVINIYDNTNYNQKFKGKAT 88

QY 61 MTRNTSISTAYMELSLRSEDATVYICAREHVLRYGMDVWGQGTFTTVSSGSAAPT 120
Db 89 MVDKSTSTAYMELSLRSEDATVYICARAAYI-----MDYWGQGTFTVTSASTKGPSV 143

QY 121 PFLVSCNSPSTSSVAVGCLAQDFLPDSITFSPKYNKNSDISSTRGPSPVL 179
Db 144 PFLAPCSRSTSE--STAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSL 200

QY 180 TSQVLLPSKDVNQGTD-----EHK 198
Db 201 SSVVTVPSNFG--GTQTYTCNVDHK 223

RESULT 3
US-07-916-098A-45
; Sequence 45, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESS: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,411
```

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; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-916-098A-45

Query Match          51.0%; Score 537.5; DB 2; Length 467;
Best Local Similarity 52.8%; Pred. No. 3.1e-40;
Matches 112; Conservative 30; Mismatches 45; Indels 25; Gaps 7;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNSGNTGYAQKPGQGRVT 60
Db 29 EVKPGASVKVSKASGYTFTSYVHWVRQAPGQGLEWMIGVINPYNDGTDYDEKFKGKAT 88

QY 61 MTRNTSISTAYMELSLRSEDATVYICAREB-----WLRYGMDVWGQGTFTTVSSG 113
Db 89 VTLPSTNTAYMELSLRSEDATVYICAREKDNATGAWFA-----YWGQGTFTTVSSA 142

QY 114 SASAPTLPLVSCNSPSTSSVAVGCLAQDFLPDSITFSPKYNKNSDISSTRGPSPVL 173
Db 143 STKGPSVFLAPCSRSTSE--STAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQ 199

QY 174 -GGKYAATSQVLLPSKDVNQGTD-----EHK 198
Db 200 SSGLYSLSSVTVPSNFG--GTQTYTCNVDHK 229

RESULT 4
US-08-397-411-13
; Sequence 13, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,411
```

```
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 279 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-411-13

Query Match 50.0%; Score 526.5; DB 3; Length 279;
Best Local Similarity 55.1%; Pred. No. 1.6e-39;
Matches 109; Conservative 26; Mismatches 56; Indels 7; Gaps 5;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQRTV 60
DB 10 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQRTV 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTTVTVSSGSASAPTL 120
DB 70 L7ADKASATAYMELSLRSEDVAVYCARSAI-YDYGPAYWGQGTFTTVTVSSASTKGPVS 128
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLR-GGKYAA 179
DB 129 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTFFPAVLQSSGLYSL 185
QY 180 TSQVLLPSKDVMOGTDEH 197
DB 186 SSVWTVPPSSSL--GTQTY 201

RESULT 5
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-09-485-737B-67

Query Match 48.5%; Score 511; DB 3; Length 468;
Best Local Similarity 49.5%; Pred. No. 7.4e-38;
Matches 98; Conservative 36; Mismatches 54; Indels 10; Gaps 5;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQRTV 60
DB 30 ELKKEGASVKISCKASGYTFTDYGNNWVKQAPGQGLKMWGINTYTGESTYYDDFKGRFV 89
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTTVTVSSGSASAPTL 120
DB 90 FSLDTSVSAAYLQISLKAEDTATYFCARR----GFYANDYWGQGTFTTVTVSSASTKGPVS 145
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLR-GGKYAA 179
DB 146 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTFFPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOGTDEH 197
DB 203 SSVWTVPPSSSL--GTQTY 218

RESULT 6
US-10-071-485-67
; Sequence 67, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-10-071-485-67

Query Match 48.5%; Score 511; DB 4; Length 468;
Best Local Similarity 49.5%; Pred. No. 7.4e-38;
Matches 98; Conservative 36; Mismatches 54; Indels 10; Gaps 5;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQRTV 60
DB 30 ELKKEGASVKISCKASGYTFTDYGNNWVKQAPGQGLKMWGINTYTGESTYYDDFKGRFV 89
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTTVTVSSGSASAPTL 120
DB 90 FSLDTSVSAAYLQISLKAEDTATYFCARR----GFYANDYWGQGTFTTVTVSSASTKGPVS 145
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLR-GGKYAA 179
DB 146 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTFFPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOGTDEH 197
DB 203 SSVWTVPPSSSL--GTQTY 218

RESULT 7
US-09-485-737B-90
; Sequence 90, Application US/09485737B
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```
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 279 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-411-13

Query Match 50.0%; Score 526.5; DB 3; Length 279;
Best Local Similarity 55.1%; Pred. No. 1.6e-39;
Matches 109; Conservative 26; Mismatches 56; Indels 7; Gaps 5;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQRTV 60
DB 10 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQRTV 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTTVTVSSGSASAPTL 120
DB 70 L7ADKASATAYMELSLRSEDVAVYCARSAI-YDYGPAYWGQGTFTTVTVSSASTKGPVS 128
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLR-GGKYAA 179
DB 129 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTFFPAVLQSSGLYSL 185
QY 180 TSQVLLPSKDVMOGTDEH 197
DB 186 SSVWTVPPSSSL--GTQTY 201

RESULT 5
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-09-485-737B-67

Query Match 48.5%; Score 511; DB 3; Length 468;
Best Local Similarity 49.5%; Pred. No. 7.4e-38;
Matches 98; Conservative 36; Mismatches 54; Indels 10; Gaps 5;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQRTV 60
DB 30 ELKKEGASVKISCKASGYTFTDYGNNWVKQAPGQGLKMWGINTYTGESTYYDDFKGRFV 89
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTTVTVSSGSASAPTL 120
DB 90 FSLDTSVSAAYLQISLKAEDTATYFCARR----GFYANDYWGQGTFTTVTVSSASTKGPVS 145
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLR-GGKYAA 179
DB 146 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTFFPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOGTDEH 197
DB 203 SSVWTVPPSSSL--GTQTY 218

RESULT 6
US-10-071-485-67
; Sequence 67, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-10-071-485-67

Query Match 48.5%; Score 511; DB 4; Length 468;
Best Local Similarity 49.5%; Pred. No. 7.4e-38;
Matches 98; Conservative 36; Mismatches 54; Indels 10; Gaps 5;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQRTV 60
DB 30 ELKKEGASVKISCKASGYTFTDYGNNWVKQAPGQGLKMWGINTYTGESTYYDDFKGRFV 89
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTTVTVSSGSASAPTL 120
DB 90 FSLDTSVSAAYLQISLKAEDTATYFCARR----GFYANDYWGQGTFTTVTVSSASTKGPVS 145
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLR-GGKYAA 179
DB 146 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTFFPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOGTDEH 197
DB 203 SSVWTVPPSSSL--GTQTY 218

RESULT 7
US-09-485-737B-90
; Sequence 90, Application US/09485737B
```

```
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-09-485-737B-90
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```
Query Match 48.5%; Score 511; DB 3; Length 711;
Best Local Similarity 49.5%; Pred. No. 1.2e-37;
Matches 98; Conservative 36; Mismatches 54; Indels 10; Gaps 5;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
DB 30 ELKPGASVKISCKASGYTFTDYGNNWVKQAPGQGLKWMGWINTYTGESTYVDDFKGRFV 89
QY 61 MTRNTSISTAYMELSSLRSEDTAVYICAREEHLVRYYGMDVWVGQGTITVTVSSGSASAPTL 120
DB 90 FSLDTSVAAYLQISLKAEDTATVFCARR----GFYAMDYWGQGTITVTVSSASTKGPVS 145
QY 121 PPLVSCENSPDTSVAVGCLAQDFLPDSITPSWKYKNNSDISSTRGFPVSILR-GGKYAA 179
DB 146 PFLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOGTDEH 197
DB 203 SSVTVTPSSSL--GIQTY 218
```

```
RESULT 8
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; FILE REFERENCE: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS-015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-10-071-485-90

Query Match 48.5%; Score 511; DB 4; Length 711;
Best Local Similarity 49.5%; Pred. No. 1.2e-37;
Matches 98; Conservative 36; Mismatches 54; Indels 10; Gaps 5;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
DB 30 ELKPGASVKISCKASGYTFTDYGNNWVKQAPGQGLKWMGWINTYTGESTYVDDFKGRFV 89
QY 61 MTRNTSISTAYMELSSLRSEDTAVYICAREEHLVRYYGMDVWVGQGTITVTVSSGSASAPTL 120
DB 90 FSLDTSVAAYLQISLKAEDTATVFCARR----GFYAMDYWGQGTITVTVSSASTKGPVS 145
QY 121 PPLVSCENSPDTSVAVGCLAQDFLPDSITPSWKYKNNSDISSTRGFPVSILR-GGKYAA 179
DB 146 PFLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOGTDEH 197
DB 203 SSVTVTPSSSL--GIQTY 218
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RESULT 9
US-09-301-593-43
; Sequence 43, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; TITLE OF INVENTION: Retting, Wolfgang J.
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-301-593-43
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Query Match 48.4%; Score 510; DB 4; Length 472;
Best Local Similarity 54.2%; Pred. No. 9.2e-38;
Matches 109; Conservative 24; Mismatches 58; Indels 10; Gaps 6;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
DB 29 EVKPGASVKVSKTSRYTFTYTHWVRQAPGQGLEWIGINPNNGIPNINQKFKGRAT 88
QY 61 MTRNTSISTAYMELSSLRSEDTAVYICAREEHLVRY---YGMVDVWGQGTITVTVSSGSASA 117
DB 89 LTVGKSASTAYMELSSLRSEDTAVYICARRIAYGYDEGHAMDYWGQGTITVTVSS-STKG 147
QY 118 PTLFPLVSCENSPDTSVAVGCLAQDFLPDSITPSWKYKNNSDISSTRGFPVSILR-GGK 176
DB 148 PSVFPPLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQSSGL 204
QY 177 YAATSOVLLPSKDVMOGTDEH 197
DB 205 YLSLSSVTVTPSSSL--GIQTY 223
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RESULT 10  
US-08-458-516-22  
; Sequence 22, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 222 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-458-516-22

Query Match 48.3%; Score 509; DB 1; Length 222;  
Best Local Similarity 53.5%; Pred. No. 4.4e-38;  
Matches 106; Conservative 28; Mismatches 56; Indels 8; Gaps 5;

QY 1 EVKPGASVKVSKASGYFTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGRTV 60  
Db 10 EVKPGSSVKVSKASGYFTFTSYDINWVRQAPGQGLEWIGVYPGSGGTNYNEKFKGRVT 69  
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTVTVSSGSASAPTL 120  
Db 70 LVVDESTNTAYMELSLRSEDVAVYFCARRDG--NYGMFAYWGQGTFTVTVSSASTKGPSV 127  
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFWSKYKNNSDISSTRGPPSVLR-GGKYAA 179  
Db 128 PFLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQSSGLYS 184  
QY 180 TSQVLLPSKDVWGQGTDEH 197  
Db 185 SSVWTVPSSSL--GTQTY 200

RESULT 11  
US-08-458-516-23  
; Sequence 23, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco

; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-458-516-23

Query Match 48.3%; Score 509; DB 1; Length 235;  
Best Local Similarity 53.5%; Pred. No. 4.7e-38;  
Matches 106; Conservative 28; Mismatches 56; Indels 8; Gaps 5;

QY 1 EVKPGASVKVSKASGYFTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGRTV 60  
Db 10 EVKPGSSVKVSKASGYFTFTSYDINWVRQAPGQGLEWIGVYPGSGGTNYNEKFKGRVT 69  
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTVTVSSGSASAPTL 120  
Db 70 LVVDESTNTAYMELSLRSEDVAVYFCARRDG--NYGMFAYWGQGTFTVTVSSASTKGPSV 127  
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFWSKYKNNSDISSTRGPPSVLR-GGKYAA 179  
Db 128 PFLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQSSGLYS 184  
QY 180 TSQVLLPSKDVWGQGTDEH 197  
Db 185 SSVWTVPSSSL--GTQTY 200

RESULT 12  
US-08-458-516-13  
; Sequence 13, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/059,159  
FILING DATE: 03-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-37-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 449 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-516-13

Query Match 48.3%; Score 509; DB 1; Length 449;  
Best Local Similarity 53.5%; Pred. No. 1.1e-37;  
Matches 106; Conservative 28; Mismatches 56; Indels 8; Gaps 5;  
QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60  
Db 10 EVKPGSSVKVSKASGYAFTNYLIEWRQAPGQGLEWIGVYPSGGTNYNEKPKGRVT 69  
QY 61 MTRNTSISTAYMELSSLRSEDTAVTYCAREEWLVRYGMDVWGQTTTVTVSSGSASAPTL 120  
Db 70 LTVDSTNTAYMELSSLRSEDTAVFYCARRDQ--NYGWFAYWGQGTTLTVTVSSASTKGPSV 127  
QY 121 PFLVSCNSPDSSTSVAVGCLAQDLPDSITFSWKYKKNDSISSTRGFPVSLR-CKGYAA 179  
Db 128 PFLAPSSKSTSG-GTALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGLYSL 184  
QY 180 TSQVLLPSKDVMOGTDEH 197  
Db 185 SSVTVPSSSL--GTQTY 200

RESULT 13  
US-08-444-644-28  
Sequence 28, Application US/08444644  
Patent No. 6015555  
GENERAL INFORMATION:  
APPLICANT: Friden, Phillip M.  
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
TITLE OF INVENTION: CONJUGATES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,644  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/232,246  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/800,458  
FILING DATE: 26-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US90/05077  
FILING DATE: 07-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/404,089  
FILING DATE: 07-SEP-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Wagner, Richard W.  
REGISTRATION NUMBER: 34,480  
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
US-08-444-644-28  
Query Match 47.6%; Score 501.5; DB 3; Length 235;  
Best Local Similarity 48.8%; Pred. No. 2.2e-37;  
Matches 100; Conservative 39; Mismatches 51; Indels 15; Gaps 6;  
QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60  
Db 29 ELVPGASMKLSCKASGYSTGYTNWVKQSHGENLEWIGRINPANGGTDYNEKFKDAP 88  
QY 61 MTRNTSISTAYMELSSLRSEDTAVTYCAREEWLVRYGMDVWGQTTTVTVSSGSASAPTL 120  
Db 89 LTVDKSSNTAYMELSLTSEDSAVTYCARGYV--YYSLDYWGQGTSTVTVSSASTKGPSV 145  
QY 121 PFLVSCNSPDSSTSVAVGCLAQDLPDSITFSWKYKKNDSISSTRGFPVSLR-CKGYAA 179  
Db 146 PFLAPCSRSTSE-STALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGLYSL 202  
QY 180 TSQVLLPSKDVMOGTD-----EKK 198  
Db 203 SSVTVPSNPF--GTQTYTCNVDPK 225

RESULT 14  
US-08-232-246A-28  
Sequence 28, Application US/08232246A  
Patent No. 6329508  
GENERAL INFORMATION:  
APPLICANT: Friden, Phillip M.  
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
TITLE OF INVENTION: CONJUGATES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,246A  
FILING DATE: 04-MAY-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/800,458  
FILING DATE: 26-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US90/05077  
FILING DATE: 07-SEP-1990  
APPLICATION NUMBER: US 07/404,089  
FILING DATE: 07-SEP-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Wagner, Richard W.  
REGISTRATION/DOCKET NUMBER: ALK88-15AAA  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
US-08-232-246A-28

Query Match 47.6%; Score 501.5; DB 3; Length 235;  
Best Local Similarity 48.8%; Pred. No. 2.2e-37;  
Matches 100; Conservative 39; Mismatches 51; Indels 15; Gaps 6;  
QY 1 EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMNPNNGNTGYAQKFGQRTV 60  
DB 29 ELVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMNPNNGNTGYAQKFGQRTV 88  
QY 61 MTRNTSISTAYMELSLRSEDATVYVCAREEWLVRYGMDVWGQGTITVTVSSGSASAPTL 120  
DB 89 LTVKSSNTAYMELSLRSEDATVYVCAREEWLVRYGMDVWGQGTITVTVSSGSASAPTL 145  
QY 121 PFLVSCNSPDTSSVAVGCLAQDFLPDSITPSWKYKNSDISSTRGPPSVLR-GGKYAA 179  
DB 146 FPLAPCSRRTSE--STAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQSSGLYSL 202  
QY 180 TSQVLLPSKDVWGQTD-----EHK 198  
DB 203 SSVTVTPSSNF--GTQTYTCNVDPK 225

RESULT 15  
US-08-444-644-42  
Sequence 42, Application US/08444644  
Patent No. 6015555  
GENERAL INFORMATION:  
APPLICANT: Fiden, Phillip M.  
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
TITLE OF INVENTION: CONJUGATES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,644  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/232,246  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/800,458  
FILING DATE: 26-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US90/05077  
FILING DATE: 07-SEP-1990  
APPLICATION NUMBER: US 07/404,089  
FILING DATE: 07-SEP-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Wagner, Richard W.  
REGISTRATION/DOCKET NUMBER: ALK88-15AAA  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
US-08-444-644-42

Query Match 47.1%; Score 496.5; DB 3; Length 235;  
Best Local Similarity 48.3%; Pred. No. 6.2e-37;  
Matches 99; Conservative 39; Mismatches 52; Indels 15; Gaps 6;  
QY 1 EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMNPNNGNTGYAQKFGQRTV 60  
DB 29 ELVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMNPNNGNTGYAQKFGQRTV 88  
QY 61 MTRNTSISTAYMELSLRSEDATVYVCAREEWLVRYGMDVWGQGTITVTVSSGSASAPTL 120  
DB 89 LTVKSSNTAYMELSLRSEDATVYVCAREEWLVRYGMDVWGQGTITVTVSSGSASAPTL 145  
QY 121 PFLVSCNSPDTSSVAVGCLAQDFLPDSITPSWKYKNSDISSTRGPPSVLR-GGKYAA 179  
DB 146 FPLAPCSRRTSE--STAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQSSGLYSL 202  
QY 180 TSQVLLPSKDVWGQTD-----EHK 198  
DB 203 SSVTVTPSSSL--GTQTYTCNVDPK 225

Search completed: March 8, 2005, 05:54:07  
Job time : 22.8813 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.4472 Seconds  
(without alignment)  
1353.842 Million cell updates/sec

Title: US-09-784-950-30

Perfect score: 769

Sequence: 1 GQSPSSLSASVGDRTVTTCR.....VCLNNFYPREXKEHOKSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567.5	73.8	215	2 J80242	Ig kappa chain NIG
2	562.5	73.1	215	2 J80244	Ig kappa chain NIG
3	529.5	68.9	215	2 J80243	Ig kappa chain NIG
4	513.5	66.8	215	2 A23746	Ig kappa chain V-I
5	500	65.0	141	2 A49134	Ig kappa chain V-I
6	500	65.0	234	2 S14237	Ig kappa chain pre
7	494	64.2	230	2 S33161	Ig kappa chain - s
8	487	63.3	234	2 S01320	Ig kappa chain pre
9	487	63.3	240	2 S06084	Ig kappa chain pre
10	482	62.7	108	1 K1HWE	Ig kappa chain V-I
11	481	62.5	125	2 S40353	Ig kappa chain V-J
12	481	62.5	216	2 J80241	Ig kappa chain Am3
13	475	61.8	210	2 A56169	Ig kappa chain V r
14	470	61.1	214	2 S68212	Ig kappa chain (Ma
15	468	60.9	108	1 K1HUGL	Ig kappa chain V-I
16	465	60.5	127	2 S40367	Ig kappa chain V-J
17	463	60.2	123	2 S40313	Ig kappa chain V-J
18	462	60.1	125	2 S40333	Ig kappa chain V-J
19	461	59.9	139	2 S40365	Ig kappa chain - h
20	460	59.8	126	2 S40335	Ig kappa chain V-J
21	457	59.4	144	2 P0105	Ig kappa chain pre
22	457	59.4	218	2 J05810	monoclonal antibody
23	456.5	59.4	124	2 S40336	Ig kappa chain V-J
24	456	59.3	130	2 S40368	Ig kappa chain - h
25	456	59.3	132	2 S40334	Ig kappa chain - h
26	455.5	59.2	225	2 S37484	Ig kappa chain - m
27	455	59.2	129	2 S40369	Ig kappa chain - h
28	454.5	59.1	235	2 S25058	Ig kappa chain - m
29	454	59.0	218	2 S68241	Ig kappa chain V r

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A:Description: Structure relationship of kappatype light chains with AL amyloidosis: Mult

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 567.5; DB 2; Length 215;

Best Local Similarity 74.5%; Pred. No. 1.6e-39;

Matches 108; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

Qy 2 QSPSSLSASVGDRTVTTCRASQDIRDN-LGVYQKPGKAPKELIYAASNLQSGVPSRSG 60

Db 6 QSPGTLSPGERATLSGRASQSVSNLYAWYQKPGQAPSLIYDASSRATGPDPSDEQ 65

Qy 61 SGSGTFTLTISLQPEDFATYVCLQYKTYPTWTFQGQTKVEIKRTVAAPSVFIPPPSDEQ 120

Db 66 SGSGTDFILTISGLEPEDFATYVCCQYDRPPTWTFQGQTKVEIKRTVAAPSVFIPPPSDEQ 125

Qy 121 LKSGTASVVCLLNNFYPREXKEHOK 145

Db 126 LKSGTASVVCLLNNFYPREAKVQWK 150

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 562.5; DB 2; Length 215;

Best Local Similarity 74.5%; Pred. No. 4.2e-39;

Matches 108; Conservative 14; Mismatches 22; Indels 1; Gaps 1;



DB 146 TSGGASVVCFLNFFPKDI 164

## RESULT 7

S33161  
IG kappa chain - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S33161  
R:Poley, R.C.; Beh, K.J.  
submitted to the EMBL Data Library, July 1990  
A:Description: Isolation and characterisation of sheep kappa light chain cDNA.  
A:Reference number: S33161  
A:Accession: S33161  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-230 <POL>  
A:Cross-references: EMBL:X54110; NID:G297103; PIDN:CAA38046.1; PID:g1364221  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:143-212/Domain: immunoglobulin homology <IMM>

		Query Match	64.2%	Score 494;	DB 2;	Length 230;
		Best Local Similarity	66.2%;	Pred. No. 1.8e-33;		
		Matches	92;	Conservative 24;	Mismatches 23;	Indels 0; Gaps 0;
<hr/>						
Qy	2	QSPSSLASVGDRTVITCRASODTRDNLGWYQQKPGKAPKELLIAAANLQGVDSRPSGS	61			
		:   :	:	:	:	:
		:   :	:	:	:	:
Dd	22	QSPSSLASLTERVSITCRTSQSVSNLYNWYQQKPGQAPKLLIYYATRLTLDVDSRPSGS	81			
		:   :	:	:	:	:
		:   :	:	:	:	:
<hr/>						
Qy	62	GSGTEFTLTLSLLOPEFATPYCYLOYKTYPTWTFQGCTKVETKRVTVAAPSVPFIPPSDEQL	121			
		:   :	:	:	:	:
		:   :	:	:	:	:
Dd	82	GSGTDYTLTISLEANDATATYCLQVYSSTPLAFGGGTVNVEIKRDAOPSVFLKFPSEQL	141			
		:   :	:	:	:	:
		:   :	:	:	:	:

## RESULT 8

S01320  
IG kappa chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 21-Jan-2000  
C:Accession: S01320  
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a  
A:Reference number: S01320; MUID:88329081; PMID:3138116  
A:Accession: S01320  
A:Molecule type: mRNA  
A:Residues: 1-234 <DE1>  
A:Cross-references: EMBL:X13187; NID:G51784; PIDN:CAA31579.1; PID:G51785  
A:Note: this sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-234/Product: Ig kappa chain #status predicted <MAT>  
F:36-110/Domain: immunoglobulin homology <IMW>

Query Match	63.3%	Score	487;	DB	2;	Length	234;
Best Local Similarity	65.5%	Pred.	No. 6.9e-33;				
Matches	91;	Conservative	21;	Mismatches	27;	Indels	0;
Gaps	0						
Qy	2	QSPSSLASGVDRVTITCRASQDTRNDLNGWTQQKPGKAPKLIIYAASNQLQGVPSPRFGSGS	61				
Db	26	QSPASLSVGSVSTITCRASENIYNSLAWYQQKGSKPLLIVYATKLVDPGVPSPRFGSGS	85				
Qy	62	GSGTFTLTSSLPEDPATYYCLOKYTYPTWFOGTVKEIKRTVAASPVIIPPDSDDL	121				
Db	86	GGTGYSLKINSLOSEPFGSYCHFWMDPTTFSGTKLEMKRADAAPTVGIFPPSSOL	145				

```

Qy      122 KSGTASVVCLLNFFPREX 140
          || || || || || || || ||
Db      146 TSGGASVVCFLNFFPKDI 164

```

## RESULT 9

S06084  
 IG kappa chain precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
 C:Accession: S06084  
 R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.  
 Nucleic Acids Res. 17, 7992, 1989  
 A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA  
 A:Reference number: S06084; MUID:90016888; PMID:2508067  
 A:Accession: S06084  
 A:Molecule type: mRNA  
 A:Residues: 1-240 <CRO>  
 A:Cross-references: EMBL:X16129; NID:S56457; PIDN:CAA34256.1; PID:g56458  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-240/Product: IG kappa chain #status predicted <MAT>  
 F:153-222/Domain: immunoglobulin homology <IMV>

[illegible]

## RESULT 10

K1HWWE  
 IG kappa chain V-I region (WEA) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 09-Jul-2004  
 C:Accession: A01876  
 R:Goni, F.; Frangione, B.  
 Proc Natl. Acad Sci. U.S.A. 80, 4837-4841, 1983  
 A:Title: Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) wit  
 A:Reference number: A93964; MUID:83273707; PMID:6410398  
 A:Accession: A01876  
 A:Molecule type: protein  
 A:Residues: 1-108 <GON>  
 A:Cross-references: UNIPROT:P01610  
 C:Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated gal  
 C:Genetics:  
 A:Gene: GDB:IGKV1  
 A:Cross-references: GDB:136264  
 A:Map position: 2p12-2p12  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp  
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer  
 F:16-90/Domain: immunoglobulin homology <IMM>  
 F:23-88/Disulfide bonds: #status predicted

Query Match 62.7%; Score 482; DB 1; Length 108;  
Best Local Similarity 87.4%; Pred. No. 8.3e-33;  
Matches 90; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

```

Db      6 QSPSSLSASVGDRVTITCRASQGRINDLTWYQKPGTAPKRLIYGATLSQSGVPSRFGS 65
QY      62 GSGTEFTLTISLQPEDFATYYCLQYKTYPTWTFQGGTKVEIKR 104
Db      66 GSGTEFTLTISLQPEDFATYYCLQYSSFPWTFQGGTKVEIKR 108

RESULT 11
S40353
IG kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40353
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:9408091; PMID:8258341
A:Accession: S40353
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match      62.5%; Score 481; DB 2; Length 125;
Best Local Similarity 87.7%; Pred. No. 1.2e-32;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY      2 QSPSSLSASVGDRVTITCRASQDIRNDLWYQKPGKAPKRLIYAASNLSQSGVPSRFGS 61
Db      20 QSPSSLSASVGDRVTITCRASQIGNDLWYQKPGKAPKRLIYAASSFGSGVPSRFGS 79

QY      62 GSGTEFTLTISLQPEDFATYYCLQYKTYPTWTFQGGTKVEIKRVA 107
Db      80 GSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTRVEIKRVA 125

RESULT 12
JE0241
IG kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R;Alim, M.A.; Yanaki, S.; Hossein, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPD, November 1998
A:Description: Structure relationship of kappatype light chains with AL amyloidosis: MUI
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match      62.5%; Score 481; DB 2; Length 216;
Best Local Similarity 66.2%; Pred. No. 2e-32;
Matches 99; Conservative 18; Mismatches 26; Indels 6; Gaps 3;

QY      2 QSPSSLSASVGDRVTITCRASQDIRDN----LGYQKPGKAPKRLIYAASNLSQSGVPSR 57
Db      6 QSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQKPGQ-PKLLIW-ANVRESGVDPDR 63

QY      58 FSGSGSGTEFTLTISLQPEDFATYYCLQYKTYPTWTFQGGTKVEIKRVAAPSVFIPPPS 117
Db      64 FRSGVGTDFTLTISNLQALVAVYICQYYSFYSFGQGRLEIKRVAAPSVFIPPPS 123

QY      118 DEOLKSGTASVCLLNNFYPREXKEHOK 145
Db      124 DEOLKSGTASVCLLNNFYPREAKVOWK 151

```



C;Accession: A01867  
R;Laure, C.J.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973  
A;Title: The primary structure of a monoclonal IGM-immunoglobulin (macroglobulin Gal), I  
A;Reference number: A01867; MUID:75059122; PMID:4215718  
A;Accession: A01867  
A;Molecule type: protein  
A;Residues: 1-108 <LAU>  
A;Cross-references: UNIPROT:P01599  
A;Note: the C region of this chain has the Inv (3) marker  
C;Comment: This chain was isolated from a Waldenstrom's macroglobulin.  
C;Genetics:  
A;Gene: GDB:IGKV1  
A;Cross-references: GDB:136264  
A;Map position: 2p12-2p12  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;16-90/Domain: immunoglobulin homology <IMM>  
F;23-88/Disulfide bonds: #status predicted

Query Match	60.9%;	Score 468;	DB 1;	Length 108;
Best Local Similarity	88.3%;	Pred No. 1.2e-31;		
Matches	91;	Conservative	5;	Mismatches 7; Indels 0; Gaps 0;
Qy	2	QSPSLSASVGDRTTTCRASQDIRDNLGWYQKFGKAPKRLIYAASNLSQGVPSRPSGS	61	
Db	6	QSPSLSASVGDRTTTCRASQDIRDNLGWYQKFGKAPKRLIYAASNLSQGVPSRPSGS	65	
Qy	62	GSCTFTLTISLQPEDFATYCYQKTYPTWTFGGTKVEIKR	104	
Db	66	GAGTEFTLTISLQPEDFATYCYQKTYPTWTFGGTKVEIKR	108	

Search completed: March 8, 2005, 06:39:25  
Job time : 11.4972 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 54.8971 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-30

Perfect score: 769

Sequence: 1 GQSPSSLSASVGRVTTCR.....VCLLNFPYEXXEHQKSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_prot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	670	87.1	236	2	Q6GMW1	Q6gmw1 homo sapien
2	639	83.1	236	2	Q7Z3Y4	Q7z3y4 homo sapien
3	633	82.3	234	2	Q7Z473	Q7z473 homo sapien
4	629	81.8	236	2	Q6GMX8	Q6gmxx8 homo sapien
5	622	80.9	236	2	Q6GMX9	Q6gmxx9 homo sapien
6	619	80.5	236	2	Q6PIH7	Q6pih7 homo sapien
7	618	80.4	236	2	Q6PIT5	Q6pit5 homo sapien
8	607	78.9	236	2	Q6GMX0	Q6gmxx0 homo sapien
9	598	77.8	236	2	Q6PIH4	Q6pih4 homo sapien
10	554.5	72.1	235	2	Q6GMW0	Q6gmw0 homo sapien
11	538	70.0	236	2	Q6PIL8	Q6pil8 homo sapien
12	535.5	69.6	235	2	Q6GMV9	Q6gmvv9 homo sapien
13	531	69.1	236	2	Q6P5S8	Q6p5s8 homo sapien
14	527.5	68.6	235	2	Q6PJF2	Q6pjf2 homo sapien
15	506	65.8	236	2	Q7TS98	Q7ts98 mus musculus
16	496	64.5	240	2	Q6PIH6	Q6pih6 homo sapien
17	492.5	64.0	239	2	Q8NEK0	Q8nek0 homo sapien
18	492.5	64.0	239	2	Q8TCD0	Q8tcd0 homo sapien
19	482	62.7	108	1	KV1R_HUMAN	P01610 homo sapien
20	470.5	61.2	239	2	Q6P491	Q6p491 homo sapien
21	468	60.9	108	1	KV1G_HUMAN	P01599 homo sapien
22	464	60.3	238	2	Q6GJS7	Q6gjs7 mus musculus
23	451	58.6	108	1	KV1B_HUMAN	P01594 homo sapien
24	444	57.7	108	2	Q9UL77	Q9ul77 homo sapien
25	440	57.2	108	1	KV1V_HUMAN	P04430 homo sapien
26	434.5	56.5	219	2	Q65ZC0	Q65zc0 mus musculus
27	434	56.4	116	2	Q9GPF6	Q9gpf6 homo sapien
28	433	56.3	108	2	Q9UL70	Q9ul70 homo sapien
29	429.5	55.9	107	2	Q9GSA9	Q9gsa9 homo sapien
30	429	55.8	108	1	KV1H_HUMAN	P01607 homo sapien
31	427	55.5	108	1	KV1H_HUMAN	P01600 homo sapien

32	425	55.3	108	1	KV1C_HUMAN	P01595 homo sapien
33	425	55.3	244	2	Q65ZC8	Q65zc8 homo sapien
34	424.5	55.2	243	2	Q6NTU5	Q6ntu5 xenopus lae
35	422	54.9	108	1	KV1L_HUMAN	P01604 homo sapien
36	421	54.7	108	2	Q9UL79	Q9ul79 homo sapien
37	420	54.6	108	1	KV1Y_HUMAN	P80362 homo sapien
38	418	54.4	237	2	Q7S236	Q7s236 xenopus lae
39	417	54.2	108	1	KV1A_HUMAN	P01593 homo sapien
40	417	54.2	240	2	Q65ZC9	Q65zc9 homo sapien
41	415	54.0	108	1	KV1E_HUMAN	P01597 homo sapien
42	415	54.0	108	1	KV1M_HUMAN	P01605 homo sapien
43	415	54.0	108	1	KV1S_HUMAN	P01611 homo sapien
44	414.5	53.9	107	1	KV1D_HUMAN	P01596 homo sapien
45	414	53.8	108	1	KV1F_HUMAN	P01598 homo sapien

#### ALIGNMENTS

#### RESULT 1

ID	Q6GMW1	PRELIMINARY;	PRT;	236 AA.
AC	Q6GMW1;			
DT	05-JUL-2004 (TREMBlrel. 27, Created)			
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Splice;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,			
RT	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Splice;			
RA	Strausberg R.;			
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC073791; AAH73791.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003006; IG MHC.			
DR	InterPro; IPR003596; IG v.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	Pfam; PF00047; IG; 2.			
DR	SMART; SM00409; IGC1; 2.			
DR	SMART; SM00407; IGC1; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			



Query Match	81.8%;	Score 629;	DB 2;	Length 236;
Best local Similarity	85.4%;	Pred. No. 6.2e-55;		
Matches 123;	Conservative	8;	Mismatches 13;	Indels 0; Gaps 0;
Qy	2	QSPSSLSASVGDRTVITTCRASQDIRNLGHVYQKQPKAPKLLIYAASNLOSQVPSRFGS	61	
Db	28	QSPSSVSASVGDRTVITTCRASQGISSLAWYQKQPKAPKLLIYAASNLOSQVPSRFGS	87	
Qy	62	GSGETFTLTSSIQPEDFATYYCLQVYKTPWTFTGQTKVEIKETVAAPSVFIFPPSPDEQL	121	
Db	88	GSGETFTLTSSIQPEDFATYYCQQAHSFPFTTGGTGKVDIKETVAAPSVFIFPPSPDEQL	147	
Qy	122	KSGTASVVCLLNNFYPREKKEHQK	145	
Db	148	KSGTASVVCLLNNFYPREAKVOMK	171	

RESULT 5  
Q6GMX9 PRELIMINARY; PRT; 236 AA.

ID Q6GMX9  
AC Q6GMX9  
DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC TTSUUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straubeberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.W., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Dattchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC TTSUUE=Primary B-Cells;  
RA Straubeberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC073763; AAR73763.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFE7 CRC64;



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KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEER351 CRC64;

Query Match      80.4%; Score 618; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 8e-54;
Matches 120; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPKAPKRLIYAASNLQSGVPSRFRSGS 61
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
28 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPKAPKRLIYAASNLQSGVPSRFRSGS 87

QY 62 GSGTEFTLTISLQPEDFATYVCLOQKTPVTFGGTQVETKRTVAAPSVFIFPPSDQL 121
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
88 GSGTEFTLTISLQPEDFATYVCLOQKTPVTFGGTQVETKRTVAAPSVFIFPPSDQL 147

QY 122 KSGTASVVCLLNFPYPRXKEHQK 145
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
148 KSGTASVVCLLNFPYPRXKEHQK 171

RESULT 8
Q6GMX0
ID Q6GMX0 PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match      78.9%; Score 607; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 1e-52;
Matches 120; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPKAPKRLIYAASNLQSGVPSRFRSGS 61
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
28 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPKAPKRLIYAASNLQSGVPSRFRSGS 87

QY 62 GSGTEFTLTISLQPEDFATYVCLOQKTPVTFGGTQVETKRTVAAPSVFIFPPSDQL 121
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
88 GSGTEFTLTISLQPEDFATYVCLOQKTPVTFGGTQVETKRTVAAPSVFIFPPSDQL 147

QY 122 KSGTASVVCLLNFPYPRXKEHQK 145
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
148 KSGTASVVCLLNFPYPRXKEHQK 171

RESULT 9
Q6PIH4
ID Q6PIH4 PRELIMINARY; PRT; 236 AA.
AC Q6PIH4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034146; AAH34146.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein_1.
SQ SEQUENCE 236 AA; 25871 MW; B501A28CD06BEE26 CRC64;

Query Match 77.8%; Score 598; DB 2; Length 236;
Best Local Similarity 82.6%; Pred. No. 8.1e-52;
Matches 119; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKQPGKAPKELIYAAASNLQSGVPSRSGS 61
Db 28 QSPSTLSASVGDRTVITCRASQISDWLAWYQKQPGKAPKELIYDASRLQSGVPSRSGS 87
Qy 62 GSGTEFTLTISLQPEDPATYCYQKYTPWTFQGTGKVEIKRTVAAPSVFIFFPSDEQL 121
Db 88 GSGTEFTLTISLQPEDPATYCYQKYTPWTFQGTGKVEIKRTVAAPSVFIFFPSDEQL 147
Qy 122 KSGTASVCLNNFYPREXKEHOK 145
Db 148 KSGTASVCLNNFYPREXKEHOK 171

RESULT 10
Q6GMW0 PRELIMINARY; PRT; 235 AA.
ID Q6GMW0
AC Q6PIL8; PRELIMINARY; PRT; 235 AA.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH3792.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
PR
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```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein_1.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 72.1%; Score 554.5; DB 2; Length 235;
Best Local Similarity 73.1%; Pred. No. 1.9e-47;
Matches 106; Conservative 18; Mismatches 20; Indels 1; Gaps 1;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKQPGKAPKELIYAAASNLQSGVPSRSGS 61
Db 26 QSPSTLSASVGDRTVITCRASQISNNLAWYQKQPGKAPKELIYDASRLQSGVPSRSGS 85
Qy 62 GSGTEFTLTISLQPEDPATYCYQKYTPWTFQGTGKVEIKRTVAAPSVFIFFPSDEQ 120
Db 86 GSGTEFTLTISLQPEDPATYCYQKYTPWTFQGTGKVEIKRTVAAPSVFIFFPSDEQ 145
Qy 121 LKSGTASVCLNNFYPREXKEHOK 145
Db 146 LKSGTASVCLNNFYPREXKEHOK 170

RESULT 11
Q6PIL8 PRELIMINARY; PRT; 236 AA.
ID Q6PIL8
AC Q6PIL8; PRELIMINARY; PRT; 236 AA.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032451; AAH32451.1; -.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
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DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS0290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match          70.0%; Score 538; DB 2; Length 236;
Best Local Similarity 71.2%; Pred. No. 8.7e-46;
Matches 104; Conservative 17; Mismatches 23; Indels 2; Gaps 2;

QY 2 QSPSLASVGDRTVITCRASQDIRDN-LGWYQKQPGKAPKRLIYAASNLOSQVPSRFSG 60
DB QSPGLTSLSPERATLSCRASQSLSSYLAWTQKPGQAPRLIYGVSSRATGIPDRFSG 85
QY 61 SGSSTFTLTSSLOPEDFATYICLQYKT-YPWTFQGTQKVEIKRTVAAPSFIIPPSDE 119
DB SGSSTFTLTSLRLEPEDFAVYCYQYGTSPRITFGQGTDLDKETVAAPSFIIPPSDE 145
QY 120 QKSGTASVCLNNFYPREKHEKOK 145
DB QKSGTASVCLNNFYPREKQVWK 171

RESULT 12
Q6GMV9 PRELIMINARY; PRT; 235 AA.
AC Q6GMV9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH3793.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.

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DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS0290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match          69.6%; Score 535.5; DB 2; Length 235;
Best Local Similarity 71.7%; Pred. No. 1.5e-45;
Matches 104; Conservative 14; Mismatches 26; Indels 1; Gaps 1;

QY 2 QSPSLASVGDRTVITCRASQDIRDN-LGWYQKQPGKAPKRLIYAASNLOSQVPSRFSG 60
DB QSPGLTSLSPERATLSCRASQSLSSYLAWTQKPGQAPRLIYGVSSRATGIPDRFSG 85
QY 61 SGSSTFTLTSSLOPEDFATYICLQYKT-YPWTFQGTQKVEIKRTVAAPSFIIPPSDEQ 120
DB SGSSTFTLTSLRLEPEDFAVYCYQYGTSPITFGGKVEIKRTVAAPSFIIPPSDEQ 145
QY 121 LKSGTASVCLNNFYPREKHEKOK 145
DB LKSGTASVCLNNFYPREKQVWK 170

RESULT 13
Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.

```

DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 953E37BEB4FF5F27 CRC64;  
  
Query Match 69.1%; Score 531; DB 2; Length 236;  
Best Local Similarity 70.5%; Pred. No. 4.4e-45;  
Matches 103; Conservative 18; Mismatches 23; Indels 2; Gaps 2;  
  
Qy 2 QSPSSLASVGDRTVITTCRASQDI-RNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSG 60  
Db 26 QSPGTLSPFGERATLSCRASQTVFSSHLAWYQKPGAPQLLIYGASSRATGIPDRFSG 85  
  
Qy 61 SGSSTFTLTISLQPEDFATYICLQYKTYT-WTFGQTKVEIKRTVAAPSVFIPPPSDE 119  
Db 86 SGSSTFTLTITLPEDEDFAVYFCQYGTSPSLTFGGTGTRVEIKRTVAAPSVFIPPPSDE 145  
  
Qy 120 QLKSGTASVCLNNFYPREKHEQK 145  
Db 146 QLKSGTASVCLNNFYPREAKVQWK 171

## RESULT 14

Q6PJF2 ID Q6PJF2 PRELIMINARY; PRT; 235 AA.  
AC Q6PJF2;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC016380; AAH16380.1; -.  
DR HSSP; P01837; 1KCU.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG.v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;  
  
Query Match 68.6%; Score 527.5; DB 2; Length 235;  
Best Local Similarity 69.7%; Pred. No. 9.9e-45;  
Matches 101; Conservative 19; Mismatches 24; Indels 1; Gaps 1;  
  
Qy 2 QSPSSLASVGDRTVITTCRASQDIRD-NLGWYQKPGKAPKRLIYAASNLQSGVPSRFSG 60  
Db 26 QSPATLSLSPGERATLSCRASQIVSSAYLAWYQKPGAPQLLMFGSSSRATGIPDRFSG 85  
  
Qy 61 SGSSTFTLTISLQPEDFATYICLQYKTYTWTGQTKVEIKRTVAAPSVFIPPPSDEQ 120  
Db 86 SGSSTFTLTITSLPEDEDFAVYFCQYGTSGTGTGKVDIKRTVAAPSVFIPPPSDEQ 145  
  
Qy 121 LKSGTASVCLNNFYPREKHEQK 145  
Db 146 LKSGTASVCLNNFYPREAKVQWK 170

## RESULT 15

Q7TS98 ID Q7TS98 PRELIMINARY; PRT; 236 AA.  
AC Q7TS98;  
DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Anti-colorectal carcinoma light chain.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93383497; PubMed=8372513;  
RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;  
RT "Cloning and characterization of 1116NS19.9 heavy and light chain  
cDNAs and expression of antibody fragments in *Escherichia coli*";  
RL Year Immunol. 7:56-62(1993).  
DR EMBL; S65921; AAB28160.1; -.  
DR HSSP; P01837; 1KBS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG.v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
SQ SEQUENCE 236 AA; 26454 MW; 2C586EBF5EA10F4C CRC64;  
  
Query Match 65.8%; Score 506; DB 2; Length 236;  
Best Local Similarity 69.1%; Pred. No. 1.4e-42;  
Matches 96; Conservative 17; Mismatches 26; Indels 0; Gaps 0;  
  
Qy 2 QSPSSLASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 61  
Db 28 QSPSSMTASGERVTITCKASQDINSYLSYFQQKPGKSPKTLIYRANRLVDGVSRFSGS 87  
  
Qy 62 SGSSTFTLTISLQPEDFATYICLQYKTYTWTGQTKVEIKRTVAAPSVFIPPPSDEQ 121  
Db 88 GSGQDYSLTISLSEYEDMGVIYCYLQYDFPRPTFGGTKLEIKRADAAPTVSIFFPSSQL 147  
  
Qy 122 KSGTASVCLNNFYPREX 140  
Db 148 TSGGASVVCFLNNFYPKDI 166

Search completed: March 8, 2005, 06:35:50  
Job time : 54.8971 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 68.1532 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-30

Perfect score: 769

Sequence: 1 GQSPSSLSASVGRVTTCR.....VCLLNFFPREXKHOKSP 147

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: geneseqp1980s.\*
  - 2: geneseqp1990s.\*
  - 3: geneseqp2000s.\*
  - 4: geneseqp2001s.\*
  - 5: geneseqp2002s.\*
  - 6: geneseqp2003as.\*
  - 7: geneseqp2003bs.\*
  - 8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	769	100.0	147	2	AAY34312 Igm antib
2	706	91.8	147	2	AAY34310 Igm antib
3	694	90.2	236	5	ABG77164 Germline
4	694	90.2	236	8	ADR28586 Human ant
5	688	89.5	236	8	ADP07905 Human imm
6	684	88.9	234	8	AD884458 Human ant
7	684	88.9	234	8	ADR68600 Human ant
8	683	88.8	184	8	AD884439 Human ant
9	683	88.8	184	8	ADR68581 Human ant
10	682	88.7	236	5	ABG77160 Germline
11	682	88.7	236	8	ADR28582 Human ant
12	680	88.4	215	8	ADH10328 Anti-HIV-
13	675	87.8	152	8	ADK52390 Human ant
14	675	87.8	152	8	ADK52354 Human ant
15	674	87.6	234	8	AD884470 Human ant
16	674	87.6	234	8	ADR68612 Human ant
17	671	87.3	234	8	AD884452 Human ant
18	671	87.3	234	8	ADR68594 Human ant
19	670	87.1	234	8	AD884464 Human ant
20	670	87.1	234	8	ADR68606 Human ant
21	668	86.9	234	8	AD884476 Human ant
22	668	86.9	234	8	ADR68618 Human ant
23	666	86.6	236	5	ABG77163 Amino aci
24	666	86.6	236	8	ADR28585 Human ant
25	663	86.2	164	7	ADD28242 Human het

26	657	85.4	236	5	ABG77159 Amino aci
27	657	85.4	236	8	ADR28581 Human ant
28	655	85.2	212	6	AAO31100 Human A2-
29	650	84.5	224	4	AAB75043 TRO005 Hu
30	649	84.4	214	7	ADC26154 Parent an
31	649	84.4	237	5	ABB81107 Anti-VEGF
32	649	84.4	237	5	ABP51952 Plasmid p
33	649	84.4	237	8	ADO14128 Plasmid p
34	649	84.4	237	8	ADO14131 Plasmid p
35	649	84.4	237	8	ADQ90703 Anti-VEGF
36	649	84.4	237	8	ADQ90701 Anti-VEGF
37	649	84.4	237	8	ADQ90705 Anti-VEGF
38	649	84.4	237	8	ADQ90709 Anti-VEGF
39	649	84.4	237	8	ADQ90723 Anti-VEGF
40	649	84.4	237	8	ADQ90721 Anti-VEGF
41	649	84.4	237	8	ADQ90707 Anti-VEGF
42	647	84.1	237	2	AAW70703 Protein e
43	647	84.1	650	5	ABP61241 Phage-dis
44	645.5	83.9	241	4	AAB82912 Human Imm
45	644	83.7	236	5	AAU74297 Anti-huma

ALIGNMENTS

RESULT 1  
AAY34312  
ID AAY34312 standard; protein; 147 AA.  
XX  
AC AAY34312;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE Igm antibody CEM 10.12 G5 kappa chain sequence.  
XX  
KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 140  
FT /label= "unknown  
FT /note= "encoded by GMC"  
XX  
PN WO9945031-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 03-MAR-1999; 99WO-US004583.  
XX  
PR 03-MAR-1998; 98US-00034507.  
PR 03-FEB-1999; 99US-00244253.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX  
DR WPI; 1999-540816/45.  
XX  
N-PSDB; AAZ20413.  
XX  
PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX  
PS Claim 61; Fig 27; 245pp; English.  
XX  
CC This sequence represents the kappa chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the Igm MAB ABX-CBL, providing that the antibody is not CBL1. The MAB

CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX  
SQ Sequence 147 AA;  
Query Match 100.0%; Score 769; DB 2; Length 147;  
Best Local Similarity 100.0%; Pred. No. 9.1e-50;  
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GQSPSSLSASVGDRTVITCRASQDIRNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSG 60  
Db 1 GQSPSSLSASVGDRTVITCRASQDIRNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSG 60  
Qy 61 SGSCTEFTLTSSLOPEDFATYYCLOYKTPWTFGQGTKEIKRTVAAPSFIFFPSDEQ 120  
Db 61 SGSCTEFTLTSSLOPEDFATYYCLOYKTPWTFGQGTKEIKRTVAAPSFIFFPSDEQ 120  
Qy 121 LKSGTASVVCLLNNFYPREXKEHQSP 147  
Db 121 LKSGTASVVCLLNNFYPREXKEHQSP 147

RESULT 2  
AAY34310  
ID AAY34310 standard; protein; 147 AA.  
XX  
AC AAY34310;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE IgM antibody CEM 10.1 G10 kappa chain sequence.  
XX  
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
OS Homo sapiens.  
XX  
FN WO9945031-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 03-MAR-1999; 99WO-US004583.  
XX  
PR 03-MAR-1998; 98US-00034607.  
PR 03-FEB-1999; 99US-00244253.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX  
DR WPI; 1999-540816/45.  
DR N-PSDB; AAZ20411.  
XX  
PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX  
PS Claim 61; Fig 25; 245pp; English.

XX This sequence represents the kappa chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft

CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX  
SQ Sequence 147 AA;  
Query Match 91.8%; Score 706; DB 2; Length 147;  
Best Local Similarity 93.2%; Pred. No. 4.4e-45;  
Matches 136; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
Qy 2 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSG 61  
Db 2 QSPSSLSASVGERVITTCRASQDIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 61  
Qy 62 GSGTEFTLTSSLOPEDFATYYCLOYKTPWTFGQGTKEIKRTVAAPSFIFFPSDEQL 121  
Db 62 GSGTEFTLTSSLOPEDFATYYCLOHNGYPRTFQGTKEIKRTVAAPSFIFFPSDEQL 121  
Qy 122 KSGTASVVCLLNNFYPREXKEHQSP 147  
Db 122 KSGTASVVCLLNNFYPREXKEHQSP 147

RESULT 3  
ABG77164  
ID ABG77164 standard; protein; 236 AA.  
XX  
AC ABG77164;  
XX  
DT 24-OCT-2002 (first entry)  
XX  
DE Germline protein sequence of anti-IGF-IR antibody AJ30/JK1.  
XX  
KW Insulin-like growth factor I receptor; antibody; human; cytostatic;  
KW osteopathic; antiatherosclerotic; antiposoriatic; IGF-IR; tumour;  
KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;  
KW acromegaly; gigantism; psoriasis; atherosclerosis.  
XX  
OS Homo sapiens.  
XX  
FN WO200253596-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-US051113.  
XX  
PR 05-JAN-2001; 2001US-0259927P.  
XX  
PA (PFIZ ) PFIZER INC.  
PA (ABGE-) ABGENIX INC.  
XX  
PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;  
XX  
DR WPI; 2002-575410/61.

XX Novel humanized, chimeric monoclonal antibody that specifically binds to  
XX insulin-like growth factor I (IGF-1) receptor useful for inhibiting  
XX binding of IGF-I or IGF-II to receptor and for treating cancer in humans.  
XX  
PS Disclosure; Fig 19E; 172pp; English.  
XX  
CC This invention relates to a novel humanised, chimeric or human monoclonal  
CC antibody or its antigen binding portion that specifically binds to  
CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the  
CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-  
CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine  
CC phosphorylation. The antibodies of the invention are useful for  
CC diagnosing the presence or location of an IGF-IR-expressing tumour in a  
CC subject. The antibody or its antigen-binding portion is also useful for  
CC treating cancer in a human. The method for this further involves an anti  
CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The  
CC antibodies may also be useful for increasing IGF-IR activity and thus

CC restoring IGF-IR activity in a condition characterised by low IGF-IR  
CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is  
CC also useful for inducing apoptosis of specific cells in a patient, and to  
CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,  
CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies  
CC minimise the immunogenic and allergic responses intrinsic to mouse or  
CC mouse-derived monoclonal antibodies and thus increase the efficacy  
CC and safety of the administered antibodies. The present sequence  
CC represents an anti-insulin-like growth factor I receptor antibody of the  
CC invention  
XX  
SQ Sequence 236 AA;

Query Match 90.2%; Score 694; DB 5; Length 236;  
Best Local Similarity 92.4%; Pred. No. 5.5e-44;  
Matches 133; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRNDLGMWYQOKPGKAPKRLIYAASNLQSGVPSRFGSGS 61

Db 28 QSPSSLSASVGDRTVITCRASQDIRNDLGMWYQOKPGKAPKRLIYAASNLQSGVPSRFGSGS 87

Qy 62 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 121

Db 88 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 147

Qy 122 KSGTASVVCLLNFPYREXKEHQK 145

Db 148 KSGTASVVCLLNFPYREXKEHQK 171

## RESULT 4

ADR28586

ID ADR28586 standard; protein; 236 AA.

XX ADR28586;

XX 18-NOV-2004 (first entry)

XX Human anti-IGF-IR antibody heavy chain A30/Jk1 protein SEQ ID NO:52.

XX aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;  
XX T-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;  
XX neurodegenerative disorder; human;  
XX anti-insulin-like growth factor I receptor antibody;  
XX anti-IGF-IR antibody; cytostatic; immunosuppressive; endocrine;  
XX vasotropic; neuroprotective; nootropic; antithyroid; vaccine;  
XX gene therapy.

XX Homo sapiens.

XX WO2004071529-A2.

XX 26-AUG-2004.

XX 03-FEB-2004; 2004WO-IB000366.

XX 13-FEB-2003; 2003US-047353P.

XX (PFIZ ) PFIZER PROD INC.

XX Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;  
XX Cuernano JD, Guyot DJ, Page KL;  
XX WPI; 2004-625776/60.

XX Treating or preventing aging or a disorder (e.g. multiple myeloma,  
XX autoimmune disease or neurodegenerative disorder) in humans comprises  
XX administering an amount of a human anti-insulin-like growth factor I  
XX receptor antibody.

XX Disclosure; SEQ ID NO 52; 105pp; English.

XX The present invention describes a method for treating or preventing aging

CC or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus  
CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,  
CC ischaemia or neurodegenerative disorder) in a mammal. The method  
CC comprises administering to the mammal an amount of a human anti-insulin-  
CC like growth factor I receptor (IGF-IR) antibody. Also described is a  
CC pharmaceutical composition for treating or preventing the above-mentioned  
CC disorder in a mammal, comprising an amount of the human anti-IGF-IR  
CC antibody and a pharmaceutical carrier. The composition has cytostatic,  
CC immunosuppressive, endocrine, vasotropic, neuroprotective, nootropic and  
CC antithyroid activities, and can be used in vaccines and in gene therapy.  
CC The method and composition are useful for preventing or treating aging or  
CC a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus  
CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,  
CC ischaemia or neurodegenerative disorder) in mammals, such as humans. The  
CC human IGF-IR antibody is used in preparing a composition for the  
CC treatment or prevention of the above-mentioned disorders. The present  
CC sequence represents a human anti-IGF-IR antibody light chain amino acid  
CC sequence, which is used in the exemplification of the present invention.

XX SQ Sequence 236 AA;

Query Match 90.2%; Score 694; DB 8; Length 236;  
Best Local Similarity 92.4%; Pred. No. 5.5e-44;  
Matches 133; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRNDLGMWYQOKPGKAPKRLIYAASNLQSGVPSRFGSGS 61

Db 28 QSPSSLSASVGDRTVITCRASQDIRNDLGMWYQOKPGKAPKRLIYAASNLQSGVPSRFGSGS 87

Qy 62 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 121

Db 88 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 147

Qy 122 KSGTASVVCLLNFPYREXKEHQK 145

Db 148 KSGTASVVCLLNFPYREXKEHQK 171

## RESULT 5

ADP07905

ID ADP07905 standard; protein; 236 AA.

XX ADP07905;

XX 29-JUL-2004 (first entry)

XX Human immunoglobulin light chain variable region.

XX monoclonal antibody; tumour growth factor-beta type II receptor;

XX TGF-beta type II receptor; kidney disease; nephrosclerosis;

XX pulmonary fibrosis; liver cirrhosis; blood-vessel restenosis;

XX arteriosclerosis; psoriasis; scleroderma; atopy; keloid; arthritis;

XX human; light chain variable region.

XX Homo sapiens.

XX JP2004121001-A.

XX 22-APR-2004.

XX 07-AUG-2002; 2002JP-00230651.

XX 07-AUG-2002; 2002JP-00230600.

XX (NISB ) JAPAN TOBACCO INC.

XX WPI; 2004-322721/30.

XX DR N-PSDB; ADP07904.

XX Novel monoclonal antibody coupled with human transforming growth factor

XX (TGF)-beta type II receptor, useful for treating or preventing

XX arteriosclerosis, psoriasis, scleroderma, atopy, keloid, arthritis.

XX

PS Claim 31; SEQ ID NO 9; 78pp; Japanese.

XX The invention comprises a monoclonal antibody coupled with human tumour

CC growth factor-beta (TGF-beta) type II receptor. The monoclonal antibody

CC coupled with human TGF-beta type II receptor of the invention is useful

CC for treating or preventing: kidney disease, nephrosclerosis, pulmonary

CC fibrosis, liver cirrhosis, blood-vessel restenosis, arteriosclerosis,

CC psoriasis, scleroderma, atopy, keloid and arthritis. The present amino

CC acid sequence represents a human immunoglobulin light chain variable

CC region.

XX

SQ Sequence 236 AA;

Query Match 89.5%; Score 688; DB 8; Length 236;

Best Local Similarity 91.7%; Pred. No. 1.5e-43;

Matches 132; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTTTCRASQDIRNDLNGWYQKPGKAPKRLIYAASNLSQGVSRFSGS 61

Db 28 QSPSSLSASVGDRTTTCRASQDIRNDLNGWYQKPGKAPKRLIYAASNLSQGVSRFSGS 87

Qy 62 GSGTEFTLTISLQPEDFATYCYCLOQNTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121

Db 88 GSGTEFTLTISLQPEDFATYCYCLOQNTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 147

Qy 122 KSGTASVVCLNNFYPREXKEHQK 145

Db 148 KSGTASVVCLNNFYPREAKVQWK 171

RESULT 6

ADSR84458

ID AD84458 standard; protein; 234 AA.

XX

AC ADS84458;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human anti-EPO-R antibody Ab412 light chain SEQ ID NO:97.

XX

KW human; erythropoietin receptor; EPO receptor;

KW erythropoietin receptor binding antibody; EPO receptor binding antibody;

KW antianaemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;

KW wound healing; neural cell damage protection;

KW neural tissue damage protection; brain injury; spinal cord injury;

KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.

XX

OS Homo sapiens.

XX

PN WO2004035603-A2.

XX

PD 29-APR-2004.

XX

PF 14-OCT-2003; 2003WO-US032243.

XX

PR 14-OCT-2002; 2002US-00269711.

PR 10-OCT-2003; 2003US-00684109.

XX

PA (ABBO ) ABBOTT LAB.

XX

FI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;

XX

DR WPI; 2004-348433/32.

DR N-PSDB; ADS84456, ADS84457.

XX

XX New antibodies that bind to or activate an endogenous human

PT erythropoietin receptor, useful for diagnosing, preventing or treating

PT disorders associated with dysfunctional erythropoietin receptor, e.g.

PT anaemia.

XX

PS Disclosure; SEQ ID NO 97; 192pp; English.

XX

CC The present invention describes an antibody or its fragment that binds to

CC or activates an endogenous activity of a human erythropoietin (EPO)

CC receptor in a mammal, but does not interact with a peptide having a

CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)

CC methods of modulating or activating an endogenous activity of a human EPO

CC receptor in a mammal, comprising administering to the mammal a

CC therapeutic amount of the above antibody or its fragment to modulate or

CC activate the receptor; (2) a method of treating a mammal suffering from

CC aplasia, comprising administering to the mammal a therapeutic amount of

CC the above antibody or its fragment to modulate or activate the receptor;

CC (3) a pharmaceutical composition comprising a therapeutic amount of the

CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)

CC an isolated and purified polynucleotide sequence, and their fragments,

CC complements and degenerate codon equivalents; and (5) an isolated and

CC purified amino acid sequence, and their fragments. The EPO receptor

CC binding antibody has antianaemic, neuroprotective and vulnary

CC activities, and can be used in gene therapy. The compositions and methods

CC from the present invention can be used for modulating an endogenous

CC activity of a human EPO receptor or for treating mammals suffering from

CC aplasia or anaemia. They may also be used for identifying mammals having

CC a dysfunctional EPO receptor. The composition may also be used in

CC promoting wound healing or in protecting against neural cell and/or

CC tissue damage resulting from brain/spinal cord injury, stroke and the

CC like. The present sequence represents a human anti-EPO-R antibody light

CC chain, which is given in the exemplification of the present invention.

XX

SQ Sequence 234 AA;

Query Match 88.9%; Score 684; DB 8; Length 234;

Best Local Similarity 92.4%; Pred. No. 3e-43;

Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTTTCRASQDIRNDLNGWYQKPGKAPKRLIYAASNLSQGVSRFSGS 61

Db 26 QSPSSLSASVGDRTTTCRASQDIRNDLNGWYQKPGKAPKRLIYAASNLSQGVSRFSGS 85

Qy 62 GSGTEFTLTISLQPEDFATYCYCLOQNTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121

Db 86 GSGTEFTLTISLQPEDFATYCYCLOQNTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 145

Qy 122 KSGTASVVCLNNFYPREXKEHQK 145

Db 146 KSGTASVVCLNNFYPREAKVQWK 169

RESULT 7

ADSR86600

ID ADR68600 standard; protein; 234 AA.

XX

AC ADR68600;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human antibody Ab412 light chain polypeptide seqid 97.

XX

KW antianaemic; respiratory; vulnary; gene therapy; vaccine;

KW erythropoietin receptor; EPO-R; anti-EPO-R antibody; aplasia; anaemia;

KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;

KW wound healing; neural cell damage; tissue damage; brain injury;

KW spinal cord injury; stroke; human; anti-EPO-R antibody; light chain;

KW AB412.

XX

OS Homo sapiens.

XX

PN US2004175379-A1.

XX

PD 09-SEP-2004.

XX

PF 10-OCT-2003; 2003US-00684109.

XX

PR 14-OCT-2002; 2002US-0418031P.

XX

PA (DEVRI/) DEVRIES P J.

FA (OSTR/) OSTROW D H.



PA (REIL/) REILLY E B.  
 PA (GREEN) GREEN L L.  
 PA (WIEL/) WIELER J.  
 XX  
 PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
 XX  
 DR WPI: 2004-661369/64.  
 DR N-PSDB; ADR68598.  
 XX  
 PT New antibody or its antibody fragment that activates an endogenous  
 PT activity or is capable of binding to a human erythropoietin receptor in a  
 PT mammal, useful for treating a mammal suffering aplasia or anemia.  
 XX  
 PS Disclosure; SEQ ID NO 97; 156pp; English.  
 XX  
 CC The invention describes an antibody or its fragment that activates an  
 CC endogenous activity or capable of binding to a human erythropoietin  
 CC receptor in a mammal, or that comprises at least one heavy or light chain  
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
 CC given in the specification. Also described are: a method of activating or  
 CC modulating an endogenous activity of a human erythropoietin receptor in a  
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
 CC isolated and purified polynucleotide sequence selected from 28 sequences  
 CC comprising 322-370 bp (even SEQ ID NOs between SEQ ID NO: 2-56) given in  
 CC the specification, and their fragments, complements, and degenerate codon  
 CC equivalents; and an isolated and purified amino acid sequence selected  
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOs between  
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
 CC their fragments. The antibody or its antibody fragment that activates or  
 CC modulates the activity of the receptor is useful in a method of treating  
 CC a mammal suffering aplasia or anemia. The antibodies are also useful for  
 CC treating disorders characterised by decreased or subnormal levels of  
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
 CC hypoxia and/or diseases characterised by inadequate blood circulation or  
 CC reduced blood flow. They are also useful for promoting wound healing or  
 CC for protecting against neural cell and/or tissue damage, resulting from  
 CC brain/spinal cord injury, stroke and the like. The antibodies are also  
 CC useful for identifying or diagnosing mammals having dysfunctional  
 CC erythropoietin receptor. This sequence represents a human Ab412 antibody  
 CC light chain polypeptide.  
 XX  
 SQ Sequence 234 AA;  
 Query Match 88.9%; Score 684; DB 8; Length 234;  
 Best Local Similarity 92.4%; Pred. No. 3e-43;  
 Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 61  
 Db 26 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 85  
 QY 62 GSGTEFTLTISLQPEDFATYICLYQKTYPTWTFQGGTKVEIKRTVAAPSVFIFFPSDQL 121  
 Db 86 GSGTEFTLTISLQPEDFATYICLYQKTYPTWTFQGGTKVEIKRTVAAPSVFIFFPSDQL 145  
 QY 122 KSGTASVVCLLNPNFYPREXKEHQK 145  
 Db 146 KSGTASVVCLLNPNFYPREXKEHQK 169  
 RESULT 8  
 ADS84439  
 ID ADS84439 standard; protein; 184 AA.  
 XX  
 AC ADS84439;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human anti-EPO-R antibody Ab12 light chain SEQ ID NO:78.  
 XX

KW human; erythropoietin receptor; EPO receptor;  
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 KW antianaemic; neuroprotective; vulnerable; gene therapy; aplasia; anaemia;  
 KW wound healing; neural cell damage protection;  
 KW neural tissue damage protection; brain injury; spinal cord injury;  
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004035603-A2.  
 XX  
 PD 29-APR-2004.  
 XX  
 PF 14-OCT-2003; 2003WO-US032243.  
 XX  
 PR 14-OCT-2003; 2002US-00269711.  
 PR 10-OCT-2003; 2003US-00684109.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
 XX  
 DR WPI: 2004-348433/32.  
 DR N-PSDB; ADS84437; ADS84438.  
 XX  
 PT New antibodies that bind to or activate an endogenous human  
 PT erythropoietin receptor, useful for diagnosing, preventing or treating  
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
 PT anemia.  
 XX  
 PS Claim 41; SEQ ID NO 78; 192pp; English.  
 XX  
 CC The present invention describes an antibody or its fragment that binds to  
 CC or activates an endogenous activity of a human erythropoietin (EPO)  
 CC receptor in a mammal, but does not interact with a peptide having a  
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 CC methods of modulating or activating an endogenous activity of a human EPO  
 CC receptor in a mammal, comprising administering to the mammal a  
 CC therapeutic amount of the above antibody or its fragment to modulate or  
 CC activate the receptor; (2) a method of treating a mammal suffering from  
 CC aplasia, comprising administering to the mammal a therapeutic amount of  
 CC the above antibody or its fragment to modulate or activate the receptor;  
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 CC an isolated and purified polynucleotide sequence, and their fragments,  
 CC complements and degenerate codon equivalents; and (5) an isolated and  
 CC purified amino acid sequence, and their fragments. The EPO receptor  
 CC binding antibody has antianaemic, neuroprotective and vulnerable  
 CC activities, and can be used in gene therapy. The compositions and methods  
 CC from the present invention can be used for modulating an endogenous  
 CC activity of a human EPO receptor or for treating mammals suffering from  
 CC aplasia or anaemia. They may also be used for identifying mammals having  
 CC a dysfunctional EPO receptor. The composition may also be used in  
 CC promoting wound healing or in protecting against neural cell and/or  
 CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 CC like. The present sequence represents a human anti-EPO-R antibody light  
 CC chain, which is given in the exemplification of the present invention.  
 XX  
 SQ Sequence 184 AA;  
 Query Match 88.8%; Score 683; DB 8; Length 184;  
 Best Local Similarity 92.4%; Pred. No. 2.8e-43;  
 Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 61  
 Db 28 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 87  
 QY 62 GSGTEFTLTISLQPEDFATYICLYQKTYPTWTFQGGTKVEIKRTVAAPSVFIFFPSDQL 121  
 Db 88 GSGTEFTLTISLQPEDFATYICLYQKTYPTWTFQGGTKVEIKRTVAAPSVFIFFPSDQL 147  
 QY 122 KSGTASVVCLLNPNFYPREXKEHQK 145

Db 148 KSGTASVCLNNFYPREAKVQWK 171  
|||||  
RESULT 9  
ADR68581  
ID ADR68581 standard; protein; 184 AA.  
XX  
AC ADR68581;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human antibody Ab12 light chain polypeptide seqid 78.  
XX  
KW antianemic; respiratory; vulnerary; gene therapy; vaccine;  
KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;  
KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;  
KW wound healing; neural cell damage; tissue damage; brain injury;  
KW spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;  
KW Ab12.  
XX  
OS Homo sapiens.  
XX  
FN US2004175379-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 10-OCT-2003; 2003US-00684109.  
XX  
PR 14-OCT-2002; 2002US-0418031P.  
XX  
PA (DEVIR/) DEVRIES P J.  
PA (OSTR/) OSTROW D H.  
PA (REIL/) REILLY E B.  
PA (GREEN/) GREEN L L.  
PA (WIEL/) WIELER J.  
XX  
PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;  
XX  
XX WPI; 2004-661369/64.  
XX  
DR N-PSDB; ADR68579, ADR68586.  
XX  
XX  
PT New antibody or its antibody fragment that activates an endogenous  
PT activity or is capable of binding to a human erythropoietin receptor in a  
PT mammal, useful for treating a mammal suffering aplasia or anemia.  
XX  
PS Claim 41; SEQ ID NO 78; 156pp; English.  
XX  
CC The invention describes an antibody or its fragment that activates an  
CC endogenous activity or capable of binding to a human erythropoietin  
CC receptor in a mammal, or that comprises at least one heavy or light chain  
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ  
CC ID NO: 3 or 5) given in the specification or its fragment, but does not  
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also  
CC given in the specification. Also described are: a method of activating or  
CC modulating an endogenous activity of a human erythropoietin receptor in a  
CC mammal; a pharmaceutical composition comprising a therapeutic amount of  
CC an antibody or antibody fragment above and a pharmaceutical excipient; an  
CC isolated and purified polynucleotide sequence selected from 28 sequences  
CC comprising 322-370 bp (even SEQ ID NOs between SEQ ID NO: 2-56) given in  
CC the specification, and their fragments, complements, and degenerate codon  
CC equivalents; and an isolated and purified amino acid sequence selected  
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOs between  
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or  
CC their fragments. The antibody or its antibody fragment that activates or  
CC modulates the activity of the receptor is useful in a method of treating  
CC a mammal suffering aplasia or anaemia. The antibodies are also useful for  
CC treating disorders characterised by decreased or subnormal levels of  
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue  
CC hypoxia and/or diseases characterised by inadequate blood circulation or  
CC reduced blood flow. They are also useful for promoting wound healing or  
CC for protecting against neural cell and/or tissue damage, resulting from  
CC brain/spinal cord injury, stroke and the like. The antibodies are also

CC useful for identifying or diagnosing mammals having dysfunctional  
CC erythropoietin receptor. This is the amino acid sequence of a human Ab12  
CC antibody light chain polypeptide.  
XX  
SQ Sequence 184 AA;  
Query Match 88.8%; Score 683; DB 8; Length 184;  
Best Local Similarity 92.4%; Pred. No. 2.8e-43;  
Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
Qy 2 QSPSSLSASVGDRTVITTCRASQDIRDNLGNWYQKPGKAPKRLIYAASNLQSGVPSRSGS 61  
Db 28 QSPSSLSASVGDRTVITTCRASQDIRDNLGNWYQKPGKAPKRLIYAASNLQSGVPSRSGS 87  
Qy 62 GSGTEFTLTITSSLPEDFATYCYLQYKTYPTWTFQGTKEIKRTVAAPSVPFPPSDEQL 121  
Db 88 GSGTEFTLTITSSLPEDFATYCYLQYKTYPTWTFQGTKEIKRTVAAPSVPFPPSDEQL 147  
Qy 122 KSGTASVCLNNFYPREXKEHQK 145  
Db 148 KSGTASVCLNNFYPREAKVQWK 171  
RESULT 10  
ABG77160  
ID ABG77160 standard; protein; 236 AA.  
XX  
AC ABG77160;  
XX  
DT 24-OCT-2002 (first entry)  
XX  
DE Germline protein sequence of anti-IGF-IR antibody AJ30/Jk2.  
XX  
KW Insulin-like growth factor I receptor; antibody; human; cytostatic;  
KW osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour;  
KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;  
KW acromegaly; gigantism; psoriasis; atherosclerosis.  
XX  
OS Homo sapiens.  
XX  
FN WO200253596-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-US051113.  
XX  
PR 05-JAN-2001; 2001US-0259927P.  
XX  
PA (PFIZ ) PFIZER INC.  
PA (ABGE-) ABGENIX INC.  
XX  
PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;  
XX  
XX WPI; 2002-575410/61.  
XX  
PT Novel humanized, chimeric monoclonal antibody that specifically binds to  
PT insulin-like growth factor I (IGF-I) receptor useful for inhibiting  
PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.  
XX  
PS Disclosure; Fig 19C; 172pp; English.  
XX  
CC This invention relates to a novel humanised, chimeric or human monoclonal  
CC antibody or its antigen binding portion that specifically binds to  
CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the  
CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-  
CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine  
CC phosphorylation. The antibodies of the invention are useful for  
CC diagnosing the presence or location of an IGF-IR-expressing tumour in a  
CC subject. The antibody or its antigen-binding portion is also useful for  
CC treating cancer in a human. The method for this further involves an anti  
CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The  
CC antibodies may also be useful for increasing IGF-IR activity and thus  
CC restoring IGF-IR activity in a condition characterised by low IGF-IR

CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is  
 CC also useful for inducing apoptosis of specific cells in a patient, and to  
 CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,  
 CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies  
 CC minimise the immunogenic and allergic responses intrinsic to mouse or  
 CC mouse-derived monoclonal antibodies and thus increase the efficacy  
 CC and safety of the administered antibodies. The present sequence  
 CC represents an anti-insulin-like growth factor I receptor antibody of the  
 CC invention  
 XX  
 SQ Sequence 236 AA;

Query Match 88.7%; Score 682; DB 5; Length 236;  
 Best Local Similarity 91.0%; Pred. No. 4.3e-43;  
 Matches 131; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 QSPSSLSASVGDRTTITCRASQDIRNDLQWYQKPGKAPKRLIYAASLQSGVPSRFGSGS 61  
 DB 28 QSPSSLSASVGDRTTITCRASQDIRNDLQWYQKPGKAPKRLIYAASLQSGVPSRFGSGS 87  
 QY 62 GSGTEFTLTISLQPEDPATYCYLYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 121  
 DB 88 GSGTEFTLTISLQPEDPATYCYLYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 147  
 QY 122 KSGTASVVCLNNFYPREXKEHQK 145  
 DB 148 KSGTASVVCLNNFYPREXKEHQK 171

RESULT 11  
 ADR28582  
 ID ADR28582 standard; protein; 236 AA.  
 AC ADR28582;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX

DE Human anti-IGF-IR antibody light chain A30/Jk2 protein SEQ ID NO:48.  
 XX aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;  
 KW T-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;  
 KW neurodegenerative disorder; human;  
 KW anti-insulin-like growth factor I receptor antibody;  
 KW anti-IGF-IR antibody; cytostatic; immunosuppressive; endocrine;  
 KW vasotropic; neuroprotective; nootropic; antithyroid; vaccine;  
 KW gene therapy.

XX Homo sapiens.  
 OS WO2004071529-A2.  
 XX  
 FN 26-AUG-2004.  
 XX  
 PD 03-FEB-2004; 2004WO-IB000366.  
 PF  
 XX 13-FEB-2003; 2003US-0447353P.  
 PR  
 XX (PFIZ ) PFIZER PROD INC.  
 PA

XX Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;  
 PI Cusmano JD, Guyot DU, Page KU;  
 FI  
 XX WPI; 2004-625776/60.  
 DR

XX Treating or preventing aging or a disorder (e.g. multiple myeloma,  
 PT autoimmune disease or neurodegenerative disorder) in humans comprises  
 PT administering an amount of a human anti-insulin-like growth factor I  
 PT receptor antibody.

XX Disclosure; SEQ ID NO 48; 105pp; English.  
 PS  
 XX The present invention describes a method for treating or preventing aging  
 CC or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus

CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,  
 CC ischaemia or neurodegenerative disorder) in a mammal. The method  
 CC comprises administering to the mammal an amount of a human anti-insulin-  
 CC like growth factor I receptor (IGF-IR) antibody. Also described is a  
 CC pharmaceutical composition for treating or preventing the above-mentioned  
 CC disorder in a mammal, comprising an amount of the human anti-IGF-IR  
 CC antibody and a pharmaceutical carrier. The composition has cytostatic,  
 CC immunosuppressive, endocrine, vasotropic, neuroprotective, nootropic and  
 CC antithyroid activities, and can be used in vaccines and in gene therapy.  
 CC The method and composition are useful for preventing or treating aging or  
 CC a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus  
 CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,  
 CC ischaemia or neurodegenerative disorder) in mammals, such as humans. The  
 CC human IGF-IR antibody is used in preparing a composition for the  
 CC treatment or prevention of the above-mentioned disorders. The present  
 CC sequence represents a human anti-IGF-IR antibody light chain amino acid  
 CC sequence, which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 236 AA;

Query Match 88.7%; Score 682; DB 8; Length 236;  
 Best Local Similarity 91.0%; Pred. No. 4.3e-43;  
 Matches 131; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 QSPSSLSASVGDRTTITCRASQDIRNDLQWYQKPGKAPKRLIYAASLQSGVPSRFGSGS 61  
 DB 28 QSPSSLSASVGDRTTITCRASQDIRNDLQWYQKPGKAPKRLIYAASLQSGVPSRFGSGS 87  
 QY 62 GSGTEFTLTISLQPEDPATYCYLYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 121  
 DB 88 GSGTEFTLTISLQPEDPATYCYLYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 147  
 QY 122 KSGTASVVCLNNFYPREXKEHQK 145  
 DB 148 KSGTASVVCLNNFYPREXKEHQK 171

RESULT 12  
 ADH10328  
 ID ADH10328 standard; protein; 215 AA.  
 AC ADH10328;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Anti-HIV-gp120-antibody light chain sequence.  
 XX  
 KW Glycoprotein; gp120; anti-HIV; vaccine; antibody S8; human; antibody S19;  
 KW antibody S20.

XX Homo sapiens.  
 OS EP1371660-A1.  
 FN  
 XX 17-DEC-2003.  
 PD  
 XX 14-JUN-2002; 2002EP-00380126.  
 PF  
 XX 14-JUN-2002; 2002EP-00380126.  
 PR

XX (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.  
 PA (PHAA ) PHARMACIA SPAIN.  
 XX  
 PI Toran JL, Martinez Alonso C;  
 XX  
 DR WPI; 2004-055251/06.  
 DR N-FSDB; ADH10327.  
 XX

PT Novel antibody or its fragment comprising a light chain and/or heavy  
 PT chain which is capable of binding to glycoprotein gp120 of human  
 PT immunodeficiency virus (HIV) useful for treating HIV infection.  
 XX  
 PS Claim 1; SEQ ID NO 2; 56pp; English.

XX The invention relates to an antibody (I) or its fragment comprising heavy  
CC chain and/or light chain, capable of binding to glycoprotein gp120  
CC protein of HIV; anti-HIV vaccine (I) or a chemical compound identified by  
CC (I) is useful for preventing and treating HIV infections. They are also  
CC useful for inhibiting binding of HIV to a viral co-receptor. The present  
CC sequence represents the light chain sequence of anti-HIV-gp120 antibody  
CC S8, S19 and S20.  
XX  
SQ Sequence 215 AA;

Query Match 88.4%; Score 680; DB 8; Length 215;  
Best Local Similarity 91.7%; Pred. No. 5.5e-43;  
Matches 132; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTTITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRSGS 61  
Db 4 QSPSSLASVGDRTTITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRSGG 63  
Qy 62 GSGTEFTLTISLQPEDFATYYCLOKTYPTWTFGGTKVEIKRTVAAPSVFIFPPSDEQL 121  
Db 64 GSGTEFTLTISLQPEDFATYYCLOHNSYPLTFGGTKVEIKRTVAAPSVFIFPPSDEQL 123  
Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145  
Db 124 KSGTASVVCLLNNFYPREAKVQWK 147

RESULT 13  
ADK52390  
ID ADK52390 standard; protein; 152 AA.  
XX  
AC ADK52390;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human anti-MCP-1 variable region light chain #24.  
XX  
KW monocytic chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;  
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.  
XX  
OS Homo sapiens.  
XX  
FN WO2004016769-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 19-AUG-2003; 2003WO-US026232.  
XX  
PR 19-AUG-2002; 2002US-0404802P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;  
XX  
DR WPI; 2004-203794/19.  
DR N-PSDB; ADK52389.  
XX  
PT New human monoclonal antibody that binds to monocytic chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.  
XX  
PS Claim 2; SEQ ID NO 96; 154pp; English.

XX The present invention relates to a human monoclonal antibody that binds  
CC to monocytic chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast

CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.  
XX  
SQ Sequence 152 AA;

Query Match 87.8%; Score 675; DB 8; Length 152;  
Best Local Similarity 90.3%; Pred. No. 9.3e-43;  
Matches 130; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTTITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRSGS 61  
Db 6 QSPSSLASVGDRTTITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRSGS 65  
Qy 62 GSGTEFTLTISLQPEDFATYYCLOKTYPTWTFGGTKVEIKRTVAAPSVFIFPPSDEQL 121  
Db 66 GSGTEFTLTISLQPEDFATYYCLOHNSYPTTFGGTKVEIKRTVAAPSVFIFPPSDEQL 125  
Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145  
Db 126 KSGTASVVCLLNNFYPREAKVQWK 149

RESULT 14  
ADK52354  
ID ADK52354 standard; protein; 152 AA.  
XX  
AC ADK52354;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human anti-MCP-1 variable region light chain #15.  
XX  
KW monocytic chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;  
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.  
XX  
OS Homo sapiens.  
XX  
FN WO2004016769-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 19-AUG-2003; 2003WO-US026232.  
XX  
PR 19-AUG-2002; 2002US-0404802P.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;  
XX  
DR WPI; 2004-203794/19.  
DR N-PSDB; ADK52353.  
XX  
PT New human monoclonal antibody that binds to monocytic chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.  
XX  
PS Claim 2; SEQ ID NO 60; 154pp; English.

XX The present invention relates to a human monoclonal antibody that binds  
CC to monocytic chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or

CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.

XX Sequence 152 AA;

Query Match 87.8%; Score 675; DB 8; Length 152;  
Best Local Similarity 90.3%; Pred. NO. 9.3e-43;  
Matches 130; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITCRASQDTRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 61  
DB 6 QSPSSLSASVGDRTVITCRASQDTRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 65  
QY 62 GSGTEFTLTISLQPEDPATYCYCLOKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121  
DB 66 GSGTEFTLTISLQPEDPATYCYCLOHNTYPTTFGGTKVDIKRTVAAPSVFIFFPSDEQL 125

QY 122 KSGTASVVCLLNFPYREXKEHQK 145  
DB 126 KSGTASVVCLLNFPYREKQVWK 149

#### RESULT 15

ADS84470  
ID ADS84470 standard; protein; 234 AA.

XX ADS84470;

XX 18-NOV-2004 (first entry)

XX Human anti-EPO-R antibody Ab467 light chain SEQ ID NO:109.

XX human; erythropoietin receptor; EPO receptor;  
KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
KW antianemic; neuroprotective; vulnerable; gene therapy; aplasia; anaemia;  
KW wound healing; neural cell damage protection;  
KW neural tissue damage protection; brain injury; spinal cord injury;  
KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.

XX Homo sapiens.

XX WO2004035603-A2.

XX 29-APR-2004.

XX 14-OCT-2003; 2003WO-US032243.

XX 14-OCT-2002; 2002US-00269711.

XX 10-OCT-2003; 2003US-00684109.

XX (ABBO ) ABBOTT LAB.

XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;

XX WPI; 2004-348433/32.

XX N-PSDB; ADS84468, ADS84469.

XX New antibodies that bind to or activate an endogenous human  
PT erythropoietin receptor, useful for diagnosing, preventing or treating  
PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
PT anemia.

XX Disclosure; SEQ ID NO 109; 192pp; English.

XX The present invention describes an antibody or its fragment that binds to

CC or activates an endogenous activity of a human erythropoietin (EPO)  
CC receptor in a mammal, but does not interact with a peptide having a  
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
CC methods of modulating or activating an endogenous activity of a human EPO  
CC receptor in a mammal, comprising administering to the mammal a  
CC therapeutic amount of the above antibody or its fragment to modulate or  
CC activate the receptor; (2) a method of treating a mammal suffering from  
CC aplasia, comprising administering to the mammal a therapeutic amount of  
CC the above antibody or its fragment to modulate or activate the receptor;  
CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
CC an isolated and purified polynucleotide sequence, and their fragments,  
CC complements and degenerate codon equivalents; and (5) an isolated and  
CC purified amino acid sequence, and their fragments. The EPO receptor  
CC binding antibody has antianemic, neuroprotective and vulnerary  
CC activities, and can be used in gene therapy. The compositions and methods  
CC from the present invention can be used for modulating an endogenous  
CC activity of a human EPO receptor or for treating mammals suffering from  
CC aplasia or anaemia. They may also be used for identifying mammals having  
CC a dysfunctional EPO receptor. The composition may also be used in  
CC promoting wound healing or in protecting against neural cell and/or  
CC tissue damage resulting from brain/spinal cord injury, stroke and the  
CC like. The present sequence represents a human anti-EPO-R antibody light  
CC chain, which is given in the exemplification of the present invention.

XX Sequence 234 AA;

Query Match 87.6%; Score 674; DB 8; Length 234;  
Best Local Similarity 90.3%; Pred. NO. 1.7e-42;  
Matches 130; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITCRASQDTRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 61

DB 26 QSPSSLSASVGDRTVITCRASQDTRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 85

QY 62 GSGTEFTLTISLQPEDPATYCYCLOKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121

DB 86 GSGTEFTLTISLQPEDPATYCYCLOHNSYPCSGGKLEIKRTVAAPSVFIFFPSDEQL 145

QY 122 KSGTASVVCLLNFPYREXKEHQK 145

DB 146 KSGTASVVCLLNFPYREKQVWK 169

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Job time : 69.1532 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 78.009 Seconds

(without alignments)  
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Title: US-09-784-950-30

Perfect score: 769

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Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	694	90.2	236	15	US-10-038-591-52
2	684	88.9	234	16	US-10-684-109-97
3	683	88.8	184	16	US-10-684-109-78
4	682	88.7	236	15	US-10-038-591-48
5	680	88.4	215	16	US-10-462-040A-2
6	674	87.6	153	15	US-10-309-762-245
7	674	87.6	234	16	US-10-684-109-109
8	671	87.3	234	16	US-10-684-109-91
9	670	87.1	234	16	US-10-684-109-103
10	668	86.9	234	16	US-10-684-109-115
11	666	86.6	236	15	US-10-038-591-51
12	657	85.4	236	15	US-10-038-591-47
13	655	85.2	212	14	US-10-320-231A-77

14	649	84.4	213	16	US-10-379-392-135	Sequence 135, Appl
15	649	84.4	214	15	US-10-364-953-1	Sequence 1, Appli
16	649	84.4	237	14	US-10-020-786-10	Sequence 10, Appl
17	647.5	84.2	163	15	US-10-364-743-20	Sequence 20, Appl
18	647	84.1	237	9	US-09-056-160B-100	Sequence 100, App
19	647	84.1	237	14	US-10-234-671-100	Sequence 100, App
20	647	84.1	491	13	US-10-011-125-2	Sequence 2, Appli
21	646	84.0	213	16	US-10-379-392-137	Sequence 137, App
22	645.5	83.9	241	14	US-10-221-945-1	Sequence 1, Appli
23	645	83.9	213	16	US-10-379-392-155	Sequence 155, App
24	644	83.7	236	9	US-09-859-053-30	Sequence 30, Appl
25	644	83.7	236	16	US-10-625-105-30	Sequence 30, Appl
26	642	83.5	214	15	US-10-408-901-44	Sequence 44, Appl
27	641	83.4	214	14	US-10-153-382-19	Sequence 19, Appl
28	640	83.2	213	16	US-10-379-392-153	Sequence 153, App
29	639	83.1	367	15	US-10-291-265-899	Sequence 899, App
30	638	83.0	214	15	US-10-364-953-3	Sequence 3, Appli
31	638	83.0	214	15	US-10-364-953-11	Sequence 11, Appl
32	638	83.0	214	16	US-10-379-392-170	Sequence 170, App
33	638	83.0	237	14	US-10-020-786-8	Sequence 8, Appli
34	638	83.0	237	14	US-10-227-694-4	Sequence 4, Appli
35	638	83.0	237	17	US-10-754-212-5	Sequence 5, Appli
36	635	82.6	208	15	US-10-634-581-1	Sequence 1, Appli
37	635	82.6	214	9	US-09-949-559-128	Sequence 128, App
38	635	82.6	214	10	US-09-875-221A-128	Sequence 128, App
39	635	82.6	214	14	US-10-310-454-4	Sequence 4, Appli
40	635	82.6	214	15	US-10-364-953-4	Sequence 4, Appli
41	635	82.6	214	17	US-10-728-420B-113	Sequence 113, App
42	634	82.4	214	15	US-10-423-299-3	Sequence 3, Appli
43	633	82.3	136	15	US-10-038-591-2	Sequence 2, Appli
44	632	82.2	213	16	US-10-379-392-157	Sequence 157, App
45	631	82.1	139	14	US-10-153-382-31	Sequence 31, Appl

#### ALIGNMENTS

RESULT 1  
US-10-038-591-52  
; Sequence 52, Application US/10038591  
; Publication No. US20040086503A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Bruce D.  
; APPLICANT: Beebe, Jean  
; APPLICANT: Miller, Penelope E.  
; APPLICANT: Moyer, James D.  
; APPLICANT: Corvalan, Jose R.  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
; FILE REFERENCE: ABX-PF2  
; CURRENT APPLICATION NUMBER: US/10/038,591  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,927  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 52  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-038-591-52

Query Match 90.2%; Score 694; DB 15; Length 236;  
Best Local Similarity 92.4%; Pred. No. 6.1e-44;  
Matches 133; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy	2	QSPSSLSASVGDRTVITCRASQDTRDNLGNWYQKPGKAPKRLIYAASNLQSGVSRFSGS	61
Db	28	QSPSSLSASVGDRTVITCRASQDTRDNLGNWYQKPGKAPKRLIYAASNLQSGVSRFSGS	87
Qy	62	GSQTEFTLTSSLOPEDPATVYCYQYKTYPTWFGQTKVEIKRTVAAPSVIFPPPSDQL	121
Db	88	GSQTEFTLTSSLOPEDPATVYCYQYKTYPTWFGQTKVEIKRTVAAPSVIFPPPSDQL	147

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Qy 122 KSGTASVCLNNFYPREXKEHQK 145
Db 148 KSGTASVCLNNFYPREAKVQWK 171

RESULT 2
US-10-684-109-97
; Sequence 97, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wiele, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-97

Query Match 88.8%; Score 684; DB 16; Length 234;
Best Local Similarity 92.4%; Pred. No. 3.3e-43;
Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGS 61
Db 26 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGS 85

Qy 62 GSGTEFTLTSSLOPEDFATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVPFPPSDEQL 121
Db 86 GSGTEFTLTSSLOPEDFATYCYLQHNSYPTFGQGTKEIKRTVAAPSVPFPPSDEQL 145

Qy 122 KSGTASVCLNNFYPREXKEHQK 145
Db 146 KSGTASVCLNNFYPREAKVQWK 169

RESULT 3
US-10-684-109-78
; Sequence 78, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wiele, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-78
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Query Match 88.8%; Score 683; DB 16; Length 184;
Best Local Similarity 92.4%; Pred. No. 3.1e-43;
Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGS 61
Db 28 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGS 87

Qy 62 GSGTEFTLTSSLOPEDFATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVPFPPSDEQL 121
Db 88 GSGTEFTLTSSLOPEDFATYCYLQHNTYPTFGQGTKEIKRTVAAPSVPFPPSDEQL 147

Qy 122 KSGTASVCLNNFYPREXKEHQK 145
Db 148 KSGTASVCLNNFYPREAKVQWK 171

RESULT 4
US-10-038-591-48
; Sequence 48, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-48

Query Match 88.7%; Score 682; DB 15; Length 236;
Best Local Similarity 91.0%; Pred. No. 4.7e-43;
Matches 131; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGS 61
Db 28 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGS 87

Qy 62 GSGTEFTLTSSLOPEDFATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVPFPPSDEQL 121
Db 88 GSGTEFTLTSSLOPEDFATYCYLQHNSYPTFGQGTKEIKRTVAAPSVPFPPSDEQL 147

Qy 122 KSGTASVCLNNFYPREXKEHQK 145
Db 148 KSGTASVCLNNFYPREAKVQWK 171

RESULT 5
US-10-462-040A-2
; Sequence 2, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Light chain
US-10-462-040A-2

Query Match      88.4%; Score 680; DB 16; Length 215;
Best Local Similarity 91.7%; Pred. No. 6.1e-43;
Matches 132; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy  2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 61
Db  4 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 63

Qy  62 GSGTEFTLTISLQPEDPATYVCLOQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121
Db  64 GSGTEFTLTISLQPEDPATYVCLOHNSYPLTFGGTKVEIKRTVAAPSVFIFFPSDEQL 123

Qy  122 KSGTASVVCLLNFPYREXKEHQK 145
Db  124 KSGTASVVCLLNFPYREXKEHQK 147

RESULT 6
US-10-309-762-245
; Sequence 245, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudae, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-245

Query Match      87.6%; Score 674; DB 15; Length 153;
Best Local Similarity 91.0%; Pred. No. 1.2e-42;
Matches 131; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy  2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 61
Db  6 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 65

Qy  62 GSGTEFTLTISLQPEDPATYVCLOQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121
Db  66 GSGTEFTLTISLQPEDPATYVCLOHNSYPLTFGGTKVEIKRTVAAPSVFIFFPSDEQL 125

Qy  122 KSGTASVVCLLNFPYREXKEHQK 145
Db  126 KSGTASVVCLLNFPYREXKEHQK 149

RESULT 7
US-10-684-109-109
; Sequence 109, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-91

Query Match      87.3%; Score 671; DB 16; Length 234;
Best Local Similarity 89.6%; Pred. No. 3e-42;
Matches 129; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy  2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 61
Db  26 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 85

Qy  62 GSGTEFTLTISLQPEDPATYVCLOQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121
Db  86 GSGTEFTLTISLQPEDPATYVCLOHNSYPCFQGGTKLEIKRTVAAPSVFIFFPSDEQL 145
```

```
Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
    |||||:|||||:|||||:|||||:
Db 146 KSGTASVVCLLNNFYPREAKVQWK 169

RESULT 9
US-10-684-109-103
; Sequence 103, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-103

Query Match 87.1%; Score 670; DB 16; Length 234;
Best Local Similarity 90.3%; Pred. No. 3.6e-42;
Matches 130; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDVRTITCRASQDIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 61
    |||||:|||||:|||||:|||||:
Db 26 QSPSSLASVGDVRTITCRASQDIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 85

Qy 62 GSGTEFTLTISLQPEDPATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVEIFFPPSDEQL 121
    |||||:|||||:|||||:|||||:
Db 86 GSGTEFTLTISLQPEDPATYCYLQHNSYPTFGGTKEIKRTVAAPSVEIFFPPSDEQL 145

Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
    |||||:|||||:|||||:|||||:
Db 146 KSGTASVVCLLNNFYPREAKVQWK 169

RESULT 10
US-10-684-109-115
; Sequence 115, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-115

Query Match 86.9%; Score 668; DB 16; Length 234;
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Best Local Similarity 90.3%; Pred. No. 5.1e-42;
Matches 130; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDVRTITCRASQDIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 61
    |||||:|||||:|||||:|||||:
Db 26 QSPSSLASVGDVRTITCRSQRIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 85

Qy 62 GSGTEFTLTISLQPEDPATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVEIFFPPSDEQL 121
    |||||:|||||:|||||:|||||:
Db 86 GSGTEFTLTISLQPEDPATYCYLQHNSYPTFGGTKEIKRTVAAPSVEIFFPPSDEQL 145

Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
    |||||:|||||:|||||:|||||:
Db 146 KSGTASVVCLLNNFYPREAKVQWK 169

RESULT 11
US-10-038-591-51
; Sequence 51, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-51

Query Match 86.6%; Score 666; DB 15; Length 236;
Best Local Similarity 90.3%; Pred. No. 7.2e-42;
Matches 130; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDVRTITCRASQDIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 61
    |||||:|||||:|||||:|||||:
Db 28 QSPSSLASVGDVRTITCRASQDIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 87

Qy 62 GSGTEFTLTISLQPEDPATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVEIFFPPSDEQL 121
    |||||:|||||:|||||:|||||:
Db 88 GSGTEFTLTISLQPEDPATYCYLQHNNYPTFGQGTKEIKRTVAAPSVEIFFPPSDEQL 147

Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
    |||||:|||||:|||||:|||||:
Db 148 KSGTASVVCLLNNFYPREAKVQWK 171

RESULT 12
US-10-038-591-47
; Sequence 47, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
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; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
; TYPE: PRT
; LENGTH: 236
; ORGANISM: Homo sapiens
US-10-038-591-47

Query Match      85.4%; Score 657; DB 15; Length 236;
Best Local Similarity 88.2%; Pred. No. 3.3e-41;
Matches 127; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFGSGS 61
DB 28 QPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYAASRLHSGVPSRFGSGS 87

QY 62 GSGTEFTLTISLQPEDPATYTCLOKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQOL 121
DB 88 GSGTEFTLTISLQPEDPATYTCLOHNSYPCSFQGGTKLEIKRTVAAPSVFIFFPSDQOL 147

QY 122 KSGTASVVCLNNFYPREKKEHQK 145
DB 148 KSGTASVVCLNNFYPREKQVQWK 171

RESULT 13
US-10-320-231A-77
; Sequence 77, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 2002-12-19
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 77
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-77

Query Match      85.2%; Score 655; DB 14; Length 212;
Best Local Similarity 88.9%; Pred. No. 4.3e-41;
Matches 128; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFGSGS 61
DB 4 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYASASSLSQGVPSRFGSGS 63

QY 62 GSGTEFTLTISLQPEDPATYTCLOKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQOL 121
DB 64 GSGTEFTLTISLQPEDPATYTCLOKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQOL 123

QY 122 KSGTASVVCLNNFYPREKKEHQK 145
DB 124 KSGTASVVCLNNFYPREKQVQWK 147

RESULT 14
US-10-379-392-135
; Sequence 135, Application US/10379392
; Publication No. US20040110226A1

; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 135
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Humanized
US-10-379-392-135

Query Match      84.4%; Score 649; DB 16; Length 213;
Best Local Similarity 87.5%; Pred. No. 1.2e-40;
Matches 126; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFGSGS 61
DB 6 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYFTSSLSHSGVPSRFGSGS 65

QY 62 GSGTEFTLTISLQPEDPATYTCLOKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQOL 121
DB 66 GSGTEFTLTISLQPEDPATYTCLOKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQOL 125

QY 122 KSGTASVVCLNNFYPREKKEHQK 145
DB 126 KSGTASVVCLNNFYPREKQVQWK 149

RESULT 15
US-10-364-953-1
; Sequence 1, Application US/10364953
; Publication No. US2003024397A1
; GENERAL INFORMATION:
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MARVIN, JONATHAN S.
; TITLE OF INVENTION: ANTIBODY VARIANTS WITH PASTER ANTIGEN ASSOCIATION RATES
; FILE REFERENCE: P1951R1
; CURRENT APPLICATION NUMBER: US/10/364,953
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/355,895
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/409,685
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: Full
; OTHER INFORMATION: Y0101-VL
US-10-364-953-1

Query Match      84.4%; Score 649; DB 15; Length 214;
Best Local Similarity 87.5%; Pred. No. 1.2e-40;
Matches 126; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFGSGS 61
DB 6 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYFTSSLSHSGVPSRFGSGS 65
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.1636 Seconds  
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678.897 Million cell updates/sec

Title: US-09-784-950-30

Perfect score: 769

Sequence: 1 QSPSSLSASVGDRTVTTCR.....VCLLNFFPREXKEHQSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647	84.1	491	4	US-10-011-125A-2
2	644	83.7	236	4	US-09-859-053-30
3	641	83.4	214	4	US-09-472-087-71
4	637	82.8	233	4	US-08-030-175-43
5	631	82.1	139	4	US-09-472-087-22
6	631	82.1	139	4	US-09-472-087-96
7	630	81.9	214	2	US-07-934-373C-39
8	630	81.9	214	3	US-08-437-642B-39
9	630	81.9	214	5	PCT-US93-07832-39
10	629	81.8	218	5	PCT-US96-13152-2
11	628	81.7	214	2	US-07-934-373C-40
12	628	81.7	214	2	US-08-788-800-11
13	628	81.7	214	3	US-08-437-642B-40
14	628	81.7	214	3	US-09-097-309-2
15	628	81.7	214	3	US-09-097-171A-2
16	628	81.7	214	3	US-09-460-587-2
17	628	81.7	214	4	US-09-940-166A-2
18	628	81.7	214	5	PCT-US93-07832-40
19	628	81.7	233	2	US-07-934-373C-25
20	628	81.7	233	3	US-08-437-642B-25
21	628	81.7	233	4	US-08-146-206C-25
22	628	81.7	233	4	US-09-705-686-25
23	628	81.7	233	4	US-09-705-392A-25
24	628	81.7	233	4	US-09-705-398-25
25	628	81.7	233	5	PCT-US93-07832-25
26	628	81.7	237	3	US-09-097-309-6
27	628	81.7	237	3	US-09-097-171A-10

28	628	81.7	237	3	US-09-422-712B-2	Sequence 2, Appli
29	628	81.7	237	3	US-09-607-756-2	Sequence 2, Appli
30	628	81.7	237	3	US-09-460-587-6	Sequence 6, Appli
31	628	81.7	237	4	US-09-940-166A-6	Sequence 6, Appli
32	627.5	81.6	232	1	US-08-704-744-80	Sequence 80, Appli
33	625	81.3	214	1	US-08-458-516-12	Sequence 12, Appli
34	624	81.1	236	1	US-08-157-101A-5	Sequence 5, Appli
35	622	80.9	214	3	US-09-679-397-1	Sequence 1, Appli
36	622	80.9	214	4	US-09-680-148-1	Sequence 1, Appli
37	622	80.9	214	4	US-09-304-465A-1	Sequence 1, Appli
38	622	80.9	237	2	US-08-463-667A-25	Sequence 25, Appli
39	622	80.9	237	2	US-08-463-667A-3	Sequence 3, Appli
40	622	80.9	237	3	US-08-923-854-25	Sequence 25, Appli
41	622	80.9	237	5	PCT-US91-09133-26	Sequence 26, Appli
42	615	80.0	218	2	US-08-887-352B-13	Sequence 13, Appli
43	615	80.0	218	3	US-08-466-151-9	Sequence 9, Appli
44	615	80.0	218	3	US-09-109-207C-13	Sequence 13, Appli
45	615	80.0	218	3	US-09-296-005-13	Sequence 13, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-011-125A-2  
; Sequence 2, Application US/10011125A  
; Patent No. 6828121  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Christina Yu-Ching  
; TITLE OF INVENTION: BACTERIAL HOST STRAINS  
; FILE REFERENCE: P1804R1  
; CURRENT APPLICATION NUMBER: US/10/011.125A  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: US 60/256,162  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 2  
; LENGTH: 491  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized.  
; Patent No. 6828121  
US-10-011-125A-2

Query Match Similarity 84.1%; Score 647; DB 4; Length 491;

Best Local Similarity 86.8%; Pred. No. 1.6e-51;

Matches 125; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVTTCRASQDTRDNLGWYQQKPGKAPKRLIYAASNLQSGVPSRPSGS 61

Db 29 QSPSSLSASVGDRTVTTCRASQDTRDNLGWYQQKPGKAPKRLIYTSSLHSGVPSRPSGS 88

Qy 62 GSGTEFTLTSSLOPEDFATVYCYQYTPWTFQGTKEIKRTVAAPSVFIFPPSDEQL 121

Db 89 GSGTDYLTSSLOPEDFATVYCYQYTPWTFQGTKEIKRTVAAPSVFIFPPSDEQL 148

Qy 122 KSGTASVVCLLNFFPREXKEHQK 145

Db 149 KSGTASVVCLLNFFPREXKEHQK 172

#### RESULT 2

US-09-859-053-30

; Sequence 30, Application US/09859053

; Patent No. 6803039

; GENERAL INFORMATION:

; APPLICANT: Tsuji, Takashi

; APPLICANT: Tezuka, Katsunari

; APPLICANT: Hori, No. 6803039uaki

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF

Query Match	83.4%	Score 641;	DB 4;	Length 214;
Best Local Similarity	87.5%;	Pred. No. 2.2e-51;		
Matches 126;	Conservative 5;	Mismatches 13;	Indels 0;	Gaps 0;
Qy	2	QSPSSLSASVGDRTVITTCRASODIRDLNGLMWQKPGKAPKELIYAANLSQSGVPSRSGS	61	
Db	6	QSPSSLSASVGDRTVITTCRASQSINSYLDWVQKPGKAPKULIYAASSLSQSGVPSRSGS	65	
Qy	62	GSGETFTLTISSLOPEDFATYCYLQYKTYPMWTFQGQKVEIKRTVAAPSVPFIFFPSDEQL	121	
Db	66	GSGETFTLTISSLOPEDFATYCCQYYSTPTTFPGGKVEIKRTVAAPSVPFIFFPSDEQL	125	
Qy	122	KSGTASVVCLLNNFYPREXKEHQK	145	
Db	126	KSGTASVVCLLNNFYPREAKVOWK	149	

RESULT 5  
US - 09-472-087-22  
Sequence 22, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, BILLEN E.  
APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PF1  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: US/09/472,087  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 139  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-472-087-22

Query Match 82.1%; Score 631; DB 4; Length 139;  
Best Local Similarity 89.1%; Pred. No. 1.1e-50;  
Matches 123; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
Qy 4 PSSLSASVGDRTTTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGSGS 63  
Db 1 PSSLSASVGDRTTTCRASQINSYLDWYQKPGKAPKLLIYAASSLSQGVPSRFSGSGS 60  
Qy 64 GTEFTLTSSLOPEDFATYICLYQKTYPTWTFQGTKEIKRTVAAPSVFIPPPSDEQLKS 123  
Db 61 GTDFLTLTSSLOPEDFATYICQYQYSTPTFTGPGTKVEIKRTVAAPSVFIPPPSDEQLKS 120  
Qy 124 GTASVVCLLNNFYPREXK 141  
Db 121 GTASVVCLLNNFYPREAK 138

RESULT 6  
US-09-472-087-96  
; Sequence 96, Application US/09472087  
; Patent No. 6862736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, ELLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PF1  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 139  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-472-087-96

Query Match 82.1%; Score 631; DB 4; Length 139;  
Best Local Similarity 89.1%; Pred. No. 1.1e-50;  
Matches 123; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
Qy 4 PSSLSASVGDRTTTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGSGS 63  
Db 1 PSSLSASVGDRTTTCRASQINSYLDWYQKPGKAPKLLIYAASSLSQGVPSRFSGSGS 60  
Qy 64 GTEFTLTSSLOPEDFATYICLYQKTYPTWTFQGTKEIKRTVAAPSVFIPPPSDEQLKS 123  
Db 61 GTDFLTLTSSLOPEDFATYICQYQYSTPTFTGPGTKVEIKRTVAAPSVFIPPPSDEQLKS 120  
Qy 124 GTASVVCLLNNFYPREXK 141

Db 121 GTASVVCLLNNFYPREAK 138  
RESULT 7  
US-07-934-373C-39  
; Sequence 39, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-07-934-373C-39

Query Match 81.9%; Score 630; DB 2; Length 214;  
Best Local Similarity 86.1%; Pred. No. 2.2e-50;  
Matches 124; Conservative 5; Mismatches 15; Indels 0; Gaps 0;  
Qy 2 QSPSSLASVGDRTTTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGS 61  
Db 6 QSPSSLASVGDRTTTCRASQDIRDNLGWYQKPGKAPKLLIYTTSTLESQGVPSRFSGS 65  
Qy 62 GSGTFTLTSSLOPEDFATYICLYQKTYPTWTFQGTKEIKRTVAAPSVFIPPPSDEQL 121  
Db 66 GSGTDTLTSSLOPEDFATYICQYQYSTPTFTGPGTKVEIKRTVAAPSVFIPPPSDEQL 125  
Qy 122 KSGTASVVCLLNNFYPREXKEHOK 145  
Db 126 KSGTASVVCLLNNFYPREAKVQWK 149  
RESULT 8  
US-08-437-642B-39  
; Sequence 39, Application US/08437642B  
; Patent No. 6054297  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta

```
;
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
;
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-437-642B-39
;
; Query Match 81.9%; Score 630; DB 3; Length 214;
; Best Local Similarity 86.1%; Pred. No. 2.2e-50;
; Matches 124; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
;
; Qy 2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKELIYAASNLSQGVPSRFSGS 61
; Db 6 QSPSSLASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYTTLSGVSFRFSGS 65
;
; Qy 62 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFQGGTKVEIKRTVAAPSVPFPPSDEQL 121
; Db 66 GSGTDYTLTISLQPEDPATYCYQCGNTLPPTFGQGTKEIKRTVAAPSVPFPPSDEQL 125
;
; Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
; Db 126 KSGTASVVCLLNNFYPREKQVQWK 149
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; RESULT 9
; PCT-US93-07832-39
; Sequence 39, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
```

```
;
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
;
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; PCT-US93-07832-39
;
; Query Match 81.9%; Score 630; DB 5; Length 214;
; Best Local Similarity 86.1%; Pred. No. 2.2e-50;
; Matches 124; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
;
; Qy 2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKELIYAASNLSQGVPSRFSGS 61
; Db 6 QSPSSLASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYTTLSGVSFRFSGS 65
;
; Qy 62 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFQGGTKVEIKRTVAAPSVPFPPSDEQL 121
; Db 66 GSGTDYTLTISLQPEDPATYCYQCGNTLPPTFGQGTKEIKRTVAAPSVPFPPSDEQL 125
;
; Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
; Db 126 KSGTASVVCLLNNFYPREKQVQWK 149
;
; RESULT 10
; PCT-US96-13152-2
; Sequence 2, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-2

Query Match 81.8%; Score 629; DB 5; Length 218;
Best Local Similarity 83.1%; Pred. No. 2.8e-50;
Matches 123; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

Qy 2 QSPSSLSASVGDRTVITCRASQDI-----RDNLGWYQKPGKAPKRLIYAASNLSQGVPSR 57
Db 6 QSPSSLSASVGDRTVITCRASQDYNMYQKPGKAPKRLIYAASNLSQGVPSR 65
Qy 58 PFGSGSGTEFTLTITSSLOPEDFATYCYQKTYPTWTFQGTGKVEIKRTVAAPSVFIIPPSS 117
Db 66 PFGSGSGTDFLTITSSLOPEDFATYCYQKTYPTWTFQGTGKVEIKRTVAAPSVFIIPPSS 125
Qy 118 DEQLKSGTASVVCLLNNFYPREXKEHQK 145
Db 126 DEQLKSGTASVVCLLNNFYPREAKVQWK 153

RESULT 11
US-07-934-373C-40
; Sequence 40, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: 07/715272
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; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-40

Query Match 81.7%; Score 628; DB 2; Length 214;
Best Local Similarity 86.1%; Pred. No. 3.4e-50;
Matches 124; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFGSGS 61
Db 6 QSPSSLSASVGDRTVITCRASQDINNMYQKPGKAPKRLIYYTSTLHSGVPSRFGSGS 65
Qy 62 GSGTEFTLTITSSLOPEDFATYCYQKTYPTWTFQGTGKVEIKRTVAAPSVFIIPPSSDEQL 121
Db 66 GSGTDYTLTITSSLOPEDFATYCYQKTYPTWTFQGTGKVEIKRTVAAPSVFIIPPSSDEQL 125
Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
Db 126 KSGTASVVCLLNNFYPREAKVQWK 149

RESULT 12
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-788-800-11
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Query Match	81.7%	Score 628;	DB 2;	Length 214;
Best Local Similarity	86.1%;	Pred. No. 3.4e-50;		
Matches 124;	Conservative 4;	Mismatches 16;	Indels 0;	Gaps 0;
Qy	2	QSPSSLSASVGDRTVITCRASQDIRDNLGNWYQOKPGKAPKELIYAASNLOGVPSRFSGS	61	
Db	6	QSPSSLSASVGDRTVITCRASQDINNNLNNWYQOKPGKAPKLLIYTTSLHSGVPSRFSGS	65	
Qy	62	GSGETFLTIISSLPQEDFATYICLQYKTYPTWTFQGTQKVEIKRTVAAPSVFIFPPSPDEQL	121	
Db	66	GSGETDYLTISSLPQEDFATYICOQGNLPTPTFGQGTQKVEIKRTVAAPSVFIFPPSPDEQL	125	
Qy	122	KSGTASVWCLLNNFYPREXKEHQK	145	
Db	126	KSGTASVWCLLNNFYPREAKVQWK	149	

Db	6	QSPSSLSASVGDRTVITCRASQDNNLYNMWQQPGKAPKULLIYYTSTLHSGVSPRFSGS	65
Qy	62	GSGETFTLTSSLPQEPFATYCYLQYKTYPMWTFQGGKVEIKRTVAAPSVFIFFPSDQL	121
Db	66	GSGETDYLTLTSSLPQEPFATYCYCOQNTLPTTFQGGKVEIKRTVAAPSVFIFFPSDQL	125
Qy	122	KSGTASVVCLLNNFYPREXKEHQK	145
Db	126	KSGTASVVCLLNNFYPREAKVQWK	149

Query Match 81.7%; Score 628; DB 3; Length 214;  
Best Local Similarity 86.1%; Pred. No. 3.4e-50;  
Matches 124; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

US-09-097-171A-2  
; Sequence 2, Application US/09097171A  
; Patent No. 6171586  
; GENERAL INFORMATION:  
; APPLICANT: Lam, Xanthe M.  
; APPLICANT: Oeswein, James Q.  
; APPLICANT: Ongpipattanakul, Booneri  
; APPLICANT: Shahrokh, Zahra  
; APPLICANT: Wang, Sharon X.  
; APPLICANT: Weissburg, Robert P.  
; APPLICANT: Wong, Rita L.  
; TITLE OF INVENTION: Antibody Formulation  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/097.171A  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/874897  
; FILING DATE: 13-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1089R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 214 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-097-171A-2

Query Match 81.7%; Score 628; DB 3; Length 214;  
Best Local Similarity 86.1%; Pred No. 3.4e-50;  
Matches 124; Conservative 4; Mismatches 16; Indels 0; Gaps 0;  
Qy 2 QSPSLSASVGDRTVITCRASQDIRDNLGWYQQKPGKAPKRLIYAASNLQSGVPSRFSGS 61  
Db 6 QSPSLSASVGDRTVITCRASQDIRDNLGWYQQKPGKAPKRLIYAASNLQSGVPSRFSGS 65  
Qy 62 GSGTEFTLTISLQPEDPATYICLYKTYPTWTFQGTQVETKRTVAAPSVFIFPPSDEQL 121  
Db 66 GSGTDYTLTISLQPEDPATYICLYKTYPTWTFQGTQVETKRTVAAPSVFIFPPSDEQL 125  
Qy 122 KSGTASVVCLLNFFPREKKEHQK 145  
Db 126 KSGTASVVCLLNFFPREKQVWK 149

Search completed: March 8, 2005, 05:54:08  
Job time : 17.1636 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 14.356 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-31

Perfect score: 1064

Sequence: 1 KLPTLSLTCAVYGSFSGY.....LP SKDVMQGTDEHVVTSKKE 202

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	911	85.6	231	2 B23746	Ig Fab region IV-J
2	734.5	69.0	627	2 S14683	Ig mu chain precu
3	574.5	54.0	143	2 B49028	Ig heavy chain V-I
4	536.5	50.4	592	2 S25705	Ig mu chain - shee
5	498	46.8	146	1 GHUH2	Ig mu chain - huma
6	494	46.4	140	2 S78052	Ig heavy chain pre
7	491.5	46.2	220	2 A49444	Ig gamma-1 heavy c
8	486	45.7	126	2 S47010	Ig heavy chain V4.
9	485.5	45.6	140	2 A49045	Ig heavy chain V r
10	475.5	44.7	288	2 S29690	Ig heavy chain VDJ
11	471.5	44.3	116	2 S37456	Ig mu chain - huma
12	465.5	43.8	155	2 S31512	Ig heavy chain - h
13	465.5	43.8	155	2 S31511	Ig heavy chain - h
14	456	42.9	137	2 S31676	Ig heavy chain V r
15	450.5	42.3	114	2 I72667	cold agglutinin FS
16	450	42.3	106	2 S37454	Ig mu chain - huma
17	449.5	42.2	130	2 S31690	Ig heavy chain V r
18	447.5	42.1	140	2 I37782	Ig variable region
19	447	42.0	452	1 MHHU	Ig mu chain C regi
20	447	42.0	453	2 S37768	Ig mu chain C regi
21	447	42.0	473	1 MHUUM	Ig mu chain C regi
22	447	42.0	474	2 S15590	Ig heavy chain - h
23	446	41.9	122	2 JL0047	Ig heavy chain V r
24	440	41.4	97	2 S26898	Ig heavy chain V r
25	437	41.1	97	2 S26805	Ig heavy chain V r
26	431	40.5	97	2 S14474	Ig heavy chain V r
27	430	40.4	97	2 S26806	Ig heavy chain V r
28	430	40.4	97	2 G34964	Ig heavy chain V-I
29	429.5	40.4	146	2 S09711	Ig heavy chain V r

ALIGNMENTS

RESULT 1

B23746

Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000

C:Accession: B23746

R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.

J. Biol. Chem. 266, 2836-2842, 1991

A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin

A:Reference number: A23746; MUID:91131575; PMID:1993660

A:Accession: B23746

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-231 <LEO>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F140-209/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 911; DB 2; Length 231;

Best Local Similarity 86.5%; Pred. No. 5.3e-65;

Matches 180; Conservative 7; Mismatches 13; Indels 8; Gaps 2;

Qy	1	KLPTLSLTCAVYGSFSGYVSWIRPPGKGLWIGWHSNSTNPNPSLKSRTISVD	60
Db	12	KPSETLSLTCAVYGSFSDYYVSWIRPPGKGLWIGWHSNSTNPNPSLKSRTISVD	71
Qy	61	TSKNQPSIKLSSVTAADTAVVYCARGAAEYVYVYGVMDVGGTTVTVSSGSASAPTLPP	120
Db	72	TSKNQPSIKLSSVTAADTAVVYCARGAAEYVYVYGVMDVGGTTVTVSSGSASAPTLPP	129
Qy	121	LVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVSLRGKYAATSQ	180
Db	130	LVSCNSPDSSTSSVAVGCLAQDFLPDSTTFGKYKNNSDISSTRGFPVSLRGKYAATSQ	189
Qy	181	VLLPSKDVMOQTDEHVV-----TGSKE	202
Db	190	VLLPSKDVMOQTDEHVVCKVQHPGNKE	217

RESULT 2

S14683

Ig mu chain precursor, membrane-bound (clone 201) - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999

C:Accession: S14683; S08047

R;Friedlander, R.M.; Nussenzeig, M.C.; Leder, P.

Nucleic Acids Res. 18, 4278, 1990

A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.

A:Reference number: S14683; MUID:90332450; PMID:2115996

A:Accession: S14683

A:Molecule type: mRNA

A:Residues: 1-827 <FRI>

A:Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451



Db 93 TSKNLSLKLSSVTAADTAVVYCARGLLRGCGNDVDYVYGMVDMVGQGTVTIVSS 146

RESULT 6  
S78052  
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Nov-1997 #sequence\_revision 05-Dec-1997 #text\_change 23-Jul-1999  
C:Accession: S78052; S23717  
R:Harindranath, N.  
A:Reference number: S78051  
A:Accession: S78052  
A:Molecule type: mRNA  
A:Residues: 1-140 <HAR>  
A:Cross-references: EMBL:X54441; NID:G37815; PIDN:CAA38308.1; PID:G930M18  
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins  
Int. Immunol. 3, 865-875, 1991  
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h  
patient.  
A:Reference number: S23716; MUID:92031262; PMID:1718404  
A:Accession: S23717  
A:Molecule type: mRNA  
A:Residues: 15-111 <HAW>  
A:Cross-references: EMBL:X54441  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>  
F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F:29-111/Domain: immunoglobulin homology <IMM>

Query Match 46.4%; Score 494; DB 2; Length 140;  
Best Local Similarity 84.2%; Pred. No. 3e-32;  
Matches 96; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

Qy 1 KLPTLSLTCAVYGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 60  
Db 27 KPSETLSLTCAVYGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 86

Qy 61 TSKNQFSLKLSVTAADTAVVYCARGAAEY----YVYVYGMVDMVGQGTVTIVSS 110  
Db 87 TSKNQFSLKLSVTAADTAVVYCARGGSLRFLWLLYPADYVYGQGLTIVSS 140

RESULT 7  
A49444  
Ig gamma-1 heavy chain (New) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 16-Jul-1999  
C:Accession: A49444  
R:Saul, F.A.; Poljak, R.J.  
Proteins 14, 363-371, 1992  
A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A res  
A:Reference number: A49444; MUID:93066153; PMID:1438175  
A:Accession: A49444  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-220 <SAU>  
A:Note: this sequence modified after extraction from NCBI backbone  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:137-202/Domain: immunoglobulin homology <IMM>

Query Match 46.2%; Score 491.5; DB 2; Length 220;  
Best Local Similarity 50.5%; Pred. No. 8e-32;  
Matches 98; Conservative 35; Mismatches 50; Indels 11; Gaps 5;

Qy 4 ETLSLTCAVYGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVDTSK 63  
Db 16 QTLSTCTVCTGSDDDYVWVWVQPPGKGLWIGVVFYVGTLLDPSLRGRVTLVNTSK 75

Qy 64 NQFSLKLSVTAADTAVVYCARGAAEYVYVYGMVDMVGQGTVTIVSSGASAPTLFPLVS 123

Db 76 NQFSLRSLSSVTAADTAVVYCARNLIA-----GGIDVWGQGLSVTVSSASTGKPSVFPPLAP 130

Qy 124 CENSPSDTSSVAVGCLAQDFLPDXITFXWKYKNNDSISSTRGPFPSVLK-CGKYAATSQVL 182  
Db 131 SSRKSTSG-GTAAALGCLVKDYFPPEVTVSW--NSGALTSGVHTFPVAVLQSSGLYSLSVVT 187

Qy 183 LPSKDVNQGTDEHV 196  
Db 188 VPSSSL--GTQTYI 199

RESULT 8  
S47010  
Ig heavy chain V4.21-UniqueD-J5 region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S47010  
R:Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.  
submitted to the EMBL Data Library, July 1994  
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin  
A:Reference number: S47009  
A:Accession: S47010  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-126 <MAH>  
A:Cross-references: EMBL:Z35492; NID:G517254; PIDN:CAA84625.1; PID:G517255  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 45.7%; Score 486; DB 2; Length 126;  
Best Local Similarity 83.6%; Pred. No. 1.2e-31;  
Matches 97; Conservative 3; Mismatches 8; Indels 8; Gaps 2;

Qy 1 KLPTLSLTCAVYGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 60  
Db 13 KPSETLSLTCAVYGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 72

Qy 61 TSKNQFSLKLSVTAADTAVVYCARG-----AAEYVYVYGMVDMVGQGTVTIVSS 110  
Db 73 TSKNQFSLKLSVTAADTAVVYCARGGCGPKKACYTKNWF--DPWGGGLTIVSS 126

RESULT 9  
A49045  
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C:Accession: A49045  
R:Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silvermar  
Eur. J. Immunol. 22, 1781-1788, 1992  
A:Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i blc  
A:Reference number: A49045; MUID:92324290; PMID:1623923  
A:Accession: A49045  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140 <GRI>  
A:Cross-references: GB:S39381; NID:G250899; PIDN:AAB22441.1; PID:G250900  
A:Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBI:P:108089)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 45.6%; Score 485.5; DB 2; Length 140;  
Best Local Similarity 86.6%; Pred. No. 1.4e-31;  
Matches 97; Conservative 1; Mismatches 9; Indels 5; Gaps 2;

Qy 1 KLPTLSLTCAVYGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 60  
Db 32 KPSETLSLTCAVYGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 91

Qy 61 TSKNQFSLKLSVTAADTAVVYCARG--AAEYVYVYGMVDMVGQGTVTIVSS 110





Search completed: March 8, 2005, 06:39:26  
Job time : 15.406 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 75.4368 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-31

Perfect score: 1064

Sequence: 1 KLPTLSLTCAVYGGSPSGY.....LPKDVQMGTDEHVVTGSKE 202

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	930.5	87.5	595	2	Q8WUX4	Q8wux4 homo sapien
2	930.5	87.5	597	2	Q6GMX5	Q6gmx5 mus sapien
3	930.5	87.5	597	2	Q9BU10	Q9bu10 homo sapien
4	930.5	87.5	625	2	Q96AA6	Q96aa6 homo sapien
5	924.5	86.9	597	2	Q9BQB8	Q9bqb8 homo sapien
6	861	80.9	620	2	Q9QCY0	Q9qcy0 mus sapien
7	800	75.2	606	2	Q6GMX2	Q6gmx2 mus sapien
8	714	67.1	613	2	Q8WUK1	Q8wuk1 mus sapien
9	712.5	67.0	597	2	Q96BB9	Q96bb9 mus sapien
10	566	53.2	465	2	Q6GMX6	Q6gmx6 mus sapien
11	559.5	52.6	576	2	Q6P4I8	Q6p4i8 mus sapien
12	539.5	50.7	613	2	Q8VCX7	Q8vcx7 mus sapien
13	526.5	49.5	476	2	Q6GMX1	Q6gmx1 mus sapien
14	517.5	48.6	477	2	Q6GMX7	Q6gmx7 mus sapien
15	498	46.8	146	1	HV21_HUMAN	P06331 mus sapien
16	498	46.8	614	2	Q7TMT6	Q7tmt6 mus sapien
17	480.5	45.2	496	2	Q96KX8	Q96kx8 mus sapien
18	478	44.9	116	2	Q7Z3Y6	Q7z3y6 mus sapien
19	473	44.5	478	2	Q6NYH3	Q6nyh3 mus sapien
20	472.5	44.4	478	2	Q7Z379	Q7z379 mus sapien
21	472	44.4	492	2	Q7Z374	Q7z374 mus sapien
22	467	43.9	473	2	Q8TC63	Q8tc63 mus sapien
23	464.5	43.7	476	2	Q6MZX7	Q6mzx7 mus sapien
24	447.5	42.1	479	2	Q9NM22	Q9nm22 mus sapien
25	447	42.0	454	1	MUC_HUMAN	P01871 mus sapien
26	440	41.4	150	2	Q95973	Q95973 mus sapien
27	431.5	40.6	472	2	Q6N089	Q6n089 mus sapien
28	428.5	40.3	478	2	Q6PI81	Q6pi81 mus sapien
29	422.5	39.7	573	2	Q8WU38	Q8wu38 mus sapien
30	416.5	39.1	119	2	Q9UL73	Q9ul73 mus sapien
31	415.5	39.1	605	2	Q6GN83	Q6gn83 xenopus lae

Query Match 87.5%; Score 930.5; DB 2; Length 595;

32	414	38.9	482	2	Q91X92	Q91x92 mus musculus
33	406	38.2	593	2	Q6INM5	Q6inm5 xenopus lae
34	405.5	38.1	470	2	Q6PJA4	Q6pja4 homo sapien
35	402.5	37.8	482	2	Q7Z351	Q7z351 homo sapien
36	400	37.6	572	2	Q661Q7	Q661q7 xenopus lae
37	398	37.4	470	2	Q7TMK1	Q7tmk1 mus musculus
38	397	37.3	225	2	Q6PAF5	Q6paf5 xenopus lae
39	394.5	37.1	464	2	Q6MZU6	Q6mzu6 homo sapien
40	394	37.0	139	2	Q86SX2	Q86sx2 homo sapien
41	390.5	36.7	129	1	HV2F_HUMAN	P01824 homo sapien
42	390	36.7	465	2	Q6P6C4	Q6p6c4 homo sapien
43	383.5	36.0	614	2	Q6DDO7	Q6ddo7 xenopus lae
44	383	36.0	472	2	Q6PJA7	Q6pja7 mus musculus
45	383	36.0	475	2	Q6MZQ6	Q6mzq6 homo sapien

#### ALIGNMENTS

RESULT 1  
Q8WUX4  
ID Q8WUX4 PRELIMINARY; PRT; 595 AA.  
AC Q8WUX4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marz M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC019235; AAH19235.2; -.  
DR PIR; G34964; G34964.  
DR HSSP; P01861; 1ADQ.  
DR PFam; PF07654; Cl-set; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 5.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;



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DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65274 MW; 2DAPAF8FB7E055851 CRC64;

Query Match      87.5%; Score 930.5; DB 2; Length 597;
Best Local Similarity 87.2%; Pred. No. 1.8e-74;
Matches 184; Conservative 4; Mismatches 14; Indels 9; Gaps 2;

QY 1 KLPETLSLTCVAVGSGFSGYWSWIRPPGKLEWIGEINHSNSTNYPNLSKRVTSVD 60
Db 32 KPSETLSLTCGVYGSFGYWSWIRPPGKLEWIGEINHSNSTNYPNLSKRVTSVD 91
QY 61 TSKNQFSIKLSVTAADTAIVYCAR---GAAYYYYYYGMVWGQGTITVSSGSASAPT 117
Db 92 TSKKQLSLKSSVNAADTAIVYCARVITRASPGTDGRYGMVWGQGTITVSSGSASAPT 151
QY 118 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNSDISSTRGPPSVLRGKYAA 177
Db 152 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKYAA 211
QY 178 TSQVLLPSKDVQMGTDEHV-----TGSKE 202
Db 212 TSQVLLPSKDVQMGTDEHVCKVQHPNGNKE 242

RESULT 4
Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kryzyski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.2; -
DR PIR; S15590; S15590.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
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DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBFE CRC64;

Query Match      87.5%; Score 930.5; DB 2; Length 625;
Best Local Similarity 87.2%; Pred. No. 1.9e-74;
Matches 184; Conservative 4; Mismatches 14; Indels 9; Gaps 2;

QY 1 KLPETLSLTCVAVGSGFSGYWSWIRPPGKLEWIGEINHSNSTNYPNLSKRVTSVD 60
Db 39 KPSETLSLTCGVYGSFGYWSWIRPPGKLEWIGEINHSNSTNYPNLSKRVTSVD 98
QY 61 TSKNQFSIKLSVTAADTAIVYCAR---GAAYYYYYYGMVWGQGTITVSSGSASAPT 117
Db 99 TSKKQLSLKSSVNAADTAIVYCARVITRASPGTDGRYGMVWGQGTITVSSGSASAPT 158
QY 118 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNSDISSTRGPPSVLRGKYAA 177
Db 159 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKYAA 218
QY 178 TSQVLLPSKDVQMGTDEHV-----TGSKE 202
Db 219 TSQVLLPSKDVQMGTDEHVCKVQHPNGNKE 249

RESULT 5
Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kryzyski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -
```





RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC015760; AAH15760.1; -.  
DR PIR; S05271; S05271.  
DR PIR; S24260; S24260.  
DR HSP; P01861; IADQ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
SQ SEQUENCE 597 AA; 65039 MW; 4FC3AD8ECE263D9 CRC64;

Query Match 67.0%; Score 712.5; DB 2; Length 597;  
Best Local Similarity 70.0%; Pred. No. 5.5e-55;  
Matches 145; Conservative 17; Mismatches 36; Indels 9; Gaps 3;

Qy 5 TSLTCAVYGGSFSGYYWSWIRQPPGKLEWIGEHNS-GSTNPNPSLKSRVTISVDTSK 63  
Db 36 SLRLSCAAGSFSGYYWSWIRQPPGKLEWIGEHNS-GSTNPNPSLKSRVTISVDTSK 95  
Qy 64 NQPSLKLSVTAADTAVYCAARGAAEY--YYGMDVWGQGTVTTVSSGSASAPTLFPL 121  
Db 96 DTLQLWNSLRAEDTAVYCAKPRGYSASGNTYREDYWGQGTTLVTVSSGSASAPTLFPL 155  
Qy 122 VSCNSPSTSSVAVGCLAQDFLPDXITEXWKYKNNSDISSTRGFPSPVLRGKYAATSQV 181  
Db 156 VSCNSPSTSSVAVGCLAQDFLPDSITTFWKYKNNSDISSTRGFPSPVLRGKYAATSQV 215  
Qy 182 LLPSKDVWGQGTDEHV-----TGSKE 202  
Db 216 LLPSKDVWGQGTDEHVCKVQHPNGKE 242

RESULT 10  
Q6GMX6 PRELIMINARY; PRT; 465 AA.  
ID Q6GMX6  
AC Q6GMX6  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Sapich M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073766; AAH73766.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IGV; 2.  
DR SMART; SM00407; IGV; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
KW Hypothetical protein.  
SQ SEQUENCE 465 AA; 51083 MW; B3A9E7D0FDB1386E CRC64;  
Query Match 53.2%; Score 566; DB 2; Length 465;  
Best Local Similarity 58.9%; Pred. No. 4.9e-42;  
Matches 116; Conservative 22; Mismatches 47; Indels 12; Gaps 5;  
Qy 1 KLPETLSLTCVAVGGSFSGYYWSWIRQPPGKLEWIGEHNSGSTNPNPSLKSRVTISVD 60  
Db 32 KPSETLSLTCVAVGGSFSGYYWSWIRQPPGKLEWIGEHNSGSTNPNPSLKSRVTISVD 91  
Qy 61 TSKNPSLKLSVTAADTAVYCAARGAAEY--YYGMDVWGQGTVTTVSSGSASAPTLFPL 120  
Db 92 TSKNPSLKLSVTAADTAVYCAARGAAEY--YYGMDVWGQGTVTTVSSGSASAPTLFPL 145  
Qy 121 LVSCNSPSTSSVAVGCLAQDFLPDXITEXWKYKNNSDISSTRGFPSPVLR-GGKYAATS 179  
Db 146 LAPSSKSTSG-GTAALGCLVKDYFPEPTVYSW-NSGALTSGVHTFPAVLQSSGLYSLSS 202  
Qy 180 QVLLPSKDVWGQGTDEHV 196  
Db 203 VTVTPSSSL--GTQTYI 217  
RESULT 11  
Q6P4I8 PRELIMINARY; PRT; 576 AA.  
ID Q6P4I8  
AC Q6P4I8  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE IGHD protein.  
GN Name=IGHD;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]









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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 93.6527 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-31

Perfect score: 1064

Sequence: 1 KLPTLSLTCAVYGGSPSGY.....LPKDVWGQTDHVVVGSKE 202

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1064	100.0	202	2 AAY34303	Aay34303 Igm antib
2	1041	97.8	205	2 AAY34299	Aay34299 Igm antib
3	920	86.5	190	2 AAY34304	Aay34304 Igm antib
4	876.5	82.4	197	2 AAY34300	Aay34300 Igm antib
5	734.5	69.0	627	7 ADE97370	Ade97370 Human imm
6	729.5	68.6	203	2 AAY34301	Aay34301 Igm antib
7	727	68.3	595	7 ADM05427	Adm05427 Human pro
8	718	67.5	223	2 AAY08598	Aay08598 Anti-huma
9	714.5	67.2	266	8 ADF69305	Adf69305 Human lun
10	713	67.0	588	2 AAU71880	Aau71880 Anti-huma
11	713	67.0	588	3 AAB12917	Aab12917 Anti-huma
12	713	67.0	596	4 AAM23924	Aam23924 Human EST
13	712	66.9	223	8 ADL70773	Adl70773 Anti-TNPa
14	706.5	66.4	228	8 ADL70776	Adl70776 Anti-TNPa
15	704.5	66.2	199	2 AAY34302	Aay34302 Igm antib
16	699	65.7	588	2 AAU71881	Aau71881 Anti-huma
17	699	65.7	588	3 AAB12918	Aab12918 Anti-huma
18	685	64.4	533	7 ADB65070	Adb65070 Human pro
19	684.5	64.3	570	8 ADR19329	Adr19329 Chimeric
20	683	64.2	569	8 ADR19330	Adr19330 Chimeric
21	675	63.4	571	8 ADP84970	Adp84970 Chimeric
22	646.5	60.8	450	6 ABP96294	Abp96294 4A5-3.1.1
23	633.5	59.5	453	6 ABP96295	Abp96295 4A5-3.1.1
24	624.5	58.7	472	2 AAR93166	Aar93166 Anti-rhes
25	617	58.0	229	7 ADJ32128	Adj32128 Human int

26	615	57.8	223	7 ADJ32112	Adj32112 Human int
27	607.5	57.1	230	7 ADJ32118	Adj32118 Human int
28	606	57.0	537	3 AAY96290	Aay96290 Human IGF
29	597.5	56.2	462	3 AAB26884	Aab26884 Human imm
30	584.5	54.9	464	7 ADE28411	Ade28411 Human ant
31	570.5	53.6	466	7 ADE28479	Ade28479 Human ant
32	568	53.4	473	4 AAB36206	Aab36206 Human imm
33	567.5	53.3	466	7 ADE28471	Ade28471 Human ant
34	563.5	53.0	580	6 AAO30915	Aao30915 di-NHS76
35	562	52.8	251	5 AEG80712	Aeg80712 Anyloid p
36	562	52.8	254	5 AEG80713	Aeg80713 Anyloid p
37	562	52.8	263	5 AEG80714	Aeg80714 Human IGF
38	559	52.5	580	6 AAO30913	Aao30913 di-NHS76
39	555.5	52.2	466	7 ADE28419	Ade28419 Human ant
40	554	52.1	152	6 ABO04857	Abo04857 Human epi
41	552	51.9	221	7 ADJ32126	Adj32126 Human int
42	545	51.2	229	3 AAB30593	Aab30593 Variable
43	544.5	51.2	172	3 AAY93713	Aay93713 The heavy
44	544.5	51.2	172	6 AAE35892	Aae35892 Human 2.1
45	544	51.1	241	8 ADS84467	Ads84467 Human ant

#### ALIGNMENTS

RESULT 1  
AAY34303  
ID AAY34303 standard; protein; 202 AA.

AC AAY34303;

DT 19-NOV-1999 (first entry)

DE Igm antibody CEM 13.12 heavy chain sequence.

KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

XX Location/Qualifiers

FT Misc-difference 147  
FT /label= "unknown  
FT /note= "encoded by TYC"

FT Misc-difference 151  
FT /label= "unknown  
FT /note= "encoded by TYC"

FT Misc-difference 151  
FT /label= "unknown  
FT /note= "encoded by TYC"

XX WO9945031-A2.

XX 10-SEP-1999.

PF 03-MAR-1999; 99WO-US004593.

PR 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

DR N-PSDB; AAZ20404.

XX New monoclonal antibody, used for treating e.g. graft versus host  
XX disease, cancers, autoimmune diseases and inflammatory diseases.

PS Claim 60; Fig 28; 245pp; English.

XX This sequence represents the heavy chain of an antibody of the invention.

CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IgM MAb ABX-CBL, providing that the antibody is not CBL1. The MAB  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX

SQ Sequence 202 AA;

Query Match 100.0%; Score 1064; DB 2; Length 202;  
Best Local Similarity 100.0%; Pred. No. 4.3e-67;  
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLPETLSLTCAVYGGSGFYWIRPPGKGLWGEINHSSTNPNPSLKSRVTISVD 60  
Db 1 KLPETLSLTCAVYGGSGFYWIRPPGKGLWGEINHSSTNPNPSLKSRVTISVD 60  
Qy 61 TSKNQFSLKLSVTAADTAVYICARGAAYYYYGYGMDVWGQGTIVTVSSGSASAPTLFP 120  
Db 61 TSKNQFSLKLSVTAADTAVYICARGAAYYYYGYGMDVWGQGTIVTVSSGSASAPTLFP 120  
Qy 121 LVSCENSPDTSVAVGCLAQDFLPDXITFPWKYKNNSDISSTRGFPSVLRGGKYAATSQ 180  
Db 121 LVSCENSPDTSVAVGCLAQDFLPDXITFPWKYKNNSDISSTRGFPSVLRGGKYAATSQ 180  
Qy 181 VLLPSKDVMOGTDEHVVTGSKE 202  
Db 181 VLLPSKDVMOGTDEHVVTGSKE 202

RESULT 2

AAAY34299  
ID AAY34299 standard; protein; 205 AA.

AC AAY34299;

DT 19-NOV-1999 (first entry)

DE IgM antibody CEM 10.1 C3 heavy chain sequence.

KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Misc-difference 150

FT /label= unknown

FT /note= "encoded by TYC"

PN WO9945031-A2.

PD 10-SEP-1999.

PF 03-MAR-1999; 99WO-US004583.

PR 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

DR N-PSDB; AAZ20400.

XX

PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.

PS Claim 60; Fig 24; 245pp; English.

XX This sequence represents the heavy chain of an antibody of the invention.  
XX The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
XX complement and a variable region that binds to the epitope on CD147 bound  
XX by the IgM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
XX can selectively kill activated T-cells, activated B-cells or resting or  
XX activated monocytes. The products and methods can be used for treating  
XX diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
XX versus host disease (GVHD), organ transplant rejection diseases (e.g.  
XX renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
XX (e.g. leukaemia and lymphomas) and pancreatic), autoimmune diseases  
XX (e.g. lupus), and inflammatory diseases (e.g. arthritis)

SQ Sequence 205 AA;

Query Match 97.8%; Score 1041; DB 2; Length 205;

Best Local Similarity 97.5%; Pred. No. 1.8e-65;

Matches 197; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KLPETLSLTCAVYGGSGFYWIRPPGKGLWGEINHSSTNPNPSLKSRVTISVD 60

Db 4 KPSETLSLTCAVYGGSGFYWIRPPGKGLWGEINHSSTNPNPSLKSRVTISVD 63

Qy 61 TSKNQFSLKLSVTAADTAVYICARGAAYYYYGYGMDVWGQGTIVTVSSGSASAPTLFP 120

Db 64 TSKNQFSLKLSVTAADTAVYICARGTTEYYYYGYGMDVWGQGTIVTVSSGSASAPTLFP 123

Qy 121 LVSCENSPDTSVAVGCLAQDFLPDXITFPWKYKNNSDISSTRGFPSVLRGGKYAATSQ 180

Db 124 LVSCENSPDTSVAVGCLAQDFLPDXITFPWKYKNNSDISSTRGFPSVLRGGKYAATSQ 183

Qy 181 VLLPSKDVMOGTDEHVVTGSKE 202

Db 184 VLLPSKDVMOGTDEHVVTGSKE 205

RESULT 3

AAAY34304

ID AAY34304 standard; protein; 190 AA.

AC AAY34304;

DT 19-NOV-1999 (first entry)

DE IgM antibody CEM 13.5 heavy chain sequence.

KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

PN WO9945031-A2.

PD 10-SEP-1999.

PF 03-MAR-1999; 99WO-US004583.

PR 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

DR N-PSDB; AAZ20405.



XX New immunoadhesin, useful for treating anthrax and rhinovirus, comprises  
PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and  
PT J chain and secretory component associated with the chimeric toxin  
PT receptor protein.  
XX  
PS Disclosure; SEQ ID NO 47; 289pp; English.  
XX  
XX The invention relates to a novel immunoadhesin comprising a chimeric  
CC toxin receptor protein consisting of a toxin receptor protein linked to  
CC at least a portion of an immunoglobulin heavy chain with a J (joining)  
CC chain and secretory component (SC) associated with the chimeric toxin  
CC receptor protein. The immunoadhesin comprises a chimeric bacterial or  
CC viral toxin receptor protein and the immunoadhesin has plant-specific  
CC glycosylation. The immunoadhesin of the invention demonstrates virucide  
CC and antibacterial activities and may be useful for reducing the binding  
CC of a viral or bacterial antigen to a host cell and thus for treating or  
CC preventing anthrax, as well as human rhinovirus infection which results  
CC in the common cold. The current sequence is that of the human  
CC immunoadhesin-related protein of the invention.  
XX  
SQ Sequence 627 AA;

Query Match 69.0%; Score 734.5; DB 7; Length 627;  
Best Local Similarity 67.9%; Pred. No. 2e-43;  
Matches 146; Conservative 23; Mismatches 29; Indels 17; Gaps 4;  
Qy 5 TSLTCAVYGGFSGYVSWIRPPGKLEWIGE-INHSQSTYNPSLKSRTVTSVDTSK 63  
Db 36 SVKVSCKASGTFSSAISVROAPGGLEWGGIPIFGPNTAQKFGQGVTTADEST 95  
Qy 64 NQFSLKLSSTVAADTAVVYCARG-----AAEYY----YYYGMDVMGQGTTVTVSSGSA 113  
Db 96 STAYMELSLRSEDTAVVYCAKTLGILGPYSSGWTGPNSDYYYGMDVMGQGTTVTVSSGSA 155  
Qy 114 SAPTLFPLVSCENSPDTSSTSSAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPSPVLRGG 173  
Db 156 SAPTLFPLVSCENSPDTSSTSSAVGCLAQDFLPDSDITFSWKYKNNSDISSTRGFPSPVLRGG 215  
Qy 174 KYAATSOVLLPSKDVMOGTDEHVV-----TGSKE 202  
Db 216 KYAATSOVLLPSKDVMOGTDEHVVCKVQHPNGNKE 250

RESULT 6  
AAY34301  
ID AAY34301 standard; protein; 203 AA.  
XX  
AC AAY34301;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE IGM antibody CEM 10.12 F3 heavy chain sequence.  
XX  
XX Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
OS Homo sapiens.  
XX  
FN WO9945031-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 03-MAR-1999; 99WO-US004583.  
XX  
PR 03-MAR-1998; 98US-00034607.  
PR 03-FEB-1999; 99US-00244253.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX  
DR WPI: 1999-540816/45.  
DR N-PSDB; AAZ20402.  
XX  
XX New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
PT  
XX  
PS Claim 60; Fig 26; 245pp; English.  
XX  
CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX  
SQ Sequence 203 AA;

Query Match 68.6%; Score 729.5; DB 2; Length 203;  
Best Local Similarity 71.4%; Pred. No. 1.4e-43;  
Matches 140; Conservative 25; Mismatches 28; Indels 3; Gaps 2;  
Qy 5 TSLTCAVYGGFSGYVSWIRPPGKLEWIGEIN-HSGSTYNPSLKSRTVTSVDTSK 63  
Db 6 SVKVSCKASGYTFTSYDINVRQATGQGLEWGMNPNFNSGTGYAQKFGQGVTVNRTSI 65  
Qy 64 NQFSLKLSSTVAADTAVVYCARG--AAEYVVVVYGMVWGQGTTVTVSSGSASAPTLPL 121  
Db 66 STAYMELSLRSEDTAVVYCAKGHGSYFYISYGMVWGQGTTVTVSSGSASAPTLPL 125  
Qy 122 VSCENSPDTSSTSSAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPSPVLRGGKYAATSQV 181  
Db 126 VSCENSPDTSSTSSAVGCLAQDFLPDSDITFSWKYKNNSDISSTRGFPSPVLRGGKYAATSQV 185  
Qy 182 LLPSKDVMOGTDEHVV 197  
Db 186 LLPSKDVMOGTDEHVV 201

RESULT 7  
ADM05427  
ID ADM05427 standard; protein; 595 AA.  
XX  
AC ADM05427;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human protein of the invention SEQ ID NO:4112.  
XX  
KW human; gene therapy; diagnostic marker; pharmaceutical.  
XX  
OS Homo sapiens.  
XX  
FN EP1347046-A1.  
XX  
PD 24-SEP-2003.  
XX  
PF 12-APR-2002; 2002EP-00008400.  
XX  
PR 22-MAR-2002; 2002JP-00137785.  
XX  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Iehii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;







XX PD 06-JUN-2000.  
XX PF 17-SEP-1999; 99JP-00263984.  
XX PR 18-SEP-1998; 98JP-00264598.  
XX PA (SANY ) SANKYO CO LTD.  
XX WPI; 2000-454476/40.  
XX DR N-PSDB; AAA78271.  
XX PT Anti-human Fas humanizing antibody-containing antirheumatic agents.  
XX PS Claim 1; Page 75-77; 109pp; Japanese.  
XX CC The present invention relates to antirheumatic agents which comprise as  
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
CC does not include a J segment, has apoptosis inducing activity, and  
CC consists of a light and heavy chain polypeptide produced synthetically.  
CC The agents of the invention exhibit antirheumatic and immunosuppressive  
CC activity and can be used to treat autoimmune diseases, especially  
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
CC binding properties. Included in the invention are nucleotide sequences of  
CC the IgM light and heavy chains (see AAA78267-A78272) and the  
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also  
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
CC chains used in the invention are represented by sequences AAA78213-  
CC A78266. Primers used for sequencing the human Ig DNA used in the  
CC invention are represented by sequences AAA78277-A78318 and AAA78335-  
CC A78337, while humanised anti-Fas Ig DNA sequencing primers are  
CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer  
CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in  
CC the production of the agent of the invention  
XX SQ Sequence 588 AA;  
Query Match 67.0%; Score 713; DB 3; Length 588;  
Best Local Similarity 67.8%; Pred No. 6.1e-42;  
Matches 139; Conservative 22; Mismatches 30; Indels 14; Gaps 3;  
Qy 5 TSLTCAVYGGFSGYYWSWIRQPGKGLEWIGEI-NHSGSTNNYPSLKRWTISVDTSK 63  
Db 36 SVKVSCKASGYTFTDYNMHWVRQAPGQGLEWMGIYPNGYGTGYNQKPKSKATLTVDNSA 95  
Qy 64 NQFSLKLSVTAADTAVTYCARGAAEYIYYIYGMVWGQGTITVTVSSGSASAPTLFPLVS 123  
Db 96 STAYMELSLRSSEDATVYTCARS-----YYAMDYWGQGTITVTVSSGSASAPTLFPLVS 148  
Qy 124 CENSPSDTSSVAVGCLAQDFPDXTITFXWKYKNNSDISSTRGFPFSLRGCKYAATSOVL 183  
Db 149 CENSPSDTSSVAVGCLAQDFPDSTITFSWKYKNNSDISSTRGFPFSLRGCKYAATSOVL 208  
Qy 184 PSKDVMOGTDEHV-----TGSKE 202  
Db 209 PSKDVMOGTDEHVCKVQHPNGNKE 233  
RESULT 12  
ID AAM23924  
XX AAM23924 standard; protein; 596 AA.  
XX AC AAM23924;  
XX DT 12-OCT-2001 (first entry)  
XX DE Human EST encoded protein SEQ ID NO: 1449.  
XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
XX gene therapy; nutrition.  
OS Homo sapiens.  
XX WO200154477-A2.  
XX PN 02-AUG-2001.  
XX PD 25-JAN-2001; 2001WO-US002687.  
XX PF 25-JAN-2000; 2000US-00491404.  
XX PR 17-JUL-2000; 2000US-00617746.  
XX PR 03-AUG-2000; 2000US-00631451.  
XX PR 15-SEP-2000; 2000US-00663870.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
XX DR WPI; 2001-476164/51.  
XX DR N-PSDB; AAH98583.  
XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
XX antibodies and research use.  
XX PS Claim 20; Page 1011-1012; 1275pp; English.  
XX CC The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a  
CC protein of the invention  
XX SQ Sequence 596 AA;  
Query Match 67.0%; Score 713; DB 4; Length 596;  
Best Local Similarity 69.9%; Pred No. 6.2e-42;  
Matches 144; Conservative 16; Mismatches 38; Indels 8; Gaps 3;  
Qy 5 TSLTCAVYGGFSGYYWSWIRQPGKGLEWIGEINHS-STNNYPSLKRWTISVDTSK 63  
Db 36 SLRLSCAASGFTFSSYWMHWVRQAPGKGLVWVSRIINTDGSSTSVADSVKGRFTISRDNAAK 95  
Qy 64 NQFSLKLSVTAADTAVTYCARG-AAEYIYYIYGMVWGQGTITVTVSSGSASAPTLFPLV 122  
Db 96 NTLYLQWNSLRAEDTAVTYCARADNCSSTSCYKCFDYWGQGTITVTVSSGSASAPTLFPLV 155  
Qy 123 SCENSPDSTSSVAVGCLAQDFPDXTITFXWKYKNNSDISSTRGFPFSLRGCKYAATSOVL 182  
Db 156 SCENSPDSTSSVAVGCLAQDFPDSTITFSWKYKNNSDISSTRGFPFSLRGCKYAATSOVL 215  
Qy 183 LPSKDVMOGTDEHV-----TGSKE 202  
Db 216 LPSKDVMOGTDEHVCKVQHPNGNKE 241  
RESULT 13  
ID ADL70773  
XX ADL70773 standard; protein; 223 AA.  
XX AC ADL70773;  
XX DT 03-JUN-2004 (first entry)  
XX DE Anti-TNFalpha antibody VH region, SEQ ID 46.  
XX KW Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;  
KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;





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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 107.196 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-31

Perfect score: 1064

Sequence: 1 KLPTLSLTCAVYCGSFSGY.....LPSKDVMOGTDEHVVTSKSE 202

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452.seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	734.5	69.0	627	13	US-10-047-542-47
2	727	68.3	595	15	US-10-108-260A-4112
3	685	64.4	533	15	US-10-104-047-3224
4	617	58.0	229	10	US-09-972-656-82
5	615	57.8	223	10	US-09-972-656-66
6	610.5	57.4	179	15	US-10-309-762-171
7	607.5	57.1	230	10	US-09-972-656-72
8	584.5	54.9	464	15	US-10-292-088-22
9	570.5	53.6	466	15	US-10-292-088-86
10	567.5	53.3	466	15	US-10-292-088-70
11	563.5	53.0	580	14	US-10-310-719-37
12	559	52.5	580	14	US-10-310-719-35
13	555.5	52.2	466	15	US-10-292-088-30

14	554	52.1	152	9	US-09-187-693-68	Sequence 68, Appl
15	552	51.9	221	10	US-09-972-656-80	Sequence 80, Appl
16	545	51.2	229	9	US-09-974-449-37	Sequence 37, Appl
17	544.5	51.2	172	14	US-10-153-382-21	Sequence 21, Appl
18	544	51.1	241	16	US-10-684-109-106	Sequence 106, Appl
19	541	50.8	241	16	US-10-684-109-71	Sequence 71, Appl
20	534	50.2	239	16	US-10-684-109-100	Sequence 100, Appl
21	533	50.1	241	16	US-10-684-109-88	Sequence 88, Appl
22	525	49.3	118	15	US-10-371-942-90	Sequence 90, Appl
23	521.5	49.0	193	15	US-10-264-049-4331	Sequence 4331, Ap
24	518	48.7	253	10	US-09-880-748-954	Sequence 954, App
25	518	48.7	253	15	US-10-293-418-954	Sequence 954, App
26	516	48.5	429	14	US-10-194-801C-6	Sequence 6, Appli
27	515	48.4	250	14	US-10-194-975-110	Sequence 110, App
28	515	48.4	255	10	US-09-880-748-1642	Sequence 1642, Ap
29	515	48.4	255	15	US-10-293-418-1642	Sequence 1642, Ap
30	512.5	48.2	250	10	US-09-880-748-993	Sequence 993, App
31	512.5	48.2	250	15	US-10-293-418-993	Sequence 993, App
32	512.5	48.2	254	10	US-09-880-748-1659	Sequence 1659, Ap
33	512.5	48.2	254	15	US-10-293-418-1659	Sequence 1659, Ap
34	510.5	48.0	252	10	US-09-880-748-1326	Sequence 1326, Ap
35	510.5	48.0	252	15	US-10-293-418-1326	Sequence 1326, Ap
36	510	47.9	235	16	US-10-684-109-112	Sequence 112, App
37	508	47.7	173	15	US-10-309-762-173	Sequence 173, App
38	508	47.7	447	14	US-10-194-801C-2	Sequence 2, Appli
39	507	47.7	249	10	US-09-880-748-957	Sequence 957, App
40	507	47.7	249	15	US-10-293-418-957	Sequence 957, App
41	505.5	47.5	250	10	US-09-880-748-1413	Sequence 1413, Ap
42	505.5	47.5	250	15	US-10-293-418-1413	Sequence 1413, Ap
43	504.5	47.4	125	15	US-10-371-942-110	Sequence 110, App
44	504.5	47.4	467	14	US-10-211-357-8	Sequence 8, Appli
45	504.5	47.4	467	14	US-10-211-357-10	Sequence 10, Appl

#### ALIGNMENTS

RESULT 1  
US-10-047-542-47  
; Sequence 47, Application US/10047542  
; Publication No. US20020168367A1  
; GENERAL INFORMATION:  
; APPLICANT: LARRICK, JAMES W.  
; APPLICANT: WYCOFF, KEITH L.  
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
; TITLE OF INVENTION: AND BACTERIAL DISEASES  
; FILE REFERENCE: 030905.0004.CIP1  
; CURRENT APPLICATION NUMBER: US/10/047,542  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: PCT/US01/13932  
; PRIOR FILING DATE: 2001-04-28  
; PRIOR APPLICATION NUMBER: 60/200,298  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 627  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-047-542-47

Query Match 69.0%; Score 734.5; DB 13; Length 627;  
Best Local Similarity 67.9%; Pred. No. 5.1e-46;  
Matches 146; Conservative 23; Mismatches 29; Indels 17; Gaps 4;

Qy 5 TLSLTCAVYCGSFSGYVWSWIRPPGKLEWIGE-INHSGSTNYPNPSLKSVRTISVDTSK 63  
Db 36 SVKVSCKASGCTFSYAIWSVRQPGQGLEWGGIIPFGTANYAQKFGQRTITADEST 95  
Qy 64 NQFSLKLSSTVAADTAVVYVYCARG-----AAEYV-----YYYGMDVMGQGTVTTVSSGSA 113  
Db 96 STAYNELLSLSESDTAVVYCAKTIILGIPYSGSWPNSDYYIYGMVWGQGTITTVSSGSA 155

Qy 114 SAPTLFPLVSCENSPDSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLRGG 173  
Db 156 SAPTLFPLVSCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGG 215  
Qy 174 KYAATSOVLLPSKDVMOGTDDEHVY-----TGSKE 202  
Db 216 KYAATSOVLLPSKDVMOGTDDEHVYKQHPNGNKE 250

RESULT 2  
US-10-108-260A-4112  
; Sequence 4112, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA  
; FILE REFERENCE: HI-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4112  
; LENGTH: 595  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-108-260A-4112

Query Match 68.3%; Score 727; DB 15; Length 595;  
Best Local Similarity 70.7%; Pred. No. 1.7e-45;  
Matches 145; Conservative 20; Mismatches 32; Indels 8; Gaps 3;

Qy 5 TSLSLTCAVYGGSPGYWMIROPPGKLEWIGINHSNSTN-YNPSLKSRVTISVDTSK 63  
Db 37 SLRLSCAASGTFNFAMHWIROPKGLLEVYVTSISNGRKYGESVKGRFTISRDSK 96  
Qy 64 NQPSLKLSVTAADTAVYICARGAAEYIIYGYGMDVMGQGTTVTVSSGSASAPTLFPLVS 123  
Db 97 NTLFLQMSLRDDTAVYICARGHS-IDNYHYGVDVMGQGTTVTVSSGSASAPTLFPLVS 155  
Qy 124 CENSPDSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLRGGKYAATSOVLL 183  
Db 156 CENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSOVLL 215  
Qy 184 PSKDVMOGTDDEHVY-----TGSKE 202  
Db 216 PSKDVMOGTDDEHVYKQHPNGNKE 240

RESULT 3  
US-10-104-047-3224  
; Sequence 3224, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: HI-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3224  
; LENGTH: 533  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3224

Query Match 64.4%; Score 685; DB 15; Length 533;  
Best Local Similarity 68.3%; Pred. No. 1.9e-42;  
Matches 140; Conservative 15; Mismatches 42; Indels 8; Gaps 3;

Qy 5 TSLSLTCAVYGGSPGYWMIROPPGKLEWIGINHSNSTNYPNPSLKSRVTISVDTSKN 64

Db 36 SLRLSCAASGDFVSSNTMSWVROSPGKPEWVATMYGGINTYYAESVKGRFTVSRDGSQN 95  
Qy 65 QPSLKLSVTAADTAVYICARGAAEYIYGYGMDVMGQGTTVTVSSGSASAPTLFPLVS 123  
Db 96 TLYLEMSLRPDDTAVYICVRDHRNYADTSPYGRK-WGQGTFLTVTVSSGSASAPTLFPLVS 154  
Qy 124 CENSPDSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLRGGKYAATSOVLL 183  
Db 155 CENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSOVLL 214  
Qy 184 PSKDVMOGTDDEHVY-----TGSKE 202  
Db 215 PSKDVMOGTDDEHVYKQHPNGNKE 239

RESULT 4  
US-09-972-656-82  
; Sequence 82, Application US/09972656  
; Publication No. US20030099647A1  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Tsai, Mei-Mei  
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
; TITLE OF INVENTION: Neutralizing Activity  
; FILE REFERENCE: A-799  
; CURRENT APPLICATION NUMBER: US/09/972,656  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 82  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-656-82

Query Match 58.0%; Score 617; DB 10; Length 229;  
Best Local Similarity 62.2%; Pred. No. 8.1e-38;  
Matches 125; Conservative 21; Mismatches 45; Indels 10; Gaps 5;

Qy 1 KLPETLSLTCAVYGGSPGYWMIROPPGKLEWIGINHSNSTNYPNPSLKSRVTISVD 60  
Db 13 KPSETLSLTCAVYGGSPGYWMIROPPGKLEWIGINHSNSTNYPNPSLKSRVTISVD 72  
Qy 61 TSKNQPSLKLSVTAADTAVYICARGAAEYIIYGYGMDVMGQGTTVTVSSGSASAP 116  
Db 73 TSKNQPSLKLSVTAADTAVYICARGWPTVYWGSIYRPGKGYFDYWGQGTFLTVTVSSASTKGP 132  
Qy 117 TLFPLVSCENSPDSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLR-GGKY 175  
Db 133 SVFELAPSPSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGLY 189  
Qy 176 AATSOVLLPSKDVMOGTDDEHV 196  
Db 190 SLSSVWTVPSSSL--GTQTYI 208

RESULT 5  
US-09-972-656-66  
; Sequence 66, Application US/09972656  
; Publication No. US20030099647A1  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Tsai, Mei-Mei  
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
; TITLE OF INVENTION: Neutralizing Activity  
; FILE REFERENCE: A-799  
; CURRENT APPLICATION NUMBER: US/09/972,656  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 66  
; LENGTH: 223





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Qy      180 QVLLPSKD 187
      |::|:
Db      206 VVTVPSSN 213

RESULT 9
US-10-292-088-86
; Sequence 86, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-86

Query Match      53.6%; Score 570.5; DB 15; Length 466;
Best Local Similarity 61.7%; Pred. No. 4.4e-34;
Matches 116; Conservative 21; Mismatches 46; Indels 5; Gaps 4;

Qy      1 KLPETLSLTCVAVGGSGFYWSWIROPKPGKLEWIGEINHSGSTNNPNSLKSRVTISVD 60
Db      32 KPSETLSLTCVSGGSIRGYWWSWIROPKPGKLEWIGIYYSGSTNNPNSLKSRVTISVD 91

Qy      61 TSKNQFSLKLSVTAADTAVYYCARGAAEYIIYGGMDVWGQGTITVTVSSGSASAPTLFP 120
Db      92 TSKNQFSLKLSVTAADTAVYYCARGGLYDYGW-FAPWGQGLTVTVSSASTKGPSVFP 150

Qy      121 LVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPSVLR-GGKYAATS 179
Db      151 LAPCSRSTSE-STAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSS 207

Qy      180 QVLLPSKD 187
      |::|:
Db      208 VVTVPSSN 215

RESULT 10
US-10-292-088-70
; Sequence 70, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-70

Query Match      53.6%; Score 570.5; DB 15; Length 466;
Best Local Similarity 61.7%; Pred. No. 4.4e-34;
Matches 116; Conservative 21; Mismatches 46; Indels 5; Gaps 4;

Qy      1 KLPETLSLTCVAVGGSGFYWSWIROPKPGKLEWIGEINHSGSTNNPNSLKSRVTISVD 60
Db      32 KPSETLSLTCVSGGSIRGYWWSWIROPKPGKLEWIGIYYSGSTNNPNSLKSRVTISVD 91

Qy      61 TSKNQFSLKLSVTAADTAVYYCARGAAEYIIYGGMDVWGQGTITVTVSSGSASAPTLFP 120
Db      92 TSKNQFSLKLSVTAADTAVYYCARGGLYDYGW-FAPWGQGLTVTVSSASTKGPSVFP 150

Qy      121 LVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPSVLR-GGKYAATS 179
Db      151 LAPCSRSTSE-STAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSS 207

Qy      180 QVLLPSKD 187
      |::|:
Db      208 VVTVPSSN 215
```

```
US-10-292-088-70

Query Match      53.3%; Score 567.5; DB 15; Length 466;
Best Local Similarity 61.2%; Pred. No. 7.4e-34;
Matches 115; Conservative 22; Mismatches 46; Indels 5; Gaps 4;

Qy      1 KLPETLSLTCVAVGGSGFYWSWIROPKPGKLEWIGEINHSGSTNNPNSLKSRVTISVD 60
Db      32 KPSETLSLTCVSGGSIRGYWWSWIROPKPGKLEWIGIYYSGSTNNPNSLKSRVTISVD 91

Qy      61 TSKNQFSLKLSVTAADTAVYYCARGAAEYIIYGGMDVWGQGTITVTVSSGSASAPTLFP 120
Db      92 TSKNQFSLKLSVTAADTAVYYCARGGLYDYGW-FAPWGQGLTVTVSSASTKGPSVFP 150

Qy      121 LVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPSVLR-GGKYAATS 179
Db      151 LAPCSRSTSE-STAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSS 207

Qy      180 QVLLPSKD 187
      |::|:
Db      208 VVTVPSSN 215

RESULT 11
US-10-310-719-37
; Sequence 37, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-NHS76(gamma4h) (FN>AQ) -ala-IL2(D20T) heavy chain fused to
; OTHER INFORMATION: IL-2 variant
US-10-310-719-37

Query Match      53.0%; Score 563.5; DB 14; Length 580;
Best Local Similarity 61.1%; Pred. No. 1.8e-33;
Matches 116; Conservative 20; Mismatches 43; Indels 11; Gaps 5;

Qy      1 KLPETLSLTCVAVGGSP-SGYWWSWIROPKPGKLEWIGEINHSGSTNNPNSLKSRVTISV 59
Db      13 KPSETLSLTCVAVSGYSISSGYWWSWIROPKPGKLEWIGSYHSGSYTNNPNSLKSRVTISV 72

Qy      60 DTSKNQFSLKLSVTAADTAVYYCARGAAEYIIYGGMDVWGQGTITVTVSSGSASAPTLF 119
Db      73 DTSKNQFSLKLSVTAADTAVYYCARGK-----WSKFDYWGQGLTVTVSSASTKGPSVF 126

Qy      120 PLVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPSVLR-GGKYAAT 178
Db      127 PLAPCSRSTSE-STAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSS 183

Qy      179 SQVLLPSKD 188
      |::|:
Db      184 SVTVPPSSSL 193

RESULT 12
US-10-310-719-35
; Sequence 35, Application US/10310719
; Publication No. US20030166163A1
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GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
TITLE OF INVENTION: Immunocytokines With Modulated Selectivity  
FILE REFERENCE: LEX-020  
CURRENT APPLICATION NUMBER: US/10/310,719  
CURRENT FILING DATE: 2002-12-04  
PRIOR APPLICATION NUMBER: 60/337,113  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/371,966  
PRIOR FILING DATE: 2002-04-12  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 35  
LENGTH: 580  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: variant

US-10-310-719-35  
Query Match 52.5%; Score 559; DB 14; Length 580;  
Best Local Similarity 61.6%; Pred. No. 3.9e-33;  
Matches 117; Conservative 20; Mismatches 41; Indels 12; Gaps 6;  
1 KLPETLSLTCVAVGSGSP-SGYWWSWIRQPPGKLEWIGSHSGSTNNPSLKSRTVISV 59  
13 KPSETLSLTCVAVGSGSISGYWWSWIRQPPGKLEWIGSHSGSTNNPSLKSRTVISV 72  
60 DTSKNQFSLKSSVTAADTAVVYCARGAAYYYYGMDVWGQGTITVTVSSG-SASAPTL 118  
73 DTSKNQFSLKSSVTAADTAVVYCARGK-----WSKFDYWGQGTITVTVSSGASTKGP 126  
119 PFLVSCENSPDSTSSVAVGCLAQDFLPDXITFXWKYKNNDISSTRGPPSVLR-GGKYAA 177  
127 PFLAPCSRSTSE-STAALGCLVKDYFPFPTVSM--NSGALTSGVHTTFAVLQSSGLYSL 183  
178 TSQVLLPSKD 187  
184 SSVTVTPSSN 193

RESULT 13  
US-10-282-088-30  
Sequence 30, Application US/10292088  
Publication No. US2003021100A1  
GENERAL INFORMATION:  
APPLICANT: BEDIAN, VAHE  
APPLICANT: GLADUE, RONALD P.  
APPLICANT: CORVALAN, JOSE  
APPLICANT: JIA, XIAO-CHI  
APPLICANT: FENG, XIAO  
TITLE OF INVENTION: ANTIBODIES TO CD40  
FILE REFERENCE: ABX-PF/3 US  
CURRENT APPLICATION NUMBER: US/10/292,088  
CURRENT FILING DATE: 2003-03-14  
PRIOR APPLICATION NUMBER: 60/348,980  
PRIOR FILING DATE: 2001-11-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 30  
LENGTH: 466  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-292-088-30

Query Match 52.2%; Score 555.5; DB 15; Length 466;  
Best Local Similarity 58.5%; Pred. No. 5.7e-33;  
Matches 113; Conservative 23; Mismatches 42; Indels 15; Gaps 5;  
1 KLPETLSLTCVAVGSGFSGYWSWIRQPPGKLEWIGSHSGSTNNPSLKSRTVISVD 60  
32 KPSETLSLTCVAVGSGSIRSYWTWIRQPPGKLEWIGSHSGSTNNPSLKSRTVISVD 91

QY 61 TSKNQFSLKSSVTAADTAVVYCAR-----GAAAYYYYGMDVWGQGTITVTVSSGSASA 115  
DB 92 MSKNQFSLKSSVTAADTAVVYCARKGDYGGNFYFHQ-----WGQGTITVTVSSASTKG 145  
QY 116 PTLFPLVSCENSPDSTSSVAVGCLAQDFLPDXITFXWKYKNNDISSTRGPPSVLR-GGK 174  
DB 146 PSVFPLAPCSRSTSE-STAALGCLVKDYFPFPTVSM--NSGALTSGVHTTFAVLQSSGL 202  
QY 175 YAATSQVLLPSKD 187  
DB 203 YLSLSSVTVTPSSN 215

RESULT 14

US-09-187-693-68  
Sequence 68, Application US/09187693  
Patent No. US20020173629A1  
GENERAL INFORMATION:  
APPLICANT: Jakobovits, Aya  
APPLICANT: Yang, Xiao-Dong  
APPLICANT: Gallo, Michael  
APPLICANT: Jia, Xiao-Chi  
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal  
TITLE OF INVENTION: Growth Factor Receptor  
FILE REFERENCE: Cell 4.20 CIP2  
CURRENT APPLICATION NUMBER: US/09/187,693  
CURRENT FILING DATE: 1998-11-05  
PRIOR APPLICATION NUMBER: 09/162,280  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 08/851,362  
PRIOR FILING DATE: 1997-05-05  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 68  
LENGTH: 152  
TYPE: PRT  
ORGANISM: human  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(152)  
OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-187-693-68

Query Match 52.1%; Score 554; DB 9; Length 152;  
Best Local Similarity 77.5%; Pred. No. 2.3e-33;  
Matches 107; Conservative 6; Mismatches 23; Indels 2; Gaps 2;

QY 8 LTCVAVGSGFSGYWSWIRQPPGKLEWIGSHSGSTNNPSLKSRTVISVDTSKNQFS 67  
DB 8 LTCVAVGSGFSGYWSWIRQPPGKLEWIGSHSGSTNNPSLKSRTVISVDTSKNQFS 67  
QY 68 LKLSVTAADTAVVYCARGAAYYYYGMDVWGQGTITVTVSSGSASAAPTLPPLVSCENS 127  
DB 68 LKLSVTAADTAVVYCARGPGG-SYYYGMDVWGQGTITVTVSSASTKGPVFLAPCSRS 126  
QY 128 PSDTSSVAVGCLAQDFLP 145  
DB 127 TSE-STAALGCLGQGLLP 143

RESULT 15

US-09-972-656-80  
Sequence 80, Application US/09972656  
Publication No. US20030099647A1  
GENERAL INFORMATION:  
APPLICANT: Deshpande, Rajendra  
APPLICANT: Tsai, Mei-Mei  
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
TITLE OF INVENTION: Neutralizing Activity  
FILE REFERENCE: A-799  
CURRENT APPLICATION NUMBER: US/09/972,656  
CURRENT FILING DATE: 2001-10-05

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; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-80

Query Match      51.9%; Score 552; DB 10; Length 221;
Best Local Similarity 58.8%; Pred. No. 4.8e-33;
Matches 117; Conservative 21; Mismatches 47; Indels 14; Gaps 6;

Qy 1 KLPETLSLTCAVYGGSPS--GYWWSWIRQPPGKGLEWIGEIHHSGSTNPNPSLKSRTIS 58
Db 13 KPSETLSLTCAVSGSISGGYSWSWIRQPPGKGLEWIGIYHSGSTVYNPSLKSRTIS 72

Qy 59 VDTSKNQFSLKLSVTAADTAVYTCARGAAYYYYYGMDVMWGQGTVTYVSSGSASAPTL 118
Db 73 VDRSKNQFSLKLSVTAADTAVYTCARGDWGYF-----DYWGQGTTLVTYVSSASTKGPSV 126

Qy 119 FPLVSCENSPSDTSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPSVLR-GGKYAA 177
Db 127 FPLAPSSKSTSG-GTAAIGCLLVKDYFPEPVTVSW-NSGALTSGVHTFPAPVLQSSGLYSL 183

Qy 178 TSQVLLPSKDVMOGTDEHV 196
Db 184 SSVVTVFSSSL--GTQTVI 200
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Search completed: March 8, 2005, 07:05:53  
Job time : 108.196 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 22.2112 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-31

Perfect score: 1064

Sequence: 1 KLPTLSLTCAVYGGSPSGY.....LPSKDVMOGTDEHVVTGSKE 202

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624.5	58.7	472	3	US-08-793-450-8
2	568	53.4	473	3	US-09-049-672A-4
3	544.5	51.2	172	4	US-09-472-087-7
4	544.5	51.2	172	4	US-09-472-087-86
5	528	49.6	832	3	US-08-630-820-7
6	528	49.6	832	4	US-09-273-453-7
7	516	48.5	429	4	US-09-372-425A-6
8	508	47.7	447	4	US-09-372-425A-2
9	504.5	47.4	467	3	US-08-523-894-8
10	504.5	47.4	467	3	US-08-523-894-10
11	504.5	47.4	467	3	US-08-523-894-12
12	502.5	47.2	123	3	US-08-793-450-4
13	496.5	46.7	476	3	US-08-487-550-12
14	496.5	46.7	476	4	US-09-526-098-12
15	496.5	46.7	476	4	US-09-383-916-12
16	496.5	46.7	487	4	US-09-800-729-145
17	492	46.2	139	4	US-09-203-768A-2
18	486.5	45.7	476	3	US-08-487-550-4
19	486.5	45.7	476	4	US-09-526-098-4
20	486.5	45.7	476	4	US-09-383-916-4
21	483.5	45.4	219	3	US-09-460-384-37
22	471	44.3	122	1	US-08-360-125-11
23	471	44.3	122	2	US-08-450-578-11
24	471	44.3	122	2	US-09-017-628-11
25	471	44.3	122	2	US-09-014-880-11
26	471	44.3	122	4	US-08-450-363-11
27	471	44.3	122	4	US-09-467-903-11

28	466.5	43.8	229	2	US-08-887-352B-20	Sequence 20, Appl
29	466.5	43.8	229	3	US-09-109-207C-20	Sequence 20, Appl
30	466.5	43.8	229	3	US-09-296-005-20	Sequence 20, Appl
31	466.5	43.8	229	4	US-09-920-171-20	Sequence 20, Appl
32	466.5	43.8	229	4	US-09-716-028-20	Sequence 20, Appl
33	466.5	43.8	229	4	US-10-113-996-20	Sequence 20, Appl
34	466.5	43.8	229	2	US-08-887-352B-25	Sequence 25, Appl
35	466.5	43.8	233	3	US-09-109-207C-25	Sequence 25, Appl
36	466.5	43.8	233	3	US-09-296-005-25	Sequence 25, Appl
37	466.5	43.8	233	4	US-09-920-171-25	Sequence 25, Appl
38	466.5	43.8	233	4	US-09-716-028-25	Sequence 25, Appl
39	466.5	43.8	233	4	US-10-113-996-25	Sequence 25, Appl
40	466.5	43.8	451	2	US-08-887-352B-14	Sequence 14, Appl
41	466.5	43.8	451	2	US-08-887-352B-16	Sequence 16, Appl
42	466.5	43.8	451	3	US-08-466-151-65	Sequence 65, Appl
43	466.5	43.8	451	3	US-09-109-207C-14	Sequence 14, Appl
44	466.5	43.8	451	3	US-09-109-207C-16	Sequence 16, Appl
45	466.5	43.8	451	3	US-09-296-005-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-08-793-450-8  
; Sequence 8, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHARABIHI, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,450  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 472 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-793-450-8

Query Match 58.7%; Score 624.5; DB 3; Length 472;  
Best Local Similarity 63.3%; Pred. No. 2.1e-49;  
Matches 126; Conservative 23; Mismatches 41; Indels 9; Gaps 6;

QY	1	KLPETLSLTCAYVGSFSGYYWMIROP	PPKGLWEIGEI	NHSGSTWYN	PSLKS	RVTISYD	60
Db	32	KPSETLSLTCYVGSFSGYYWMIROP	PPKGLWEIGEI	NHSGSTWYN	PSLKS	RVTISYD	91
QY	61	TSKNQFSLKLSVTAADTAVYCYARG	AAEYYYYYG--MDV	WQGGTTVT	VSGS	ASAPTL	118
Db	92	TSKNQFSLKLSVTAADTAVYCYAR	--APEYKWKYHGDW	FDPWGGTTVT	VSSAS	TGKPSV	150
QY	119	FFLVGENSEPSTSSVAVGCLAQD	PLPDXTFXWKYKRN	SDIS	STRG	FFPSVLR--G	177
Db	151	FFLAPSSKXSTG--GTAALGCLVK	QDYFPEPVT	VSW--NSG	ALTSQVHT	FFPAVLQSSGL	207
QY	178	TSQVLLPSPKQVMQGTDEHV	196				
Db	208	SSWTVTPSSSL--GTOTVI	224				

RESULT 2  
 US-09-049-672A-4  
 ; Sequence 4, Application US/09049672A  
 ; Patent No. 6135941  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Yue, Henry  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Cotley, Neil C.  
 ; APPLICANT: Guegler, Karl J.  
 ; APPLICANT: Baughn, Mariah R.  
 ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/049,672A  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cerrone, Michael C  
 ; REGISTRATION NUMBER: 39,132  
 ; REFERENCE/DOCKET NUMBER: PF-0497 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 473 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: PANCTUT01  
 ; CLONE: 1513264  
 US-09-049-672A-4

	Matches	119;	Conservative	22;	Mismatches	50;	Indels	8;	Gaps	5
Qy	1	KL	PETLSLTCAVYGGSPS--GYWSWIRPPGKGLEWIGEINHSGSTNNP	SLKSRVTIS	58					
Db	32	KP	SETTSLTCAVSGSGSITSGGYWSWIRPPGKLEWIGIYYSGSTLYNP	SLKSRVTIS	91					
Qy	59	VD	TSKQFSLKLSVTAADTAVYCAARGAAEYYYYYGMVGMGGT	TTVTSGGSASAPTL	118					
Db	92	VD	TSKQFSLKLSVTAADTAVYCARDDVGLRGNGYGMVGMGGT	TLVTVSASTKGP	SV 151					
Qy	119	FP	IVSCENSPSDTSSVAVGCLCAODFLPDXTFTXWKYKNNSDIS	STRGPPSVLR--CGKTA	177					
Db	152	FP	LAPSKSTSG--CTAALGCLVKDYFEPVPTVSW--NSGALT	SGVHTTFAVLQSSGL	SL 208					
Qy	178	TS	QVLLPSKDVMOGTDEHV	196						
Db	209	SS	VTVPSSSL--GTQTYI	225						

```

RESULT 3
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-EF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

      Query Match      51.2%      Score 544.5; DB 4; Length 172;
      Best Local Similarity 62.4%; Pred. No. 1.3e-42;
      Matches 108; Conservative 22; Mismatches 34; Indels 9; Gaps 4

Qy      1      KLPETLSLTCAVYGGSF--GYWSWIRQPPGKGLEWIGEHSGSTNNPSLKSRVTIS 58
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
Db      7      KPSQLSLTCTVSGGSISSGHHYWSWIRQHPGKGLEWIGIYVYIGNTVYNPDLKSRVTIS 66
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
Qy      59      VDTSKNQFSLKSSVTAADTAVVYCARGAAEYHYHYGMDVWGQGTTVTVSSGSASAPTL 118
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
Db      67      VDTSKNQFSLKSSVTAADTAVVYCARGDSGD-----YIGIDVWGQGTTVTVSSASTKGPSV 122
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
Qy      119     FRLVSCENSPDSTSSVAVGCLADFLPDXTTFXWKYKKNSSDISSRGPFPVLRL 171
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
Db      123     FPLAPCSRSTSE-STAAIGCLVDYDFPEPVTVSW--NSGALTSGVHTFPAVLQ 172
      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |

RESULT 4
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY

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QY 139 LAQDFL--PDXITXKWKYKNNDSISST 163  
Db 212 PAPELGGPSVFLPPKPKOTLMISRT 238

RESULT 9  
US-08-523-894-8  
; Sequence 8, Application US/08523894  
; Patent No. 6136310  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Newman, Roland A.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; TITLE OF INVENTION: Therapy  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314-3187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/523,894  
; FILING DATE: 06-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 467 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-523-894-8

Query Match 47.4%; Score 504.5; DB 3; Length 467;  
Best Local Similarity 55.0%; Pred. No. 2.5e-38;  
Matches 105; Conservative 27; Mismatches 50; Indels 9; Gaps 6;

QY 1 KLPETLSLTCAVYGGSFSG-YVWSWIRPPGKGLEWIGEHNS-GSTNPNPILKSRVTIS 58  
Db 32 KPSETLSLTCSVSGSISGDYWFIRSPGKLEWIGIYVSGGGTNYNPSLNNRVIS 91

QY 59 VDTSKNQPSLKLSSVTAADTAVYICARGAAYYYYYYGMVWGQGTITTVSSGSASAPTL 118  
Db 92 IDTSKNLPSLKLRSVTAADTAVYICASNILKYLHW---LLYWGQGLVTVSSASTKGPSV 148

QY 119 FPLVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNNDSISSTRGFPVLR-GGKYAA 177  
Db 149 FPLAPCSRSTSE-STAAALGCLVKDYFPFVPTVSW--NSGALTSGVHTFPVQLQSSGLYS 205

QY 178 TSQVLLPSKDV 188  
Db 206 SSVTVTPSSSL 216

RESULT 10  
US-08-523-894-10  
; Sequence 10, Application US/08523894  
; Patent No. 6136310  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Newman, Roland A.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; TITLE OF INVENTION: Therapy  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria

; APPLICANT: Hanna, Nabil  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; TITLE OF INVENTION: Therapy  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314-3187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/523,894  
; FILING DATE: 06-SEP-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 467 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-523-894-10

Query Match 47.4%; Score 504.5; DB 3; Length 467;  
Best Local Similarity 55.0%; Pred. No. 2.5e-38;  
Matches 105; Conservative 27; Mismatches 50; Indels 9; Gaps 6;

QY 1 KLPETLSLTCAVYGGSFSG-YVWSWIRPPGKGLEWIGEHNS-GSTNPNPILKSRVTIS 58  
Db 32 KPSETLSLTCSVSGSISGDYWFIRSPGKLEWIGIYVSGGGTNYNPSLNNRVIS 91

QY 59 VDTSKNQPSLKLSSVTAADTAVYICARGAAYYYYYYGMVWGQGTITTVSSGSASAPTL 118  
Db 92 IDTSKNLPSLKLRSVTAADTAVYICASNILKYLHW---LLYWGQGLVTVSSASTKGPSV 148

QY 119 FPLVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNNDSISSTRGFPVLR-GGKYAA 177  
Db 149 FPLAPCSRSTSE-STAAALGCLVKDYFPFVPTVSW--NSGALTSGVHTFPVQLQSSGLYS 205

QY 178 TSQVLLPSKDV 188  
Db 206 SSVTVTPSSSL 216

RESULT 11  
US-08-523-894-12  
; Sequence 12, Application US/08523894  
; Patent No. 6136310  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; TITLE OF INVENTION: Therapy  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria

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; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-523-894-12

Query Match 47.4%; Score 504.5; DB 3; Length 467;
Best Local Similarity 55.0%; Pred. No. 2.5e-38;
Matches 105; Conservative 27; Mismatches 50; Indels 9; Gaps 6;

Qy 1 KLPETLSLTCAVYGGSPG-YVWSWIROPKGLWIGELNHS-GSTNYPNLSKSRVTIS 58
Db 32 KPSETLSLTCTVYGGSPGYWIRPOPGKGLWIGELNHSSTNYPNLSKSRVTISVD 91
Qy 59 VDTSKNQFSLKSSVTAADTAVVYCARGAAEYVYVYG--MDVWGQGTVTVTSS 118
Db 92 IDTSKNLPSLKLRSVTAADTAVVYCASNILKYLHW---LLVWGQGLVTVTVSSASTKGPSV 148
Qy 119 PPLVSCNPSDTSVAVGCLAQFLDXITFXWKYKNSDISSTRFPSPVLR-GGKYAA 177
Db 149 FPLAPCSRSTSE-STAAIGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAPVLQSSGLYS 205
Qy 178 TSQVLLPSKDV 188
Db 206 SSVTVFSSSL 216

RESULT 12
US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-793-450-4

Query Match 47.2%; Score 502.5; DB 3; Length 123;
Best Local Similarity 87.5%; Pred. No. 6.2e-39;
Matches 98; Conservative 3; Mismatches 8; Indels 3; Gaps 2;

Qy 1 KLPETLSLTCAVYGGSPGYWIRPOPGKGLWIGELNHSSTNYPNLSKSRVTISVD 60
Db 13 KPSETLSLTCTVYGGSPGYWIRPOPGKGLWIGELNHSSTNYPNLSKSRVTISVD 72
Qy 61 TSKNQFSLKSSVTAADTAVVYCARGAAEYVYVYG--MDVWGQGTVTVTSS 110
Db 73 TSKNQFSLKLSVTAADTAVVYCARGAAEYVYVYG--MDVWGQGTVTVTSS 123

RESULT 13
US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-12

Query Match
Best Local Similarity 46.7%; Score 496.5; DB 3; Length 476;
Matches 108; Conservative 27; Mismatches 53; Indels 17; Gaps 8;

Qy 1 KLPETLSLTCVAVGSGFS-GYYWSWIROPCKGLEWIGE1-NHSGSTYNPSPKSRVTIS 58
Db 32 KPSETLSLTCVAVGSGSISGGYGWIRQPPCKGLEWIGSFYSSSGNTYNNPSPKSKQVTIS 91
Qy 59 VDTSGNQPSLKLSSVTAADTAAYVCARGAAEYVYVGM-----DVMGQGTTVTVSSGS 112
Db 92 TDTSGNQPSLKLNSMTAADTAAYVCVR---DRLFSVVGWVNNWFDVWGPGLVTVSSAS 148
Qy 113 ASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNSDSSSTRGPPSVLR- 171
Db 149 TKGPSVFLPAPSSKSTSG-GTAALGCLVKDYPPEPVTYSW--NSGALTSGVHTTTPAVLQS 205
Qy 172 GGYAATSQVLLPSKDVMOGTDEHV 196
Db 206 SGLYSLSSVTVTPSSSL--GTQTYI 228

RESULT 14
US-09-526-098-12
; Sequence 12, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-526-098-12

Query Match
Best Local Similarity 46.7%; Score 496.5; DB 4; Length 476;
Matches 108; Conservative 27; Mismatches 53; Indels 17; Gaps 8;

Qy 1 KLPETLSLTCVAVGSGFS-GYYWSWIROPCKGLEWIGE1-NHSGSTYNPSPKSRVTIS 58
Db 32 KPSETLSLTCVAVGSGSISGGYGWIRQPPCKGLEWIGSFYSSSGNTYNNPSPKSKQVTIS 91
Qy 59 VDTSGNQPSLKLSSVTAADTAAYVCARGAAEYVYVGM-----DVMGQGTTVTVSSGS 112
Db 92 TDTSGNQPSLKLNSMTAADTAAYVCVR---DRLFSVVGWVNNWFDVWGPGLVTVSSAS 148
Qy 113 ASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNSDSSSTRGPPSVLR- 171
Db 149 TKGPSVFLPAPSSKSTSG-GTAALGCLVKDYPPEPVTYSW--NSGALTSGVHTTTPAVLQS 205
Qy 172 GGYAATSQVLLPSKDVMOGTDEHV 196
Db 206 SGLYSLSSVTVTPSSSL--GTQTYI 228

RESULT 15
US-09-383-916-12
; Sequence 12, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-383-916-12

Query Match
Best Local Similarity 46.7%; Score 496.5; DB 4; Length 476;
Matches 108; Conservative 27; Mismatches 53; Indels 17; Gaps 8;

Qy 1 KLPETLSLTCVAVGSGFS-GYYWSWIROPCKGLEWIGE1-NHSGSTYNPSPKSRVTIS 58
Db 32 KPSETLSLTCVAVGSGSISGGYGWIRQPPCKGLEWIGSFYSSSGNTYNNPSPKSKQVTIS 91
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Qy	59	VDTSKNQFSLKLSVTAADTAVYYCARGAAEYYYYYIGM-----DWMGQGTTVTVSSGS	112
Db	92	TDTSKNQFSLKLSMTAADTAVYYCVR---DRLFSVVGVVYNNWFDYWGPGVLTVSSAS	148
Qy	113	ASAPTLPLVSCENSPSDTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPSVLR-	171
Db	149	TKGPSVFPFLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQS	205
Qy	172	GGKYAATSQVLLPSKDVMOGTDEHV	196
Db	206	SGLYSLSSVTVTPSSSL--GIQTYY	228

Search completed: March 8, 2005, 05:54:09  
Job time : 23.2112 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.1629 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-32  
Perfect score: 752  
Sequence: 1 MPVTPGPASISCRSSQSL.....TASVVCLLSNFPYPREAKVQW 143

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.\*
- 2: pir2.\*
- 3: pir3.\*
- 4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	74.1	219	2	PC4203
2	555	73.8	197	2	S29593
3	548	72.9	219	2	S52028
4	543	72.2	135	2	S40342
5	538	71.5	121	2	S40371
6	537	71.4	219	2	S46112
7	535	71.1	217	2	S42772
8	531	70.6	219	2	S38865
9	525	69.8	215	2	J20242
10	525	69.8	225	2	J10029
11	520	69.1	136	2	S40357
12	519	69.0	125	2	S40356
13	509	67.7	215	2	J20244
14	508	67.6	124	2	S03876
15	506	67.3	132	2	S26882
16	502	66.8	112	2	S58207
17	502	66.8	117	1	K2HUGM
18	498	66.2	112	2	S58206
19	494	65.7	215	2	A23746
20	483.5	64.3	126	2	S40339
21	481	64.0	215	2	J20243
22	480.5	63.9	240	2	S06084
23	479.5	63.8	216	2	J20241
24	464	61.7	131	2	S40372
25	463.5	61.6	214	2	S68212
26	463	61.6	113	1	K2HUTW
27	460	61.2	123	2	S40319
28	459.5	61.1	220	2	A31790
29	457.5	60.8	210	2	A56169

30	454	60.4	96	2	S40320	Ig kappa chain - h
31	451	60.0	87	2	S34091	Ig kappa chain v r
32	451	60.0	100	2	S24681	Ig kappa chain - h
33	450.5	59.9	112	1	K2HUML	Ig kappa chain v-I
34	450.5	59.9	218	2	JC5810	monoclonal antibod
35	447.5	59.5	218	2	S68241	Ig kappa chain v r
36	447	59.4	114	2	S40375	Ig kappa chain - h
37	432.5	57.5	130	2	S40321	Ig kappa chain - h
38	426	56.6	112	2	F27887	Ig kappa chain v r
39	425	56.5	116	2	S27008	Ig kappa chain v r
40	423.5	56.3	115	1	K2HUCM	Ig kappa chain v-I
41	421	56.0	131	2	D29380	Ig kappa chain pre
42	419.5	55.8	140	2	S22658	Ig kappa chain pre
43	415	55.2	112	2	S53750	antibody Fab Jel 1
44	414	55.1	112	2	C36317	Ig kappa chain v r
45	414	55.1	112	2	G26317	Ig kappa chain v r

ALIGNMENTS

RESULT 1

PC4203

Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 11-Jan-2000

C:Accession: PC4203

R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.

Gene 173, 257-259, 1996

A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mor

A:Reference number: PC4202; MUID:97082978; PMID:8964510

A:Accession: PC4203

A:Molecule type: mRNA

A:Residues: 1-219 <KWA>

A:Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226

C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:1-112/Domain: V region #status predicted <VRG>

F:113-219/Domain: C region #status predicted <CRG>

Query Match

Best Local Similarity 74.1%; Score 557; DB 2; Length 219;

Matches 103; Conservative 18; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSNGYLDWYLOKPGOSPQLLIYLGSNRAGVDPDRFSGS 60

Db 11 LPVSLGDAQASISCRSSQSIHTNGTNTVLEWYLOKPGOSPQLLIYKVSNRFGVDPDRFSGS 70

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVIFPPSDSQL 120

Db 71 GSGTDFTLKISRVEADLVGVYCFQSGHVPRTFGGTKLEIKRADAAPTV8IFPPSSSQL 130

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143

Db 131 TSGGASVVCFLNFPKDINVKW 153

RESULT 2

S29593

Ig kappa chain (WM65) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 11-Jan-2000

C:Accession: S29593

R:Seymour, R.

submitted to the EMBL Data Library, February 1991

A:Reference number: S29593

A:Accession: S29593

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197 <SEV>

A:Cross-references: EMBL:X57856; NID:g52588; PIDN:CAA40991.1; PID:g52589

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

```
Query Match          73.8%; Score 555; DB 2; Length 197;
Best Local Similarity 74.1%; Pred. No. 1.1e-40;
Matches 106; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 26 IPVTPGESASISCRSSKSLHSGNDTYLWYLFQPGQSPQLLIYRMNLSAGVDPDRFSGS 85
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGTDFTLKISRVEADVGIYWCQSLQIPRLFPGTKVDIKRTVAAPSFIPPPSDEQL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 86 GSGTSFTLRISRVEADVGFYCWQHELYPYTFGGTKLEIKRADAAPTVSIFPPSDEQL 145
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 146 TSGGASVVCFLNNFYPKDINKW 168
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52028
R;van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roostien, J.; Dirkse, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994
A;Description: Coordinate expression of antibody subunit genes yields high levels of fun
A;Reference number: S52028
A;Accession: S52028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <VAN>
A;Cross-references: EMBL:L35138; NID:9522336; PIDN:AAA67525.1; PID:g522337
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match          72.9%; Score 548; DB 2; Length 219;
Best Local Similarity 71.3%; Pred. No. 5e-40;
Matches 102; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 11 LPVSLGDAQASISCRSSQSIHSGNTYLEWYLOKPGQSPKLLIYKNSRFGVDPDRFSGS 70
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGTDFTLKISRVEADVGIYWCQSLQIPRLFPGTKVDIKRTVAAPSFIPPPSDEQL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 71 GSGTDFTLKISRVEADVGVYCFQGSHPVPTFGGTNLEIKRADAAPTVSIFPPSDEQL 130
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 131 TSGGASVVCFLNNFYPKDINKW 153
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
S40342
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S40342
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40342
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-135 <KLE>
A;Cross-references: UNIPROT:Q8NEK0; EMBL:X72452; NID:g441372; PID:g441373
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;29-108/Domain: immunoglobulin homology <IMM>
```

```
Query Match          72.2%; Score 543; DB 2; Length 135;
Best Local Similarity 93.6%; Pred. No. 8.2e-40;
Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24 LPVTPGPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 83
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGTDFTLKISRVEADVGIYWCQSLQIPRLFPGTKVDIKRTVAAPS 109
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 GSGTDFTLKISRVEADVGVYCMQALQTPRTFGQGTKVEIKRTVAAPS 132
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
S40371
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40371
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40371
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-121 <KLE>
A;Cross-references: EMBL:X72481; NID:g441430; PIDN:CAA51149.1; PID:g441431
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;13-92/Domain: immunoglobulin homology <IMM>

Query Match          71.5%; Score 538; DB 2; Length 121;
Best Local Similarity 88.6%; Pred. No. 2e-39;
Matches 101; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 8 LPVTPGPASISCRSSQSLIYSTGYNDWYLOKPGKSPQLLIYLGSKRAGVDPDRFSGS 67
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGTDFTLKISRVEADVGIYWCQSLQIPRLFPGTKVDIKRTVAAPSFIFF 114
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 68 GSGTDFTLKISRVEADVGVYCMQGLQTPRTFGQGTKLEIKRTVAAPSFIFF 121
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
S16112
Ig kappa chain V region (G2a) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S16112
R;Vaesen, M.; Prosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.; f
Biochem. Hoppe-Seyler 372, 451-453, 1991
A;Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(
A;Reference number: S16112; MUID:92000313; PMID:1910583
A;Accession: S16112
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-219 <BIT>
A;Cross-references: UNIPROT:Q8VC16; UNIPROT:Q99M37
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match          71.4%; Score 537; DB 2; Length 219;
Best Local Similarity 70.6%; Pred. No. 4.4e-39;
Matches 101; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 11 LPVSLGDAQASISCRSSQSLHSGNTYLEWYLOKPGQSPKLLIYRNSRFGVDPDRFSGS 70
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGTDFTLKISRVEADVGIYWCQSLQIPRLFPGTKVDIKRTVAAPSFIFFPSDEQL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

Db      71 GSGGDFTLKISRVAEDLGVVFCQGTHTVPYTFGGTGLRLEIKRADAAPTVSIFPPSSSQL 130
Qy      121 KSGTASVVCLLSNFPYPRKQVQW 143
Db      131 TSGGASVVCFLLNFPYPRKDINVKW 153

RESULT 7
S42772
IG kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 71.1%; Score 535; DB 2; Length 217;
Best Local Similarity 69.9%; Pred. No. 1.5e-39;
Matches 100; Conservative 18; Mismatches 25; Indels 0; Gaps 0

Qy      1 MPVTGPGPASISCRSSQSLHNSGNYLDWLQKPGQSPQLLIYLGNSRASGVPPDRFSGS 60
Db      9 LPVSLGDAQSISCRSSQSLVHTNGTYLHWYLLQKPGQPKVLIYKSTRFSGVPPDRFSGS 68
Qy      61 GSGGDFTLKISRVAEDVGIIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFPPSDEQL 120
Db      69 GSGGDFTLKISRVAEDLGVVFCQSTVVPVTFGGTGLRLEIKRADAAPTVSIFPPSSEQ 128
Qy      121 KSGTASVVCLLSNFPYPRKQVQW 143
Db      129 TSGGASVVCFLLNFPYPRKDINVKW 151

RESULT 8
S38865
IG kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S38865
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning
A:Reference number: S38864
A:Accession: S38865
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <KIP>
A:Cross-references: EMBL:Z27396; NID:g416538; PIDN:CAA81787.1; PID:g416539
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.6%; Score 531; DB 2; Length 219;
Best Local Similarity 69.9%; Pred. No. 1.5e-38;
Matches 100; Conservative 18; Mismatches 25; Indels 0; Gaps 0

Qy      1 MPVTGPGPASISCRSSQSLHNSGNYLDWLQKPGQSPQLLIYLGNSRASGVPPDRFSGS 60
Db      11 LSVSLGDAQSISCRSSQSLVHTNGTYLHWYLLQKGLSPKLLIYVSNRFSGVPPDRFSGS 70
Qy      61 GSGGDFTLKISRVAEDVGIIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFPPSDEQL 120
Db      71 GSGGDFTLKISRVAEDLGVVFCQSTVVPVTFGGTGLRLEIKRADAAPTVSIFPPSSEQ 130

```

```
db      |||||:::|||||:::|||::|||::|||::|||::|||::|||:
77 GSGTDFLEISRVAEDLGVYVCQSSHRWTFGGGTGLEIKRADAAPTVSIFPPTSQL 136

Qy     121 KSGTASVVCLLSNFYPREAKYW 143

Db     137 TSGGASVVCFLNFFYPKDIYNKW 159
```

RESULT 11

IG kappa chain V-J-C region - human  
S40357

C:Species: Homo sapiens (man)  
C:date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C:Accession: S40357

R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993

A:title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40357

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-136 <IE>

A:Cross-references: UNIPROT:Q8N8K0; EMBL:X72467

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-115/Domain: immunoglobulin homology <IMM>

	Query Match	69.1%; Score 520; DB 2; Length 136;
	Best Local Similarity	92.5%; Pred. No. 7.8e-38;
	Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0	
Qy	1 MPVTPGPASISCTSSOSLLHSNGNYLDWLQKPGSQPLLIIYLGSNRAGVDPDRFGS	60
Dd	31 LPVTPGPASISCTSSOSLLHSNGNYLDWLQKPGSQPLLIIYLGSNRAGVDPDRFGS	90
Qy	61 GSGTDFTLKISRVAEDVGIIYCQSLOIPLRFEGTKVDIKRTVA	106
Dd	91 GSGTDFTLKISRVAEDVGVIYICMAALQTPTWFGOTKVEIKRTVA	136

```

RESULT 12
S40356
IG kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40356
R:klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312, MUID:94080891, PMID:8258341
A:Accession: S40356
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <LX>
A:Cross-references: EMBL:X72466; NID:G441400; PIDN:CAAS51134.1; PID:G441401
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-104/Domain: immunoglobulin homology <IMM>

```

Query Match 69.0%; Score 519; DB 2; Length 125;  
Best Local Similarity 92.5%; Pred. No. 8.7e-38;  
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0

Qy 1 MPVTPGEPASISCRSSQSLLHSNGNYLDWLQKPGSQPOLLIYLGSRASGVPPDRFSGS 60  
:  
:  
Db 20 LPVTPGEPASISCRSSQSLLHNNGYLDWLQKPGSQPOLLIYLGSRASGVPPDRFSGS 79  
:  
:  
Qy 61 GSGTDFTLKISRVAEDVGVIYYCWSQLPIRLFGPGTKVDIKRTYA 106  
:  
:  
Db 80 GSGTDFTLKISRVAEDVGVIYYCWSQLPIRLFGPGTKVEIKRTYA 125  
:  
:

RESULT 13

JE0244  
Ig kappa chain NIG2 precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C/Accession: JE0244  
R/Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Te  
submitted to JIPID, November 1998  
A/Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy  
A/Reference number: JE0243  
A/Accession: JE0244  
A/Molecule type: protein  
A/Residues: 1-215 <ALI>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

	Query Match	67.7%	Score 509;	DB 2;	Length 215;
	Best Local Similarity	70.8%;	Pred. No. 1.1e-36;		
	Matches 102;	Conservative 16;	Mismatches 20;	Indels 6;	Gaps 3
Qy	1	MPVTEGSPASICRSSOSLHSGNYVLDWLQKPGQSPQLLIYLGSRNASGVDPDFSGS	60		
Db	11	LSVSPGERATLSCRASOS-VHSN---LAWTQQPGQAPRLIIYVASTRATGICIPARFSGS	65		
Qy	61	GSGETDFTLKISRVAEADVGVIYCMQSLQIPRL-FGPGTKVDIKRTVAAPSPVIFPPPSDQ	119		
Db	66	GSGETDFLITLSSQSEDFALYYCOQYNTWPLTFTGGGTKVKEIKRTVAAPSPVIFPPPSDQ	125		
Qy	120	LKSGTASVWCLLNNFYPREAKVQW	143		
Db	126	LKSGTASVWCLLNNFYPREAKVQW	149		

```

RESULT 14
S03876
IG kappa chain V-II region (Inc) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C/Accession: S03876
A/Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.
Biochim. Biophys. Acta 995, 103-108, 1989
A/Reference number: S03876; MUID:89194238; PMID:2495028
A/Accession: S03876
A/Molecule type: protein
A/Residues: 1-124 <PER>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
P:16-95/Domain: immunoglobulin homology <IMM>

```

[illegible]

RESULT 15  
S26882  
Ig kappa chain V region (V507) - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
C/Accession: S26882  
R/R/Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combiato, G.; Zachau, H.G.  
Nature 347, 90-92, 1990  
A/Title: Megabase inversions in the human genome as physiological events.  
A/Reference number: S26882; MUID:90370099; PMID:2118596  
A/Accession: S26882



A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-132 <WEI>  
A;Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367  
C;Genetics:  
A;Introns: 17/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;36-115/Domain: immunoglobulin homology <IMM>

	Query Match	67.3%	Score 506;	DB 2;	Length 132;
	Best Local Similarity	92.2%	Pred. No. 1.2e-36;		
	Matches 94;	Conservative 5;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	MPVTPGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGS	60		
Db	31	LPVTPGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGS	90		
Qy	61	GSQTDFTLKISRVEADVGYYCQSLQIPRLFGPGTKVDIK	102		
Db	91	GSQTDFTLKISRVEADVGYYCQALQTPQTFGQGTKVEIK	132		

Search completed: March 8, 2005, 06:39:26  
Job time : 10.2129 secs

**This Page Blank (uspic,**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 53.4033 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-32  
Perfect score: 752  
Sequence: 1 MPVTPGPASISCRSSQSL.....TASVVCLLSNFYPRKXQV 143

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_cremli.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	708	94.1	239	Q8NEK0	Q8nek0 homo sapien
2	681.5	90.6	240	Q6PIH6	Q6pih6 homo sapien
3	613	81.5	239	Q6P491	Q6p491 homo sapien
4	597	79.4	239	Q8TCD0	Q8tcd0 homo sapien
5	538	71.5	219	Q65ZC0	Q65zc0 mus musculus
6	525.5	69.9	236	Q6PII8	Q6pii8 homo sapien
7	523	69.5	235	Q6GMV9	Q6gmv9 homo sapien
8	523	69.5	235	Q6PJF2	Q6pjf2 homo sapien
9	507.5	67.5	236	Q6P588	Q6p588 homo sapien
10	502	66.8	117	1 KV2E HUMAN	Q6gmw8 homo sapien
11	495.5	65.9	236	Q6GMX8	Q6gmw8 homo sapien
12	488.5	65.0	236	Q6GMX0	Q6gmw0 homo sapien
13	486.5	64.7	234	Q7Z473	Q7z473 homo sapien
14	486.5	64.7	236	Q6GMW1	Q6gmw1 homo sapien
15	486	64.6	235	Q6GMW0	Q6gmw0 homo sapien
16	477.5	63.5	236	Q6PIH7	Q6pih7 homo sapien
17	464.5	61.8	236	Q7Z3Y4	Q7z3y4 homo sapien
18	463.5	61.6	236	Q6PIT5	Q6pit5 homo sapien
19	463	61.6	113	1 KV2D HUMAN	Q6pih4 homo sapien
20	456.5	60.7	236	Q6GMX9	Q6gmw9 homo sapien
21	450.5	59.9	112	1 KV2C HUMAN	Q6pih6 homo sapien
22	444.5	59.1	236	Q6PIH4	Q6pih4 homo sapien
23	439.5	58.4	238	Q66JS7	Q66js7 mus musculus
24	437	58.1	243	Q6NTU5	Q6ntu5 xenopus lae
25	423.5	56.3	115	1 KV2A HUMAN	Q6pih4 homo sapien
26	416.5	55.4	236	Q7TS98	Q7ts98 mus musculus
27	416.5	55.4	237	Q7SZ36	Q7sz36 xenopus lae
28	415.5	55.3	241	Q63ZX4	Q63zx4 mus musculus
29	411	54.7	113	1 KV2B HUMAN	Q6pih5 homo sapien
30	407	54.1	113	1 KV2B_MOUSE	Q6pih6 mus musculus
31	405	53.9	113	1 KV2G_MOUSE	P01631 mus musculus

32	403	53.6	248	2	Q65ZQ7	Q65zq7 mus sp. b3(
33	400	53.2	113	1	KV2F_MOUSE	P01630 mus musculus
34	395	52.5	133	1	KV2F_HUMAN	P06310 homo sapien
35	381	50.7	112	2	Q6LEM8	Q6lem8 mus musculus
36	378.5	50.3	114	2	Q9UL80	Q9ul80 homo sapien
37	377	50.1	112	1	KV2D_MOUSE	P01629 mus musculus
38	374	49.7	113	1	KV2C_MOUSE	P01628 mus musculus
39	368	48.9	112	1	KV2A_MOUSE	P01626 mus musculus
40	352.5	46.9	108	1	KV1_CANFA	P01618 canis famli
41	351	46.7	120	1	KV2B_MOUSE	P01627 mus musculus
42	343.5	45.7	134	1	KV4C_HUMAN	P06314 homo sapien
43	341.5	45.4	114	1	KV4A_HUMAN	P01625 homo sapien
44	337.5	44.9	236	2	Q8NEJ1	Q8nej1 homo sapien
45	337	44.8	133	1	KV4B_HUMAN	P06313 homo sapien

ALIGNMENTS

RESULT 1

ID	Q8NEK0	PRELIMINARY;	PRT;	239 AA.
AC	Q8NEK0;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,			
RT	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RP	Strausberg R.;			
RC	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC030814; ANH30814.1; -			
DR	PIR; S23638; S23638.			
DR	PIR; S34091; S34091.			
DR	PIR; S40342; S40342.			
DR	PIR; S40357; S40357.			
DR	HSSP; P01834; 117Z.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig cl.			
DR	InterPro; IPR003006; Ig MHC.			
DR	InterPro; IPR003596; Ig v.			
DR	Pfam; PF07654; C1-set; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			

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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA;  F5E20AD3B0552COA CRC64;

Query Match      94.1%; Score 708; DB 2; Length 239;
Best Local Similarity 93.0%; Pred. No. 2.8e-64;
Matches 133; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGSPQLLIYLGNSRAGVDPDRFSGS 60
   : |||||:
Db 31 LPVTPGPASISCRSSQSLHSGDGYNDWYLOKPGSPQLLIYLGNSRAGVDPDRFSGS 90
   : |||||:
Qy 61 GSGTDFTLKISRVEADVGIYCMQSIQI-PRLFPGTGVKVDIKRTVAAPSVFIPPSPDEQL 120
   : |||||:
Db 91 GSGTDFTLKISRVEADVGIYCMQSIQIQTPTFGGTVKVKRTVAAPSVFIPPSPDEQL 150
   : |||||:
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
   : |||||:
Db 151 KSGTASVVCLLNNFYPREAKVQW 173
   : |||||:

RESULT 2
Q6PIH6 PRELIMINARY; PRT; 240 AA.
ID Q6PIH6
AC Q6PIH6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RC Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC034142; AAH34142.1; -.
DR HSSP; P01837; 1KB5.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA;  26234 MW;  188D4DD8BB781EC4 CRC64;

Query Match      90.6%; Score 681.5; DB 2; Length 240;
Best Local Similarity 90.3%; Pred. No. 1.5e-61;
Matches 130; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGSPQLLIYLGNSRAGVDPDRFSGS 60
   : |||||:
Db 31 LSVTPGPASISCRSSQSLHSGNYFDWYLOKPGSPQLLIYWGNSRAGVDPDRFSGS 90
   : |||||:
Qy 61 GSGTDFTLKISRVEADVGIYCMQSIQI-PRLFPGTGVKVDIKRTVAAPSVFIPPSPDEQ 119
   : |||||:
Db 91 GSGTDFTLKISRVEADVGIYCMQSIQIQTPTFGGTVKVKRTVAAPSVFIPPSPDEQ 150
   : |||||:
Qy 120 LKSGTASVVCLLSNFYPREAKVQW 143
   : |||||:
Db 151 LKSGTASVVCLLNNFYPREAKVQW 174
   : |||||:

RESULT 3
Q6P491 PRELIMINARY; PRT; 239 AA.
ID Q6P491
AC Q6P491
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Skin;
RC Strausberg R.;
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC063599; AAH63599.1; -.
DR HSSP; P01837; 1KC0.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
```

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DR SMART: SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26245 MW; CD71313DDFFD358B3 CRC64;

Query Match 81.5%; Score 613; DB 2; Length 239;
Best Local Similarity 82.4%; Pred. No. 1.6e-54;
Matches 117; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 2 PVTGEPASISCRSSQSLHNSGNYLDWYKQPGQSPQLLIYLGSNRASGVDPDRFSGS 61
Db 32 PVTLGQPASISCRSSQSLHNSGNYLDWYKQPGQSPQLLIYKISNRASGVDPDRFSGS 91

Qy 62 SGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQLK 121
Db 92 AGTDFTLKISRVEADVGIYCMQSVHPFRTFGQTRVEIKRTVAAPSVFIFFPSDEQLK 151

Qy 122 SGTASVWCLLSNFPYPRKQVQW 143
Db 152 SGTASVWCLLSNFPYPRKQVQW 173

RESULT 4
Q8TCDO PRELIMINARY; PRT; 239 AA.
ID Q8TCDO
AC Q8TCDO;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smalios D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AA022362.1; -.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSP; P01834; I17Z.
InterPro; IPR007110; Ig-like.
```

```
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match 79.4%; Score 597; DB 2; Length 239;
Best Local Similarity 78.3%; Pred. No. 6.9e-53;
Matches 112; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MPVTGEPASISCRSSQSLHNSGNYLDWYKQPGQSPQLLIYLGSNRASGVDPDRFSGS 60
Db 31 LPVTLGQPASISCRSTQSLVSDGNTYLNWFQPGQSPRLIYKVSNRDSGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQL 120
Db 91 GSGTDFTLKISRVEADVGIYCMQSGTHWPSTFGQTKLEIKRTVAAPSVFIFFPSDEQL 150

Qy 121 KSGTASVWCLLSNFPYPRKQVQW 143
Db 151 KSGTASVWCLLSNFPYPRKQVQW 173

RESULT 5
Q6SZCO PRELIMINARY; PRT; 219 AA.
ID Q6SZCO
AC Q6SZCO;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
recognizing a defined linear epitope of Chironomus thummi major
allergen Chi t.1.";
RT Int. Arch. Allergy Immunol. 110:348-353(1996).
RL EMBL; Z37499; CAA85724.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IG LIKE; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON TER 1 219
FT NON TER 219 219
SQ SEQUENCE 219 AA; 23944 MW; 7B1B82A14EAF8445 CRC64;

Query Match 71.5%; Score 538; DB 2; Length 219;
Best Local Similarity 70.6%; Pred. No. 6.9e-47;
Matches 101; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MPVTGEPASISCRSSQSLHNSGNYLDWYKQPGQSPQLLIYLGSNRASGVDPDRFSGS 60
Db 11 LSVSLGDAQSISCRSSQSLVHTNGTYLHWYKQPGLSFKLLIYVSNRFSGVDPDRFSGS 70
InterPro; IPR007110; Ig-like.
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Db 31 LSLSPGERAALSCRASQSV-----NSKYLAWYQKQPGQAPRLMYAASIRATGIPDRFSGS 86
Qy 61 GSGTDFTLKISRVAEDVGIIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDBQL 120
Db 87 GSGTDFTLTISRLSESDPALYFCQYGTGTSPLTFGGGTRKVEIKRTVAAPSVFIFFPSDBQL 146
Qy 121 KSGTASVVCLLSNFPYBREAKVQW 143
Db 147 KSGTASVVCLLNNFPYBREAKVQW 169

RESULT 8
Q6PJF2 PRELIMINARY; PRT; 235 AA.
AC Q6PJF2
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RL Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; I.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 69.5%; Score 523; DB 2; Length 235;
Best Local Similarity 69.9%; Pred. No. 2.6e-45;
Matches 100; Conservative 18; Mismatches 21; Indels 4; Gaps 1;

Qy 1 MPVTGEPASISCRSSQSLHSGNYLDWYLRKPGSQPLLIIYIGSNRSGVDPDRFSGS 60
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Db 31 LSLSPGERATLSCRASQIVSSA-----YLAWTQQKPGQAPRLMFGSSSRATGIPDRFSGS 86
Qy 61 GSGTDFTLKISRVAEDVGIIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDBQL 120
Db 87 GSGTDFTLTISRLSEDPFAVYICQYGSQGTGFGTKVDIKRTVAAPSVFIFFPSDBQL 146
Qy 121 KSGTASVVCLLSNFPYBREAKVQW 143
Db 147 KSGTASVVCLLNNFPYBREAKVQW 169

RESULT 9
Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RL Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; I.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BBE4FF5F27 CRC64;

Query Match 67.5%; Score 507.5; DB 2; Length 236;
Best Local Similarity 69.5%; Pred. No. 1e-43;
Matches 98; Conservative 20; Mismatches 18; Indels 5; Gaps 2;
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Qy 4 TPGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLYLGSNRASGVDPDRFSGSG 63
Db 34 SPGERATLSKRSASQTVFSS----HLAWQQRPGQAPRLIYAGSSRATGIPDRFSGSGSG 89
Qy 64 TDFTLKISRVEADVGIIYCMQSLQIPRL-FPGTKVDIKRTVAAPSVFPPSPDEQLKS 122
Db 90 TDFTLITRIPEPEFAVYFCQYGTSPSLTFGGGTRVEIKRTVAAPSVFPPSPDEQLKS 149
Qy 123 GTASVCLLSNFYFREAKVOW 143
Db 150 GTASVCLLNNFYFREAKVOW 170

RESULT 10
KV2E HUMAN
ID _KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RL Nature 309:73-76(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PR; A01889; K2HUGM.
DR HSPP; Q99M37; I191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1
FT SIGNAL <1 4
FT CHAIN 5 117 Ig kappa chain V-II region GM607.
FT DOMAIN 5 27 Framework-1.
FT DOMAIN 28 43 Complementarity-determining-1.
FT DOMAIN 44 58 Framework-2.
FT DOMAIN 59 65 Complementarity-determining-2.
FT DOMAIN 66 97 Framework-3.
FT DOMAIN 98 106 Complementarity-determining-3.
FT DOMAIN 107 116 Framework-4.
FT DISULFID 27 97 By similarity.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12864 MW; 92C57DC719B558B1 CRC64;

Query Match 66.8%; Score 502; DB 1; Length 117;
Best Local Similarity 91.3%; Pred. No. 1.6e-43;
Matches 94; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLYLGSNRASGVDPDRFSGS 60
:
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Db 15 LPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLYLGSNRASGVDPDRFSGS 74
Qy 61 GSGTDFTLKISRVEADVGIIYCMQSLQIPRLFPGTKVDIKR 103
Db 75 GSGTDFTLKISRVEADVGIIYCMQSLQIPRLFPGTKVDIKR 117

RESULT 11
Q6GMX8 PRELIMINARY; PRT; 236 AA.
ID Q6GMX8
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 65.9%; Score 495.5; DB 2; Length 236;
Best Local Similarity 68.8%; Pred. No. 1.7e-42;
Matches 95; Conservative 15; Mismatches 23; Indels 5; Gaps 1;

Qy 6 GEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLYLGSNRASGVDPDRFSGSGSGTD 65
Db 38 GDRVTITCRASQGI-----SSWLAWYQKPKAPKLLIYAASSLQSGVPSFSGSGSGTD 92
Qy 66 FTLKISRVEADVGIIYCMQSLQIPRLFPGTKVDIKRTVAAPSVFPPSPDEQLKS 125
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Db 91 FTLISCLQSEDFATYYCQQYYTPWTFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTA 150
Qy 126 SVVCLLSNFFYPREAKVQW 143
Db 151 SVVCLLNFFYPREAKVQW 168

RESULT 14
Q6GMW1 O6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFEGA087AFAC437 CRC64;

Query Match 64.7%; Score 486.5; DB 2; Length 236;
Best Local Similarity 68.1%; Pred. No. 1.4e-41;
Matches 94; Conservative 14; Mismatches 25; Indels 5; Gaps 1;

Qy 6 GEPASISCRSSQSLHNSNGVNYLDWYLOKPGSQSPQLLIYLGNSRASGVDFSGSGSTD 65
Db 38 GDRVITICRASQGI-----SNDLGEYQOKPGAPLLIYAASLSQSGVPSFGSGSTD 92
Qy 66 FTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTA 125
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Db 93 FTLTISLQSEDFATYYCQQYYTPWTFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTA 152
Qy 126 SVVCLLSNFFYPREAKVQW 143
Db 153 SVVCLLNFFYPREAKVQW 170

RESULT 15
Q6GMW0 O6GMW0 PRELIMINARY; PRT; 235 AA.
AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 64.6%; Score 486; DB 2; Length 235;
Best Local Similarity 65.3%; Pred. No. 1.6e-41;
Matches 94; Conservative 23; Mismatches 21; Indels 6; Gaps 2;

Qy 1 MPVTPGPASISCRSSQSLHNSNGVNYLDWYLOKPGSQSPQLLIYLGNSRASGVDFRSGS 60
Db 31 LSVSPGGRATLISCRASQSI-----SNNLAWYQORPGQAPRLIYIGASRVGTGIPGRFSGS 85
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Qy	61	GS	GTDFTLKIISRVAEDVGIIYCHQ-SLIQIPRLFGFGTKVDIKRTVAAPSVFIFPPSDEQ	119
		:	: : :	
Db	86	GS	GTEFTLSISLOSSEDFAVYFCQYNWLLLYTFQGQTKLEIKRTVAAPSVFIFPPSDEQ	145
		:	: : :	
Qy	120	LK	SCTASVCLLSNFPYPREAKVQW	143
		:	: : :	
Db	146	LK	SCTASVCLLSNFPYPREAKVQW	169
		:	: : :	

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Job time : 54.4033 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 66.2987 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-32

Perfect score: 752

Sequence: 1 MPVTPGPASISCRSSQSL.....TASVVCLLSNFPYPREAKVQW 143

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	752	100.0	143	2	AAY34313 IgM antib
2	720	95.7	239	3	AAY82616 Human PTH
3	719	95.6	238	8	ADL93653 Human CD4
4	713	94.8	239	3	AAY82618 Human PTH
5	712	94.7	238	8	ADL93649 Human CD4
6	712	94.7	238	8	ADL93654 Human CD4
7	712	94.7	239	7	ADE28461 Human ant
8	710	94.4	239	7	ADE28405 Human ant
9	709	94.3	238	8	ADL93650 Human CD4
10	709	94.3	239	7	ADE28465 Human ant
11	707	94.0	239	7	ADE28521 Human ant
12	707	94.0	239	7	ADE28397 Human ant
13	707	94.0	239	7	ADE28477 Human ant
14	705	93.8	239	3	AAY82611 Human PTH
15	704	93.6	219	8	ADL16817 Human bre
16	702	93.4	239	3	AAY82615 Human PTH
17	702	93.4	239	7	ADE28421 Human ant
18	701.5	93.3	237	8	ADL93657 Human CD4
19	697	92.7	239	3	AAY82617 Human PTH
20	695	92.4	148	2	AAY34309 IgM antib
21	695	92.4	219	7	ADJ32150 Human int
22	694	92.3	238	8	ADL93652 Human CD4
23	693.5	92.2	237	8	ADL93658 Human CD4
24	693.5	92.2	237	8	ADL93651 Human CD4
25	693	92.2	239	6	ABR48456 Human Cal

ALIGNMENTS

RESULT 1

AAY34313  
ID AAY34313 standard; protein; 143 AA.

AC AAY34313;

DT 19-NOV-1999 (first entry)

DE IgM antibody CEM 13.12 kappa chain sequence.

KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

FN WO9945031-A2.

PD 10-SEP-1999.

PF 03-MAR-1999; 99WO-US004583.

PR 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

PA (ABGE-) ABGENIX INC.

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;

DR WPI; 1999-540816/45.

DR N-PSDB; AAZ20414.

PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.

PS Claim 61; Fig 28; 245pp; English.

XX This sequence represents the kappa chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 MAB  
CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX  
SQ Sequence 143 AA;  
  
Query Match 100.0%; Score 752; DB 2; Length 143;  
Best Local Similarity 100.0%; Pred. No. 6.1e-55;  
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 60  
Db 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 60  
  
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIFFPPSDEQL 120  
Db 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIFFPPSDEQL 120  
  
Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143  
Db 121 KSGTASVVCLLSNFPYPREAKVQW 143  
  
RESULT 2  
AAY82616  
ID AAY82616 standard; protein; 239 AA.  
XX  
AC AAY82616;  
XX  
DT 02-AUG-2000 (first entry)  
XX  
DE Human PTHrP monoclonal antibody clone 2G4-12-20 protein SEQ ID NO:16.  
XX  
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;  
KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
KW antiarthritic; cytostatic; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 5 /label= Val, Ala, Asp, Gly  
FT FT Misc-difference 13 /note= "possibly Leu"  
FT FT Misc-difference 25 /note= "possibly Leu"  
FT FT Misc-difference 27 /label= Ile, Thr, Asn, Ser  
FT FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys  
FT FT Misc-difference 216 /note= "possible Val"  
XX  
FN JP2000080100-A.  
XX  
PD 21-MAR-2000.  
XX  
PF 12-OCT-1998; 98JP-00304793.  
XX  
PR 17-JUN-1998; 98JP-00188196.  
PR 26-JUN-1998; 98JP-00196729.  
XX  
PA (NIBS) JAPAN TOBACCO INC.  
XX  
DR WPI; 2000-286723/25.  
DR N-PSDB; AAA13926.  
XX  
PT A human monoclonal antibody to parathyroid hormone related protein. -  
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
PT including metastasis, and pain.  
XX  
PS Claim 31; Page 48-49; 88pp; Japanese.  
XX  
CC The present invention describes a human monoclonal antibody to

CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
CC its fragments, following the stimulation of PTHrP has the following  
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
CC the release of calcium from bone; or (c) inhibits elevation of blood  
CC calcium content. The monoclonal antibody can be used in the treatment of  
CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
CC antiinflammatory activities. The present sequence represents a human  
CC PTHrP monoclonal antibody clone protein sequence from the present  
XX invention  
XX  
SQ Sequence 239 AA;  
  
Query Match 95.7%; Score 720; DB 3; Length 239;  
Best Local Similarity 94.4%; Pred. No. 4.8e-52;  
Matches 135; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 60  
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 90  
  
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIFFPPSDEQL 120  
Db 91 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIFFPPSDEQL 150  
  
Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143  
Db 151 KSGTASVVCLLSNFPYPREAKVQW 173  
  
RESULT 3  
ADL93653  
ID ADL93653 standard; protein; 238 AA.  
XX  
AC ADL93653;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human CD44-binding antibody light chain BE-D7-kappa-light SEQ ID NO:148.  
XX  
KW Human; CD44; light chain immunoglobulin variable domain;  
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;  
KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
KW dermatological; vasotropic; neuroprotective; antibody therapy;  
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
KW graft versus host response; multiple sclerosis; neoplastic disorder;  
KW cancer; antibody.  
XX  
OS Homo sapiens.  
XX  
FN WO2004024750-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 15-SEP-2003; 2003WO-US029318.  
XX  
PR 13-SEP-2002; 2002US-0410758P.  
PR 09-MAY-2003; 2003US-0469123P.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Rondon IJ, Edge A, Baribault Kent R;  
XX  
DR WPI; 2004-270003/25.  
XX  
PT New protein comprising a light chain (LC) immunoglobulin variable domain  
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
PT useful for preparing a composition for treating inflammatory or  
PT neoplastic disorders.  
XX  
PS Disclosure; SEQ ID NO 148; 128pp; English.

XX The invention relates to a novel isolated protein comprising a light  
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
 CC immunoglobulin variable domain sequence that form an antigen binding site  
 CC with binding affinity for the human CD44 extracellular domain and where  
 CC CD44 of the LC variable domain sequence. A protein of the invention has  
 CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,  
 CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,  
 CC and may have a use in antibody therapy. The protein is useful for  
 CC preparing a composition for treating inflammatory disorders, e.g.,  
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
 CC multiple sclerosis or neoplastic disorder, which is a malignant or  
 CC metastatic cancer. The present sequence represents a human CD44-binding  
 CC antibody light chain.

XX SQ Sequence 238 AA;

Query Match 95.6%; Score 719; DB 8; Length 238;  
 Best Local Similarity 94.4%; Pred. No. 5.8e-52;  
 Matches 135; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MPVTGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPLLIIYLGNSRAGVDFRSGS 60  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 30 LPVTGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPLLIIYLGNSRAGVDFRSGS 89  
 QY 61 GSGTDFTLKISRVEAEDVGIIYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIFFPSDEQL 120  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 90 GSGTDFTLKISRVEAEDVGIIYCMQALQTPRTFGGKVEIKRTVAAPSFIFFPSDEQL 149  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 121 KSGTASVVCLLSNFYPREAKVQW 143  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 150 KSGTASVVCLLSNFYPREAKVQW 172  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4

AAV82618  
 ID AAV82618 standard; protein; 239 AA.  
 XX  
 AC AAV82618;  
 XX  
 DT 02-AUG-2000 (first entry)  
 XX  
 DE Human PTHrP monoclonal antibody clone 4B4-6-21 protein SEQ ID NO:20.  
 XX  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingivitis; sepsis;  
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
 KW antiarthritic; cytostatic; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 25 /label= Ile, Thr, Asn, Ser  
 FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys  
 FT Misc-difference 213 /label= Gln, Lys, Glu  
 FT Misc-difference 215 /label= Gln, Lys, Glu  
 FT Misc-difference 219 /label= Cys, Trp  
 FT Misc-difference 220 /label= Val, Ala, Glu, Gly  
 FT Misc-difference 222 /label= Ile, Thr, Asn, Ser  
 XX  
 JN JP2000080100-A.  
 XX  
 PD 21-MAR-2000.  
 XX  
 PF 12-OCT-1998; 98JP-00304793.

XX 17-JUN-1998; 98JP-00188196.  
 PR 26-JUN-1998; 98JP-00196729.  
 XX  
 PA (NISR) JAPAN TOBACCO INC.  
 XX  
 DR WPI; 2000-286723/25.  
 DR N-PSDB; AAA13928.  
 XX  
 PT A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain.  
 XX  
 XX Claim 31; Page 55; 88pp; Japanese.  
 XX  
 CC The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment of  
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a human  
 CC PTHrP monoclonal antibody clone protein sequence from the present  
 CC invention  
 XX  
 SQ Sequence 239 AA;

Query Match 94.8%; Score 713; DB 3; Length 239;  
 Best Local Similarity 93.7%; Pred. No. 1.9e-51;  
 Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MPVTGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPLLIIYLGNSRAGVDFRSGS 60  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 31 LPVTGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPLLIIYLGNSRAGVDFRSGS 90  
 QY 61 GSGTDFTLKISRVEAEDVGIIYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIFFPSDEQL 120  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 91 GSGTDFTLKISRVEAEDVGIIYCMQTLQTPRTFGGKVEIKRTVAAPSFIFFPSDEQL 150  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 121 KSGTASVVCLLSNFYPREAKVQW 143  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 151 KSGTASVVCLLSNFYPREAKVQW 173  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5

ADL93649  
 ID ADL93649 standard; protein; 238 AA.  
 XX  
 AC ADL93649;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Human CD44-binding antibody light chain HAE-A3-kappa-light SEQ ID NO:144.  
 XX  
 KW human; CD44; light chain immunoglobulin variable domain;  
 KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;  
 KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
 KW dermatological; vasotropic; neuroprotective; antibody therapy;  
 KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
 KW graft versus host response; multiple sclerosis; neoplastic disorder;  
 KW cancer; antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 JN WO2004024750-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 15-SEP-2003; 2003WO-US029318.

```
XX 13-SEP-2002; 2002US-0410758P.  
PR 09-MAY-2003; 2003US-0469123P.  
XX  
XX (DYAX-) DYAX CORP.  
XX  
PI Rondon IU, Edge A, Baribault Kent R;  
XX  
XX WPI; 2004-270003/25.  
XX  
PT New protein comprising a light chain (LC) immunoglobulin variable domain  
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
PT useful for preparing a composition for treating inflammatory or  
PT neoplastic disorders.  
XX  
XX Disclosure; SEQ ID NO 144; 128pp; English.  
XX  
CC The invention relates to a novel isolated protein comprising a light  
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
CC immunoglobulin variable domain sequence that form an antigen binding site  
CC with binding affinity for the human CD44 extracellular domain and where  
CC CD3 of the LC variable domain sequence. A protein of the invention has  
CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,  
CC antirheumatic, dermatological, vasotrophic, and neuroprotective activity,  
CC and may have a use in antibody therapy. The protein is useful for  
CC preparing a composition for treating inflammatory disorders, e.g.,  
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
CC multiple sclerosis or neoplastic disorder, which is a malignant or  
CC metastatic cancer. The present sequence represents a human CD44-binding  
CC antibody light chain.  
XX  
XX Sequence 238 AA;  
SQ  
Query Match 94.7%; Score 712; DB 8; Length 238;  
Best Local Similarity 93.7%; Pred. No. 2.2e-51;  
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGSPOLLYLGSNRASGVDPDRSGS 60  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
30 LPVTPGPASISCRSSQSLHSGNYLDWYLOKPGSPOLLYLGSNRASGVDPDRSGS 89  
QY 61 GSGTDFTLKISRVEADVGIYQCWSLIQIRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
90 GSGTDFTLKISRVEADVGIYQCWSLIQIRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 149  
QY 121 KSGTASVVCLLSNFYPREAKVQW 143  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
150 KSGTASVVCLLSNFYPREAKVQW 172  
RESULT 6  
ADL93654  
ID ADL93654 standard; protein; 238 AA.  
XX  
XX ADL93654;  
XX  
XX 17-JUN-2004 (first entry)  
XX  
DE Human CD44-binding antibody light chain BE-H10-kappa-light SEQ ID NO:149.  
XX  
XX human; CD44; light chain immunoglobulin variable domain;  
XX heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;  
XX antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
XX dermatological; vasotrophic; neuroprotective; antibody therapy;  
XX inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
XX graft versus host response; multiple sclerosis; neoplastic disorder;  
XX cancer; antibody.  
XX  
XX Homo sapiens.  
XX  
XX WO2004024750-A2.  
XX  
XX 25-MAR-2004.  
XX  
XX
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XX 15-SEP-2003; 2003WO-US029318.  
XX  
XX 13-SEP-2002; 2002US-0410758P.  
PR 09-MAY-2003; 2003US-0469123P.  
XX  
XX (DYAX-) DYAX CORP.  
XX  
XX Rondon IU, Edge A, Baribault Kent R;  
XX  
XX WPI; 2004-270003/25.  
XX  
PT New protein comprising a light chain (LC) immunoglobulin variable domain  
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
PT useful for preparing a composition for treating inflammatory or  
PT neoplastic disorders.  
XX  
XX Disclosure; SEQ ID NO 149; 128pp; English.  
XX  
CC The invention relates to a novel isolated protein comprising a light  
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
CC immunoglobulin variable domain sequence that form an antigen binding site  
CC with binding affinity for the human CD44 extracellular domain and where  
CC CD3 of the LC variable domain sequence. A protein of the invention has  
CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,  
CC antirheumatic, dermatological, vasotrophic, and neuroprotective activity,  
CC and may have a use in antibody therapy. The protein is useful for  
CC preparing a composition for treating inflammatory disorders, e.g.,  
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
CC multiple sclerosis or neoplastic disorder, which is a malignant or  
CC metastatic cancer. The present sequence represents a human CD44-binding  
CC antibody light chain.  
XX  
XX Sequence 238 AA;  
SQ  
Query Match 94.7%; Score 712; DB 8; Length 238;  
Best Local Similarity 93.7%; Pred. No. 2.2e-51;  
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGSPOLLYLGSNRASGVDPDRSGS 60  
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
30 LPVTPGPASISCRSSQSLHSGNYLDWYLOKPGSPOLLYLGSNRASGVDPDRSGS 89  
QY 61 GSGTDFTLKISRVEADVGIYQCWSLIQIRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
90 GSGTDFTLKISRVEADVGIYQCWSLIQIRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 149  
QY 121 KSGTASVVCLLSNFYPREAKVQW 143  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
150 KSGTASVVCLLSNFYPREAKVQW 172  
RESULT 7  
ADE28461  
ID ADE28461 standard; protein; 239 AA.  
XX  
XX ADE28461;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX Human anti-CD40 antibody 23-28-1 variable region light chain protein.  
XX  
XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
XX bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
XX human; variable region light chain; 23-28-1.  
XX  
XX Homo sapiens.  
XX  
XX WO2003040170-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX
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PF 08-NOV-2002; 2002WO-US036107.
XX
PR 09-NOV-2001; 2001US-0348980P.
XX
PA (PFIZ ) PFIZER PROD INC.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
DR WPI; 2003-441521/41.
XX
DR N-PSDB; ADE28405.
XX
PT New chimeric or human monoclonal antibody or its antigen-binding portion
XX
PT that specifically binds to and activates human CD40, useful for enhancing
XX
PT an immune response in a human, or treating cancer, HIV, neutropenia or
XX
PT viral infections.
XX
PS Claim 1; SEQ ID NO 68; 177pp; English.
XX
CC The invention relates to a novel chimeric or human monoclonal antibody or
XX
CC its antigen-binding portion that specifically binds to and activates
XX
CC human CD40. The anti-CD40 antibody of the invention demonstrates
XX
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
XX
CC activities and may be useful for treating a hyperproliferative disorder
XX
CC such as cancer, viral and bacterial infection or genetic, primary or
XX
CC combined immunodeficiency conditions including neutropenia or HIV
XX
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
XX
CC in a biological sample in vitro or in vivo, as well as during gene
XX
CC therapy procedures. The current sequence is that of the human anti-CD40
XX
CC antibody variable region light chain protein of the invention.
XX
SQ Sequence 239 AA;

Query Match 94.7%; Score 712; DB 7; Length 239;
Best Local Similarity 93.7%; Pred. No. 2.2e-51;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPLLIIYLGSRASGVDPDRFSGS 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 31 LPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPLLIIYLGSRASGVDPDRFSGS 90
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 GSGTDFTLKISRVEADVGIYVCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFPPSDEQL 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 91 GSGTDFTLKISRVEADVGIYVCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFPPSDEQL 150
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 151 KSGTASVVCLLSNFYPREAKVQW 173
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
ADE28405
ID ADE28405 standard; protein; 239 AA.
XX
AC ADE28405;
XX
XX
XX 29-JAN-2004 (first entry)
XX
DE Human anti-CD40 antibody 7-1-2 variable region light chain protein.
XX
XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
XX
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
XX
XX bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
XX
XX human; variable region light chain; 7-1-2.
XX
OS Homo sapiens.
XX
XX WO2003040170-A2.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002WO-US036107.
XX
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PR 09-NOV-2001; 2001US-0348980P.
XX
PA (PFIZ ) PFIZER PROD INC.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
DR WPI; 2003-441521/41.
XX
DR N-PSDB; ADE28404.
XX
PT New chimeric or human monoclonal antibody or its antigen-binding portion
XX
PT that specifically binds to and activates human CD40, useful for enhancing
XX
PT an immune response in a human, or treating cancer, HIV, neutropenia or
XX
PT viral infections.
XX
PS Claim 1; SEQ ID NO 12; 177pp; English.
XX
CC The invention relates to a novel chimeric or human monoclonal antibody or
XX
CC its antigen-binding portion that specifically binds to and activates
XX
CC human CD40. The anti-CD40 antibody of the invention demonstrates
XX
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
XX
CC activities and may be useful for treating a hyperproliferative disorder
XX
CC such as cancer, viral and bacterial infection or genetic, primary or
XX
CC combined immunodeficiency conditions including neutropenia or HIV
XX
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
XX
CC in a biological sample in vitro or in vivo, as well as during gene
XX
CC therapy procedures. The current sequence is that of the human anti-CD40
XX
CC antibody variable region light chain protein of the invention.
XX
SQ Sequence 239 AA;

Query Match 94.4%; Score 710; DB 7; Length 239;
Best Local Similarity 93.0%; Pred. No. 3.3e-51;
Matches 133; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPLLIIYLGSRASGVDPDRFSGS 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 31 LPVTGEPASISCRSSQSLHSGNYLDWYLOKPGSQPLLIIYLGSRASGVDPDRFSGS 90
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 GSGTDFTLKISRVEADVGIYVCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFPPSDEQL 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 91 GSGTDFTLKISRVEADVGIYVCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFPPSDEQL 150
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 151 KSGTASVVCLLSNFYPREAKVQW 173
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
ADL93650
ID ADL93650 standard; protein; 238 AA.
XX
AC ADL93650;
XX
XX
XX 17-JUN-2004 (first entry)
XX
XX Human CD44-binding antibody light chain HAF-G2-kappa-light SEQ ID NO:145.
XX
XX heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;
XX
XX antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
XX
XX dermatological; vasotropic; neuroprotective; antibody therapy;
XX
XX inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
XX
XX graft versus host response; multiple sclerosis; neoplastic disorder;
XX
XX cancer; antibody.
XX
OS Homo sapiens.
XX
XX WO2004024750-A2.
XX
XX 25-MAR-2004.
XX
XX 15-SEP-2003; 2003WO-US029318.
XX
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XX 13-SEP-2002; 2002US-0410758P.  
PR 09-MAY-2003; 2003US-0469123P.  
XX (DYAX-) DYAX CORP.  
XX Rondon IJ, Edge A, Baribault Kent R;  
PI WPI; 2004-270003/25.  
XX  
XX New protein comprising a light chain (LC) immunoglobulin variable domain  
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
PT useful for preparing a composition for treating inflammatory or  
PT neoplastic disorders.  
XX  
XX Disclosure; SEQ ID NO 145; 128pp; English.  
XX  
XX The invention relates to a novel isolated protein comprising a light  
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
CC immunoglobulin variable domain sequence that form an antigen binding site  
CC with binding affinity for the human CD44 extracellular domain and where  
CC CD83 of the LC variable domain sequence. A protein of the invention has  
CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,  
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,  
CC and may have a use in antibody therapy. The protein is useful for  
CC preparing a composition for treating inflammatory disorders, e.g.,  
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
CC multiple sclerosis or neoplastic disorder, which is a malignant or  
CC metastatic cancer. The present sequence represents a human CD44-binding  
CC antibody light chain.  
XX  
SQ Sequence 238 AA;  
Query Match 94.3%; Score 709; DB 8; Length 238;  
Best Local Similarity 93.0%; Pred. No. 4e-51;  
Matches 133; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 MPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGSPOLLIYLGSNRAGVDPDRFSGS 60  
Db 30 LPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGSPOLLIYLGSNRAGVDPDRFSGS 89  
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPSPDEQL 120  
Db 90 GSGTDFTLKISRVEADVGIYCMQALQTPWTFGQTKLEIKRTVAAPSVFIPPSPDEQL 149  
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143  
Db 150 KSGTASVVCLLNNFYPREAKVQW 172  
RESULT 10  
ADE28465  
ID ADE28465 standard; protein; 239 AA.  
XX ADE28465;  
XX 29-JAN-2004 (first entry)  
XX Human anti-CD40 antibody 23-28-1 full length light chain protein.  
DE anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; light chain; 23-28-1.  
XX Homo sapiens.  
OS WO2003040170-A2.  
XX 15-MAY-2003.  
XX 08-NOV-2002; 2002WO-US036107.  
XX 08-NOV-2002; 2002WO-US036107.  
XX

PR 09-NOV-2001; 2001US-0348980P.  
XX (PFIZ ) PFIZER PROD INC.  
PA (ABGE-) ABGENIX INC.  
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;  
PI WPI; 2003-441521/41.  
XX N-PSDB; ADE28464.  
XX  
XX New chimeric or human monoclonal antibody or its antigen-binding portion  
PT that specifically binds to and activates human CD40, useful for enhancing  
PT an immune response in a human, or treating cancer, HIV, neutropenia or  
PT viral infections.  
XX  
XX Claim 7; SEQ ID NO 72; 177pp; English.  
XX  
XX The invention relates to a novel chimeric or human monoclonal antibody or  
CC its antigen-binding portion that specifically binds to and activates  
CC human CD40. The anti-CD40 antibody of the invention demonstrates  
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
CC activities and may be useful for treating a hyperproliferative disorder  
CC such as cancer, viral and bacterial infection or genetic, primary or  
CC combined immunodeficiency conditions including neutropenia or HIV  
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
CC in a biological sample in vitro or in vivo, as well as during gene  
CC therapy procedures. The current sequence is that of the human anti-CD40  
CC antibody full length light chain protein of the invention.  
XX  
SQ Sequence 239 AA;  
Query Match 94.3%; Score 709; DB 7; Length 239;  
Best Local Similarity 93.0%; Pred. No. 4e-51;  
Matches 133; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 MPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGSPOLLIYLGSNRAGVDPDRFSGS 60  
Db 31 LPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGSPHLLIYLGSNRAGVDPDRFSGS 90  
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPSPDEQL 120  
Db 91 GSGTDFTLKISRVEADVGIYCMQALQTPRTFGQTKVEIKRTVAAPSVFIPPSPDEQL 150  
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143  
Db 151 KSGTASVVCLLNNFYPREAKVQW 173  
RESULT 11  
ADE28521  
ID ADE28521 standard; protein; 239 AA.  
XX ADE28521;  
XX 29-JAN-2004 (first entry)  
XX Human anti-CD40 antibody 23-29-1L-R174K mutant VL light chain protein.  
DE anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;  
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;  
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;  
KW human; light chain; mutein; mutant; 23-29-1L-R174K.  
XX Homo sapiens.  
OS WO2003040170-A2.  
XX 15-MAY-2003.  
XX 08-NOV-2002; 2002WO-US036107.  
XX 09-NOV-2001; 2001US-0348980P.  
XX



XX WPI; 2003-441521/41.  
 DR N-PSDB; ADE28476.  
 XX  
 PT New chimeric or human monoclonal antibody or its antigen-binding portion  
 PT that specifically binds to and activates human CD40, useful for enhancing  
 PT an immune response in a human, or treating cancer, HIV, neutropenia or  
 PT viral infections.  
 XX  
 PS Claim 1; SEQ ID NO 84; 177pp; English.  
 CC  
 CC The invention relates to a novel chimeric or human monoclonal antibody or  
 CC its antigen-binding portion that specifically binds to and activates  
 CC human CD40. The anti-CD40 antibody of the invention demonstrates  
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV  
 CC activities and may be useful for treating a hyperproliferative disorder  
 CC such as cancer, viral and bacterial infection or genetic, primary or  
 CC combined immunodeficiency conditions including neutropenia or HIV  
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40  
 CC in a biological sample in vitro or in vivo, as well as during gene  
 CC therapy procedures. The current sequence is that of the human anti-CD40  
 CC antibody variable region light chain protein of the invention.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 94.0%; Score 707; DB 7; Length 239;  
 Best Local Similarity 93.7%; Pred. No. 5.9e-51;  
 Matches 134; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 MPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 60  
 DB 31 LPVTPGPASISCRSSQSLPGNGYNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 90  
 QY 61 GSGTDFTLKISRVEADVGIYQCWSLQIPRLFGPGTKVDIKRTVAAPSVPFPPSDEQL 120  
 DB 91 GSGTDFTLKISRVEADVGIYQCWSLQIPRLFGPGTKVDIKRTVAAPSVPFPPSDEQL 150  
 QY 121 KSGTASVVCLLSNFYPREAKVQW 143  
 DB 151 KSGTASVVCLLSNFYPREAKVQW 173  
 RESULT 14  
 AAY82611  
 ID AAY82611 standard; protein; 239 AA.  
 XX  
 AC AAY82611;  
 XX  
 DT 02-AUG-2000 (first entry)  
 XX  
 DE Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.  
 XX  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;  
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;  
 KW antiarthritic; cytostatic; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 FN JP2000080100-A.  
 XX  
 PD 21-MAR-2000.  
 XX  
 PF 12-OCT-1998; 98JP-00304793.  
 XX  
 PR 17-JUN-1998; 98JP-00188196.  
 PR 26-JUN-1998; 98JP-00196729.  
 XX  
 PA (NISR) JAPAN TOBACCO INC.  
 XX  
 DR WPI; 2000-286723/25.  
 DR N-PSDB; AAA13921.

XX A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain.  
 XX  
 PS Claim 31; Page 34-35; 88pp; Japanese.  
 XX  
 CC The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment of  
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a human  
 CC PTHrP monoclonal antibody clone protein sequence from the present  
 CC invention  
 XX  
 SQ Sequence 239 AA;  
 Query Match 93.8%; Score 705; DB 3; Length 239;  
 Best Local Similarity 92.3%; Pred. No. 8.6e-51;  
 Matches 132; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 60  
 DB 31 LPVTPGPATISCRSSQSLHNRNGNYLDWFLQKPGQSPQLLIYLGSRASGVDPDRFSGS 90  
 QY 61 GSGTDFTLKISRVEADVGIYQCWSLQIPRLFGPGTKVDIKRTVAAPSVPFPPSDEQL 120  
 DB 91 GSGTDFTLKISRVEADVGIYQCWSLQIPRLFGPGTKVDIKRTVAAPSVPFPPSDEQL 150  
 QY 121 KSGTASVVCLLSNFYPREAKVQW 143  
 DB 151 KSGTASVVCLLSNFYPREAKVQW 173  
 RESULT 15  
 ADR16817  
 ID ADR16817 standard; protein; 219 AA.  
 XX  
 AC ADR16817;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Human breast cancer-specific antibody Fab fragment, Fab14.6.19 #2.  
 XX  
 KW Breast cancer; diagnosis; therapy; human; antibody; Fab 14.6.19.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2004151724-A1.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 30-OCT-2003; 2003US-00698041.  
 XX  
 PR 31-OCT-2002; 2002US-0423052P.  
 XX  
 PA (CORO/) CORONELLA-WOOD J.  
 XX  
 PI Coronella-Wood J;  
 XX  
 DR WPI; 2004-570704/55.  
 DR N-PSDB; ADR16814.  
 XX  
 PT New isolated polynucleotides encoding breast cancer-specific antibody Fab  
 PT fragments 14.6.19 and 14.6.20, useful as clinical reagents for diagnosing  
 PT or treating breast cancer.  
 XX

PS Claim 8; SEQ ID NO 4; 36pp; English.

XX The invention provides a breast cancer-specific antibody fragment  
CC polynucleotide and its corresponding polypeptide. The invention is useful  
CC as clinical reagents for the diagnosis and therapy of breast cancer. The  
CC present sequence is human breast cancer-specific antibody Fab fragment,  
CC Fab14.6.19.

XX SQ Sequence 219 AA;

Query Match	93.6%	Score 704;	DB 8;	Length 219;
Best Local Similarity	91.6%	Pred. No. 9.5e-51;		
Matches 131;	Conservative 7;	Mismatches 5;	Indels 0;	Gaps 0;

  

Qy	1	MPVTPGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDRFSGS	60
Db	11	LPVTPGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGFNRASGVDPDRFSGS	70
Qy	61	GGTDPPTLKISRVEADGVYICMQSLQIPRLFGPTKVDIKRTVAAPSVFIAPPDDEQL	120
Db	71	GGTDPPTLKISRVEADGVYICMQSLQIPRTFGQGTLEIKRTVAAPSVFIAPPDDEQL	130
Qy	121	KSGTASVVCLLSNFPYFREAKVQW	143
Db	131	KSGTASVVCLLNNFPYFREAKVQW	153

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Job time : 66.2987 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 75.8864 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-32

Perfect score: 752

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Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUBCOMB.pep.\*
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- 13: /cgn2\_6/ptodata/2/pubaa/US10A\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	719	95.6	238	16	US-10-663-244-148
2	712	94.7	238	16	US-10-663-244-144
3	712	94.7	238	16	US-10-663-244-149
4	712	94.7	239	15	US-10-292-088-40
5	710	94.4	239	15	US-10-292-088-16
6	709	94.3	238	16	US-10-663-244-145
7	709	94.3	239	15	US-10-292-088-56
8	707	94.0	239	15	US-10-292-088-8
9	707	94.0	239	15	US-10-292-088-80
10	707	94.0	239	15	US-10-292-088-102
11	704	93.6	219	16	US-10-698-041-4
12	702	93.4	239	15	US-10-292-088-32
13	701.5	93.3	237	16	US-10-663-244-152

14	695	92.4	219	10	US-09-972-656-104	Sequence 104, App
15	694	92.3	238	16	US-10-663-244-147	Sequence 147, App
16	693.5	92.2	237	16	US-10-663-244-146	Sequence 146, App
17	693.5	92.2	237	16	US-10-663-244-153	Sequence 153, App
18	693	92.2	239	10	US-09-992-600A-8	Sequence 8, Appli
19	693	92.2	239	10	US-09-924-340-8	Sequence 8, Appli
20	693	92.2	239	10	US-09-992-095B-8	Sequence 8, Appli
21	693	92.2	239	10	US-09-999-570-8	Sequence 8, Appli
22	693	92.2	239	14	US-10-000-489-8	Sequence 8, Appli
23	693	92.2	239	14	US-10-000-986-8	Sequence 8, Appli
24	693	92.2	239	14	US-10-154-678-8	Sequence 8, Appli
25	693	92.2	239	17	US-10-838-854-8	Sequence 8, Appli
26	692	92.0	239	15	US-10-292-088-64	Sequence 64, Appl
27	684	91.0	239	15	US-10-108-260A-4028	Sequence 4028, Ap
28	682.5	90.8	220	9	US-09-822-698A-24	Sequence 24, Appl
29	677	90.0	247	15	US-10-466-164-69	Sequence 69, Appl
30	666	88.6	219	10	US-09-972-656-94	Sequence 94, Appl
31	666	88.6	219	10	US-09-972-656-106	Sequence 106, App
32	658	87.5	133	14	US-10-153-382-39	Sequence 39, Appl
33	656	87.2	239	15	US-10-404-724-12	Sequence 12, Appl
34	656	87.2	239	17	US-10-816-276-8	Sequence 8, Appli
35	654	87.0	239	15	US-10-404-724-49	Sequence 49, Appl
36	654	87.0	239	17	US-10-816-276-45	Sequence 45, Appl
37	646	85.9	239	15	US-10-404-724-41	Sequence 41, Appl
38	646	85.9	239	15	US-10-404-724-45	Sequence 45, Appl
39	646	85.9	239	17	US-10-816-276-37	Sequence 37, Appl
40	646	85.9	239	17	US-10-816-276-41	Sequence 41, Appl
41	644	85.6	239	15	US-10-404-724-43	Sequence 43, Appl
42	644	85.6	239	15	US-10-404-724-47	Sequence 47, Appl
43	644	85.6	239	17	US-10-816-276-39	Sequence 39, Appl
44	644	85.6	239	17	US-10-816-276-43	Sequence 43, Appl
45	636	84.6	239	15	US-10-404-724-10	Sequence 10, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-663-244-148  
; Sequence 148, Application US/10663244  
; Publication No. US20040110933A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac J.  
; APPLICANT: Edge, Albert  
; APPLICANT: Kent, Rachel Baribault  
; TITLE OF INVENTION: CD44 LIGANDS  
; FILE REFERENCE: 10280-063001  
; CURRENT APPLICATION NUMBER: US/10/663,244  
; CURRENT FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US 60/410,758  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: US 60/469,123  
; PRIOR FILING DATE: 2003-05-09  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 148  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
US-10-663-244-148

Query Match 95.6%; Score 719; DB 16; Length 238;

Best Local Similarity 94.4%; Pred. No. 1.7e-49;

Matches 135; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLLHSNGYLDWYLPKPGSPQLLYLGSNRASGVDPDRFGS 60

Db 30 LPVTPGPASISCRSSQSLLHSNGYLDWYLPKPGSPQLLYLGSNRASGVDPDRFGS 89

Qy 61 GSGTDFTLKTSRVEAEVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIIPPSDEQL 120

```
Db 90 GSGTDFTLKISRVEAEDGVVYCMQALQTPTFGGKVEIKRTVAAPSVFIPPPSDEQL 149
Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 150 KSGTASVVCLLSNFPYREAKVQW 172

RESULT 2
US-10-663-244-144
; Sequence 144, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-144

Query Match 94.7%; Score 712; DB 16; Length 238;
Best Local Similarity 93.7%; Pred. No. 6.1e-49;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 60
Db 30 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEAEDGVVYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
Db 90 GSGTDFTLKISRVEAEDGVVYCMQALQTPTFGGKVEIKRTVAAPSVFIPPPSDEQL 149

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 150 KSGTASVVCLLSNFPYREAKVQW 172

RESULT 3
US-10-663-244-144
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-144

Query Match 94.7%; Score 712; DB 16; Length 238;
Best Local Similarity 93.7%; Pred. No. 6.1e-49;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 60
Db 30 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEAEDGVVYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
Db 90 GSGTDFTLKISRVEAEDGVVYCMQALQTPTFGGKVEIKRTVAAPSVFIPPPSDEQL 149

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 150 KSGTASVVCLLSNFPYREAKVQW 172

RESULT 3
US-10-663-244-149
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-149

Query Match 94.7%; Score 712; DB 15; Length 239;
Best Local Similarity 93.7%; Pred. No. 6.1e-49;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 60
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEAEDGVVYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
Db 91 GSGTDFTLKISRVEAEDGVVYCMQVLTPTFTFGPGTKVDIKRTVAAPSVFIPPPSDEQL 150

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 151 KSGTASVVCLLSNFPYREAKVQW 173

RESULT 5
US-10-292-088-16
; Sequence 16, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
```

```
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-149

Query Match 94.7%; Score 712; DB 16; Length 238;
Best Local Similarity 93.7%; Pred. No. 6.1e-49;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 60
Db 30 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEAEDGVVYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
Db 90 GSGTDFTLKISRVEAEDGVVYCMQALQTPTFGGKVEIKRTVAAPSVFIPPPSDEQL 149

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 150 KSGTASVVCLLSNFPYREAKVQW 172

RESULT 4
US-10-292-088-40
; Sequence 40, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-40

Query Match 94.7%; Score 712; DB 15; Length 239;
Best Local Similarity 93.7%; Pred. No. 6.1e-49;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 60
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEAEDGVVYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
Db 91 GSGTDFTLKISRVEAEDGVVYCMQVLTPTFTFGPGTKVDIKRTVAAPSVFIPPPSDEQL 150

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 151 KSGTASVVCLLSNFPYREAKVQW 173

RESULT 5
US-10-292-088-16
; Sequence 16, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
```



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; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-16

Query Match          94.4%; Score 710; DB 15; Length 239;
Best Local Similarity 93.0%; Pred. No. 8.8e-49;
Matches 133; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEADVGIYVCMQSLQIPRLFGGTVKVDIKRTVAAPSVFIFFPSDEQL 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 91 GSGTDFTLKISRVEADVGIYVCMQALQTPRTFGGTVKVEIKRTVAAPSVFIFFPSDEQL 150

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 151 KSGTASVVCLLSNFPYREAKVQW 173

RESULT 6
US-10-663-244-145
; Sequence 145, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-145

Query Match          94.3%; Score 709; DB 16; Length 238;
Best Local Similarity 93.0%; Pred. No. 1.1e-48;
Matches 133; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 30 LPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEADVGIYVCMQSLQIPRLFGGTVKVDIKRTVAAPSVFIFFPSDEQL 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 90 GSGTDFTLKISRVEADVGIYVCMQALQTPWTFFGGTKLEIKRTVAAPSVFIFFPSDEQL 149

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 150 KSGTASVVCLLSNFPYREAKVQW 172

RESULT 7
```

```
US-10-292-088-56
; Sequence 56, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-56

Query Match          94.3%; Score 709; DB 15; Length 239;
Best Local Similarity 93.0%; Pred. No. 1.1e-48;
Matches 133; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEADVGIYVCMQSLQIPRLFGGTVKVDIKRTVAAPSVFIFFPSDEQL 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 91 GSGTDFTLKISRVEADVGIYVCMQALQTPRTFGGTVKVEIKRTVAAPSVFIFFPSDEQL 150

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 151 KSGTASVVCLLSNFPYREAKVQW 173

RESULT 8
US-10-292-088-8
; Sequence 8, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-8

Query Match          94.0%; Score 707; DB 15; Length 239;
Best Local Similarity 92.3%; Pred. No. 1.5e-48;
Matches 132; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEADVGIYVCMQSLQIPRLFGGTVKVDIKRTVAAPSVFIFFPSDEQL 120
```



```
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-32

Query Match          93.4%; Score 702; DB 15; Length 239;
Best Local Similarity 91.6%; Pred. No. 3.8e-48;
Matches 131; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 60
Db 31 LPVTPGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVPFIFFPSDEQL 120
Db 91 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVPFIFFPSDEQL 150

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db 151 KSGTASVVCLLSNFPYPREAKVQW 173

RESULT 13
US-10-663-244-152
; Sequence 152, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Kent, Rachel Baribault
; APPLICANT: Edge, Albert
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-152

Query Match          93.3%; Score 701.5; DB 16; Length 237;
Best Local Similarity 93.0%; Pred. No. 4.1e-48;
Matches 133; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MPVTPGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 60
Db 30 LPVTPGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVPFIFFPSDEQL 120
Db 90 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVPFIFFPSDEQL 148

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db 149 KSGTASVVCLLSNFPYPREAKVQW 171

RESULT 14
US-09-972-656-104
; Sequence 104, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
```

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; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 104
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-104

Query Match          92.4%; Score 695; DB 10; Length 219;
Best Local Similarity 90.2%; Pred. No. 1.3e-47;
Matches 129; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 60
Db 11 LPVTPGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 70

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVPFIFFPSDEQL 120
Db 71 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVPFIFFPSDEQL 130

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db 131 KSGTASVVCLLSNFPYPREAKVQW 153

RESULT 15
US-10-663-244-147
; Sequence 147, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-147

Query Match          92.3%; Score 694; DB 16; Length 238;
Best Local Similarity 91.6%; Pred. No. 1.6e-47;
Matches 131; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 60
Db 30 LPVTPGEPASISCRSSQSLHNSGYNLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVPFIFFPSDEQL 120
Db 90 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVPFIFFPSDEQL 149

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db 150 KSGTASVVCLLSNFPYPREAKVQW 172

Search completed: March 8, 2005, 07:05:54
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Job time : 76.8864 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 15.7238 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-32

Perfect score: 752

Sequence: 1 MPVTPGSPASISCRSSQSLL.....TASVVCLLSNFYPREKQVW 143

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	693	92.2	239	4	US-10-000-489-8
2	658	87.5	133	4	US-09-472-087-26
3	658	87.5	133	4	US-09-472-087-116
4	618	82.2	238	4	US-09-698-705-10
5	612	81.4	239	3	US-08-487-550-6
6	612	81.4	239	4	US-09-526-098-6
7	612	81.4	239	4	US-09-383-916-6
8	587	78.1	218	4	US-09-698-705-12
9	586	77.9	242	1	US-08-398-613A-56
10	586	77.9	242	1	US-08-398-612A-56
11	586	77.9	242	1	US-08-398-611A-56
12	586	77.9	242	2	US-08-491-334A-56
13	586	77.9	242	3	US-09-027-449-42
14	586	77.9	242	3	US-08-804-444A-42
15	586	77.9	242	3	US-09-026-985-42
16	586	77.9	242	4	US-09-121-952A-42
17	586	77.9	242	4	US-09-234-340A-42
18	561	74.6	139	4	US-09-472-087-25
19	561	74.6	139	4	US-09-472-087-114
20	555	73.8	222	4	US-09-479-614-26
21	555	73.8	242	4	US-09-479-614-20
22	552	73.4	238	3	US-09-192-545-4
23	547	72.7	173	5	PCT-US91-02942-3
24	547	72.7	173	5	PCT-US91-02946-3
25	544.5	72.4	146	4	US-09-472-087-21
26	544.5	72.4	146	4	US-09-472-087-93
27	542.5	72.1	240	4	US-09-301-593-36

28 542 72.1 216 4 US-09-254-180C-132 Sequence 132, Appl  
29 542 72.1 216 4 US-09-254-180C-183 Sequence 183, Appl  
30 540 71.6 226 4 US-09-254-180C-182 Sequence 182, Appl  
31 538.5 71.6 226 4 US-09-456-090A-38 Sequence 38, Appl  
32 538.5 71.6 226 4 US-09-453-234-38 Sequence 38, Appl  
33 538 71.5 239 4 US-09-627-896B-22 Sequence 22, Appl  
34 537 71.4 219 3 US-09-027-449-72 Sequence 72, Appl  
35 537 71.4 219 3 US-09-026-985-72 Sequence 72, Appl  
36 537 71.4 219 4 US-09-121-952A-72 Sequence 72, Appl  
37 537 71.4 219 4 US-09-234-340A-72 Sequence 72, Appl  
38 537 71.4 242 3 US-09-027-449-51 Sequence 51, Appl  
39 537 71.4 242 3 US-09-027-449-56 Sequence 56, Appl  
40 537 71.4 242 3 US-09-027-449-62 Sequence 62, Appl  
41 537 71.4 242 3 US-08-804-444A-51 Sequence 51, Appl  
42 537 71.4 242 3 US-08-804-444A-56 Sequence 56, Appl  
43 537 71.4 242 3 US-09-026-985-51 Sequence 51, Appl  
44 537 71.4 242 3 US-09-026-985-56 Sequence 56, Appl  
45 537 71.4 242 3 US-09-026-985-62 Sequence 62, Appl

#### ALIGNMENTS

RESULT 1  
US-10-000-489-8  
; Sequence 8, Application US/10000489  
; Patent No. 6794363  
; GENERAL INFORMATION:  
; APPLICANT: Benjanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.USE.DIV  
; CURRENT APPLICATION NUMBER: US/10/000,489  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: US 09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: JPatent  
; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
US-10-000-489-8

Query Match 92.2%; Score 693; DB 4; Length 239;  
Best Local Similarity 91.6%; Pred. No. 4.1e-60;  
Matches 131; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MPVTPGSPASISCRSSQSLLHSNYSYLDWYLPKQSGSPQLLIYLGSRASGVDPDRFSGS 60  
Db 31 LPVTPGSPASISCRSSQSLLHSNYSYLDWYLPKQSGSPQLLIYLGSRASGVDPDRFSGS 90  
Qy 61 GSGTDFTLKISRVAEDVGIYCMOSLQIPRLFGPGTKVDIKRTVAAPSVIFPPSDSQL 120  
Db 91 GSGTDFTLKISRVAEDVGIYCMOSLQIPRLFGPGTKVDIKRTVAAPSVIFPPSDSQL 150  
Qy 121 KSGTASVVCLLSNFYPREKQVW 143  
Db 151 KSGTASVVCLLSNFYPREKQVW 173

RESULT 2  
US-09-472-087-26  
; Sequence 26, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILEEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PF1  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-26

Query Match 87.5%; Score 658; DB 4; Length 133;  
Best Local Similarity 93.2%; Pred. No. 5.4e-57;  
Matches 124; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
  
QY 5 PGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGSGT 64  
DB 1 PGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGSGT 60  
  
QY 65 DFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIIPPSPDEQLKSGT 124  
DB 61 DFTLKISRVEADVGIYCMQALQTLPTLFGGGTKVEIKRTVAAPSVFIIPPSPDEQLKSGT 120  
  
QY 125 ASVVCLLSNFPYR 137  
DB 121 ASVVCLLSNFPYR 133

RESULT 3  
US-09-472-087-116  
; Sequence 116, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILEEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PF1  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 116  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-116

Query Match 87.5%; Score 658; DB 4; Length 133;  
Best Local Similarity 93.2%; Pred. No. 5.4e-57;  
Matches 124; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGSGT 64  
DB 1 PGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGSGT 60  
  
QY 65 DFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIIPPSPDEQLKSGT 124  
DB 61 DFTLKISRVEADVGIYCMQALQTLPTLFGGGTKVEIKRTVAAPSVFIIPPSPDEQLKSGT 120  
  
QY 125 ASVVCLLSNFPYR 137  
DB 121 ASVVCLLSNFPYR 133  
  
RESULT 4  
US-09-698-705-10  
; Sequence 10, Application US/09698705  
; Patent No. 6824780  
; GENERAL INFORMATION:  
; APPLICANT: Devaux, B.  
; APPLICANT: Keller, G.  
; APPLICANT: Koeppe, H.  
; APPLICANT: Lasky, L.  
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use  
; FILE REFERENCE: P1777R1  
; CURRENT APPLICATION NUMBER: US/09/698,705  
; CURRENT FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/162,558  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 60/182,872  
; PRIOR FILING DATE: 2000-02-16  
; NUMBER OF SEQ ID NOS: 25  
; SEQ ID NO 10  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is chimeric mouse/human  
US-09-698-705-10

Query Match 82.2%; Score 618; DB 4; Length 238;  
Best Local Similarity 81.8%; Pred. No. 8.9e-53;  
Matches 117; Conservative 12; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 MPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60  
DB 30 VPVTPGESVSIICRSKSLHNSGNTLYLWFLQPGQSPQLLIYRMSNLASGVDPDRFSGS 89  
  
QY 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIIPPSPDEQL 120  
DB 90 GSGTAPTLRISRVEADVGIYCMQALQTLPTLFGGGTKVEIKRTVAAPSVFIIPPSPDEQL 149  
  
QY 121 KSGTASVVCLLSNFPYR 143  
DB 150 KSGTASVVCLLSNFPYR 172

RESULT 5  
US-08-487-550-6  
; Sequence 6, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA

COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/487,550  
APPLICATION NUMBER: US/08/487,550  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-550-6

Query Match 81.4%; Score 612; DB 3; Length 239;  
Best Local Similarity 81.1%; Pred. No. 3.4e-52;  
Matches 116; Conservative 10; Mismatches 17; Indels 0; Gaps 0;  
  
Qy 1 MPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60  
Db 31 LPITGEPASISCRSSQSLHNSGDTFLSWYQKPGQPRLLIYKVSNRDSGVDPDRFSGS 90  
  
Qy 61 GSGTDFTLKISRVAEDVGIIYCMQSLQIPRLFGGTGKVDIKRTVAAPSVFIFFPSDEQL 120  
Db 91 GAGTDFTLKISAVEAEDVGIVFCGGTPTPTFGGTGKVEIKRTVAAPSVFIFFPSDEQL 150  
  
Qy 121 KSGTASVVCLLSNFPYREAKVQW 143  
Db 151 KSGTASVVCLLSNFPYREAKVQW 173

RESULT 6  
US-09-526-098-6  
Sequence 6, Application US/09526098  
Patent No. 6492134  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESS: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/526,098  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:

APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-526-098-6

Query Match 81.4%; Score 612; DB 4; Length 239;  
Best Local Similarity 81.1%; Pred. No. 3.4e-52;  
Matches 116; Conservative 10; Mismatches 17; Indels 0; Gaps 0;  
  
Qy 1 MPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60  
Db 31 LPITGEPASISCRSSQSLHNSGDTFLSWYQKPGQPRLLIYKVSNRDSGVDPDRFSGS 90  
  
Qy 61 GSGTDFTLKISRVAEDVGIIYCMQSLQIPRLFGGTGKVDIKRTVAAPSVFIFFPSDEQL 120  
Db 91 GAGTDFTLKISAVEAEDVGIVFCGGTPTPTFGGTGKVEIKRTVAAPSVFIFFPSDEQL 150  
  
Qy 121 KSGTASVVCLLSNFPYREAKVQW 143  
Db 151 KSGTASVVCLLSNFPYREAKVQW 173

RESULT 7  
US-09-383-916-6  
Sequence 6, Application US/09383916  
Patent No. 670654  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESS: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/383,916  
FILING DATE: 26-AUG-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-383-916-6
Query Match      81.4%; Score 612; DB 4; Length 239;
Best Local Similarity 81.1%; Pred. No. 3.4e-52;
Matches 116; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRAGVDPDRFSGS 60
Db 31 LPITPGEPASISCRSSQSLHSGNDTFLSWYQKQPRLIIYKVNRSQGVDPDRFSGS 90
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
Db 91 GAGTDFTLKISRVEADVGVYFCQGTPTPTFGGKTKVEIKRTVAAPSVFIPPPSDEQL 150
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
Db 151 KSGTASVVCLLNNFYPREAKVQW 173

RESULT 8
US-09-698-705-12
; Sequence 12, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Laaky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P1777R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
;
US-09-698-705-12
Query Match      78.1%; Score 587; DB 4; Length 218;
Best Local Similarity 78.3%; Pred. No. 8.6e-50;
Matches 112; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRAGVDPDRFSGS 60
Db 11 LSVTIGQPASISCRSSQSLSDCKTYLWLLQRPQSPKRLIYLVSTLDSGVDPDRFTGS 70
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
Db 71 GSGTDFTLKISRVEADLVGVYCMQGTHTFPTFGGKTKVEIKRTVAAPSVFIPPPSDEQL 130
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
Db 131 KSGTASVVCLLNNFYPREAKVQW 153

RESULT 9
US-08-398-613A-56
; Sequence 56, Application US/08398613A
; Patent No. 5677426
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
```

```
;
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory I
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,613A
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 874P1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1489
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-398-613A-56
Query Match      77.9%; Score 586; DB 1; Length 242;
Best Local Similarity 76.9%; Pred. No. 1.2e-49;
Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRAGVDPDRFSGS 60
Db 34 LPVSLGQASISCRSSQSLVHGIGNTYLVHLYLOKPGQSPKLLIYKVNRSQGVDPDRFSGS 93
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
Db 94 GSGTDFTLRISRVEADLVGYFCQSQSTHVLTFGAGTKLKLKRAVAAPTVFIFPPSSEQL 153
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
Db 154 KSGTASVVCLLNNFYPREAKVQW 176

RESULT 10
US-08-398-612A-56
; Sequence 56, Application US/08398612A
; Patent No. 5686070
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
; TITLE OF INVENTION: Treatment of Inflammatory Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
```





; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0874P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-491-334A-56

Query Match 77.9%; Score 586; DB 2; Length 242;  
Best Local Similarity 76.9%; Pred. No. 1.2e-49;  
Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFSGS 60  
Db 34 LPVSLGDAQSISCRSSQSLVHGIGNTYLLHWYLOKPGSQPKLLIYKVSNRFSGVDPDRFSGS 93

Qy 61 GSGTDFTLKISRVEAEDVGIIYCMQSLQIPLRFGPGTKVDIKRTVAAPSVFIFFPPSDEQL 120  
Db 94 GSGTDFTLRISRVEAEDLGLYFCQSQSTHVPLTFGAGTKLELKRVAAPTTFIFFPPSDEQL 153

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143  
Db 154 KSGTASVVCLLNFPYPREAKVQW 176

RESULT 13  
US-09-027-449-42  
; Sequence 42, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027,449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,664  
; FILING DATE: 21-Feb-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P108SR3-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-027-449-42

Query Match 77.9%; Score 586; DB 3; Length 242;  
Best Local Similarity 76.9%; Pred. No. 1.2e-49;  
Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFSGS 60  
Db 34 LPVSLGDAQSISCRSSQSLVHGIGNTYLLHWYLOKPGSQPKLLIYKVSNRFSGVDPDRFSGS 93

Qy 61 GSGTDFTLKISRVEAEDVGIIYCMQSLQIPLRFGPGTKVDIKRTVAAPSVFIFFPPSDEQL 120  
Db 94 GSGTDFTLRISRVEAEDLGLYFCQSQSTHVPLTFGAGTKLELKRVAAPTTFIFFPPSDEQL 153

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143  
Db 154 KSGTASVVCLLNFPYPREAKVQW 176

RESULT 14  
US-08-804-444A-42  
; Sequence 42, Application US/0880444A  
; Patent No. 6117980  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania N  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,44A  
; FILING DATE: 21-Feb-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-804-444A-42

Query Match 77.9%; Score 586; DB 3; Length 242;  
Best Local Similarity 76.9%; Pred. No. 1.2e-49;  
Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPOLLIYLGNSRAGVDPDRFSGS 60  
Db 34 LPVSLGDAQSISCRSSQSLVHGIGNTYLLHWYLOKPGSQPKLLIYKVSNRFSGVDPDRFSGS 93

Qy 61 GSGTDFTLKISRVEAEDVGIIYCMQSLQIPLRFGPGTKVDIKRTVAAPSVFIFFPPSDEQL 120  
Db 94 GSGTDFTLRISRVEAEDLGLYFCQSQSTHVPLTFGAGTKLELKRVAAPTTFIFFPPSDEQL 153

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143  
Db 154 KSGTASVVCLLNFPYREAKVQW 176

## RESULT 15

US-09-026-985-42  
; Sequence 42, Application US/09026985  
; Patent No. 6133426  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,985  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-026-985-42

Query Match 77.9%; Score 586; DB 3; Length 242;  
Best Local Similarity 76.9%; Pred. No. 1.2e-49;  
Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGVNYLDWYLQKPGQSPQLLIYLGNSNRASGVDPDRFSGS 60  
Db 34 LPVSLGQASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKVNRFSGVDPDRFSGS 93  
Qy 61 GSGTDFTLKISRVAEDVGIYYCMQSLQIPRLFGEGTKVDIKRTVAAPSVEIFPPPSDEQL 120  
Db 94 GSGTDFTLKISRVAEDVGLYFCQSQSTHVPLTFCAGTKLEKRAVAAPTVEIFPPPSDEQL 153  
Qy 121 KSGTASVVCLLSNFPYREAKVQW 143  
Db 154 KSGTASVVCLLNFPYREAKVQW 176

Search completed: March 8, 2005, 05:54:09  
Job time : 15.7238 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 13.5032 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-33  
Perfect score: 998  
Sequence: 1 SETLSLTCVAVGSGFSGYW.....YAATSQVLLPSKDVMOQTDE 190  
Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	902	90.4	231	2	Ig Fab region IV-J
2	678.5	68.0	627	2	Ig mu chain precur
3	556.5	55.8	143	2	Ig heavy chain V-I
4	535.5	53.7	592	2	Ig mu chain - shee
5	519	52.0	140	2	Ig heavy chain pre
6	517.5	51.9	140	2	Ig heavy chain V r
7	506	50.7	126	2	Ig heavy chain V4
8	503.5	50.5	288	2	Ig heavy chain VDJ
9	492.5	49.3	220	2	Ig gamma-1 heavy c
10	470	47.1	139	2	Ig heavy chain V r
11	461	46.2	146	1	Ig heavy chain pre
12	451	45.2	106	2	Ig mu chain - huma
13	450.5	45.1	130	2	Ig heavy chain V r
14	450.5	45.1	140	2	Ig variable region
15	449	45.0	122	2	Ig heavy chain V r
16	443	44.4	97	2	Ig heavy chain V r
17	440	44.1	97	2	Ig heavy chain V r
18	437	43.8	130	2	Ig heavy chain V r
19	436	43.7	568	2	Ig heavy chain pre
20	434.5	43.5	155	2	Ig heavy chain - h
21	434	43.5	97	2	Ig heavy chain V r
22	433.5	43.4	155	2	Ig heavy chain - h
23	433	43.4	97	2	Ig heavy chain V r
24	433	43.4	97	2	Ig heavy chain V r
25	433	43.4	452	1	Ig mu chain C regi
26	433	43.4	453	2	Ig mu chain C regi
27	433	43.4	473	1	Ig mu chain C regi
28	433	43.4	474	2	Ig heavy chain - h
29	431	43.2	137	2	Ig heavy chain V r

30	430.5	43.1	114	2	I72667	cold agglutinin FS
31	427.5	42.8	116	2	S37456	Ig mu chain - huma
32	427.5	42.8	135	2	S78051	Ig heavy chain pre
33	425.5	42.6	139	2	S31696	Ig heavy chain V r
34	425.5	42.6	147	2	S13519	Ig heavy chain V r
35	422	42.3	129	2	S44114	Ig heavy chain V r
36	421	42.2	470	2	S22080	Ig heavy chain pre
37	420	42.1	118	2	S20780	Ig heavy chain V r
38	419.5	42.0	123	2	S30530	Ig heavy chain V r
39	418	41.9	145	2	S78055	Ig heavy chain pre
40	416.5	41.7	134	2	S54906	Ig heavy chain V r
41	410	41.1	110	2	S44110	Ig heavy chain V-D
42	409.5	41.0	121	2	S44113	Ig heavy chain V r
43	408	40.9	97	2	JH0428	Ig gamma chain V r
44	408	40.9	118	2	S24443	Ig heavy chain V r
45	407.5	40.8	146	2	S09711	Ig heavy chain V r

ALIGNMENTS

RESULT 1

B23746  
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: B23746  
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin C region: immunoglobulin homology  
A:Reference number: A23746; MUID:91131575; PMID:1993660  
A:Accession: B23746  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-231 <L80>  
C:Superfamily: immunoglobulin C region: immunoglobulin homology  
F:140-209/Domain: immunoglobulin homology <IM>

Query Match 90.4%; Score 902; DB 2; Length 231;  
Best Local Similarity 92.1%; Pred. No. 4e-64;  
Matches 175; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy	1	SETLSLTCVAVGSGFSGYNSWIRQPPGKGLEWGEINHSGSTNTNPSLKSRVTISVDTS	60
Db	14	SETLSLTCVAVGSGFSGYNSWIRQPPGKGLEWGEINHSGSTNTNPSLKSRVTISVDTS	73
Qy	61	KNQFSLKLSSTVAADTAVVYCARGGTTVPDAFDIWGQTMVTVSSGGSASAPTLFPLVSC	120
Db	74	KNQFSLKLSSTVAADTAVVYCARGPHDTSGHYNWMVGQTLTVTVSSGGSASAPTLFPLVSC	133
Qy	121	ENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSPVLRGKYAATSQVLLP	180
Db	134	ENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSPVLRGKYAATSQVLLP	193
Qy	181	SKDVMQGTDE	190
Db	194	SKDVMQGTDE	203

RESULT 2

SI4683  
Ig mu chain precursor, membrane-bound (clone 201) - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
C:Accession: SI4683; S08047  
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.  
Nucleic Acids Res. 18, 4278, 1990  
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.  
A:Reference number: SI4683; MUID:90332450; PMID:2115996  
A:Accession: SI4683  
A:Molecule type: mRNA  
A:Residues: 1-627 <FRI>  
A:Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451



## RESULT 6

Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)  
A;Species: Homo sapiens (man)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
A;Accession: A49045  
R;Grillot-Courvalin, C.; Brouet, J.C.; Pillier, F.; Rasseenti, L.Z.; Labaume, S.; Silverma  
Bur, J. Immunol. 22, 1781-1788, 1992  
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl  
A;Reference number: A49045; MUID:92324290; PMID:1623923  
A;Accession: A49045  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-140 <GRI>  
A;Cross-references: GB:839381; NID:9250899; PIDN:AAB22441.1; PID:9250900  
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBI:P:108089)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
P;34-116/Domain: immunoglobulin homology <IMM>

Query Match 51.9%; Score 517.5; DB 2; Length 140;  
Best Local Similarity 91.6%; Pred. No. 5e-34;  
Matches 98; Conservative 3; Mismatches 5; Indels 1; Gaps 1;  
Qy 1 SETLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEINHGSGTNNPNSLKSRTVISVDT 60  
Db 34 SETLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEINHGSGTNNPNSLKSRTVISVDT 93  
Qy 61 KNQPSLKLSSVTAADTAVYVCARGTWTFF-DAFDIWGQGTMTVSS 106  
Db 94 KNQPSLKLSSVTAADTAVYVCARGGPAATIVESFDYWGQGTMTVSS 140

## RESULT 7

S47010  
Ig heavy chain V4.21-UniqueJ5 region - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
A;Accession: S47010  
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.  
submitted to the EMBL Data Library, July 1994  
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin  
A;Reference number: S47009  
A;Accession: S47010  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-126 <MAH>  
A;Cross-references: EMBL:Z35492; NID:9517254; PIDN:CAA84625.1; PID:9517255  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
P;15-97/Domain: immunoglobulin homology <IMM>

Query Match 50.7%; Score 506; DB 2; Length 126;  
Best Local Similarity 87.5%; Pred. No. 3.6e-33;  
Matches 98; Conservative 3; Mismatches 5; Indels 6; Gaps 1;  
Qy 1 SETLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEINHGSGTNNPNSLKSRTVISVDT 60  
Db 15 SETLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEINHGSGTNNPNSLKSRTVISVDT 74  
Qy 61 KNQPSLKLSSVTAADTAVYVCARGG-----TTTTFDAFDIWGQGTMTVSS 106  
Db 75 KNQPSLKLSSVTAADTAVYVCARGGQCPKASCYTKNWFDPWGQGTMTVSS 126

## RESULT 8

S29690  
Ig heavy chain VDJ region - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 06-Jan-1995 #sequence\_revision 30-Jan-1998 #text\_change 20-Jun-2000  
A;Accession: S29690  
R;Dammers, P.M.; Bos, N.A.; Kroese, F.G.M.  
submitted to the EMBL Data Library, October 1992

A;Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.  
A;Reference number: S29690  
A;Accession: S29690  
A;Molecule type: mRNA  
A;Residues: 1-288 <DAM>  
A;Cross-references: EMBL:X68782; NID:956442; PID:gi334294  
A;Experimental source: strain DZB  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 50.5%; Score 503.5; DB 2; Length 288;  
Best Local Similarity 51.1%; Pred. No. 1.4e-32;  
Matches 97; Conservative 36; Mismatches 52; Indels 5; Gaps 3;  
Qy 3 TSLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEIN-HSGSTNNPNSLKSRTVISVDTSK 61  
Db 14 SVKISKASGYTFTDYYMHVWKQRPQGLVWIGRINPANGNTEYAEKFKSRATLTADKSS 73  
Qy 62 NQPSLKLSSVTAADTAVYVCARGTWTFFDAFDIWGQGTMTVSSGSASAPTLPLVSC 121  
Db 74 NTAQMQLSLTSEDATYFCTIWTGVV---PPDYWGQGVMTVSSSESQSSTPLVPLVSC 130  
Qy 122 NSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDI-SSTRGFPSVLRGKGYAATSQVLLP 180  
Db 131 SPUSDENLVAMGCLARDFLPSSISFSWNYQNTEVMQGVRTFFPLRTGDKTATTSQVLLS 190  
Qy 181 SKDVMOQTDE 190  
Db 191 AKNVLEGSDE 200

## RESULT 9

A49444  
Ig gamma-1 heavy chain (New) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 16-Jul-1999  
A;Accession: A49444  
R;Saul, F.A.; Poljak, R.J.  
Proteins 14, 363-371, 1992  
A;Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A res  
A;Reference number: A49444; MUID:93066153; PMID:1438175  
A;Accession: A49444  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-220 <SAU>  
A;Note: sequence modified after extraction from NCBI backbone  
A;Note: this sequence report includes corrections based on crystal structure refinement  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
P;137-202/Domain: immunoglobulin homology <IMM>

Query Match 49.3%; Score 492.5; DB 2; Length 220;  
Best Local Similarity 51.9%; Pred. No. 7.8e-32;  
Matches 99; Conservative 32; Mismatches 44; Indels 15; Gaps 5;  
Qy 1 SETLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEINHGSGTNNPNSLKSRTVISVDT 60  
Db 15 SQTLSLTCTVSGTSDDDYYMTWVRQPPGKGLEWIGYVYTGTTLLDPSLRGRTMLVNTS 74  
Qy 61 KNQPSLKLSSVTAADTAVYCAR-----GGTTFDAFDIWGQGTMTVSSGSASAPTLFP 116  
Db 75 KNQPSLKLSSVTAADTAVYCARNLIAAG-----IDVMGQGSLLTVSSASTGPSVFP 127  
Qy 117 LVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRL-GGKYAATS 175  
Db 128 LAPSSKSTSG-GTAALGCLVKDIFPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSS 184  
Qy 176 QVLLPSKDV 184  
Db 185 VVTVPSSSL 193





Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A;Title: Somatic diversification in the heavy chain variable region genes expressed by h  
A;Reference number: A36876; MUID:94119917; PMID:8290556

A;Accession: J37782  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140 <RES>  
A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 45.1%; Score 450.5; DB 2; Length 140;  
Best Local Similarity 82.2%; Pred. No. 9.7e-29;  
Matches 88; Conservative 5; Mismatches 13; Indels 1; Gaps 1;  
Qy 1 SETLSLTCVYGGSFSGYYWIRQPPGKGLWIGEINHGSGTNNPGLKSRVTISVDTS 60  
Db 34 SETLSLTCVGGGSISSYYWIRQPPGKGLWIGIYVYSGSTNNPGLKSRVTISVDTS 93  
Qy 61 KNQFSLKLSSTVAADTAVYTCARGTTFDA-PDINGQGTMTVSS 106  
Db 94 KNQFSLKLSSTVAADTAVYTCARHNSSSWYGRYFDYWGQGLTVSS 140

## RESULT 15

JL0047  
Ig heavy chain V region precursor (clone cR18) - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 16-Aug-1996  
C;Accession: JL0047  
R;Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.  
J. Exp. Med. 167, 2011-2016, 1988  
A;Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5  
A;Reference number: JL0047; MUID:88258392; PMID:3133445  
A;Accession: JL0047  
A;Molecule type: mRNA  
A;Residues: 1-122 <BAE>  
A;Experimental source: T-cell line RPMI 8402  
A;Note: the authors translated the reading frame which extends to the stop codon; the se  
A;Note: this sequence belongs to the VH II subgroup  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;23-105/Domain: immunoglobulin homology <IMM>

Query Match 45.0%; Score 449; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.1e-28;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SETLSLTCVYGGSFSGYYWIRQPPGKGLWIGEINHGSGTNNPGLKSRVTISVDTS 60  
Db 23 SETLSLTCVYGGSFSGYYWIRQPPGKGLWIGIYVYSGSTNNPGLKSRVTISVDTS 82  
Qy 61 KNQFSLKLSSTVAADTAVYTCARG 84  
Db 83 KNQFSLKLSSTVAADTAVYTCARG 106

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Job time : 14.5532 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 70.9554 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-33

Perfect score: 998

Sequence: 1 SETLSLCAVYGGSFSGYV.....YAATSOVLPSKDVMOQTDE 190

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_cremli: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	900.5	90.2	595	2	Q8WUX4	Q8WUX4	homo sapien
2	900.5	90.2	597	2	Q6GMX5	Q6GMX5	homo sapien
3	900.5	90.2	597	2	Q9BU10	Q9BU10	homo sapien
4	900.5	90.2	625	2	Q96AA6	Q96AA6	homo sapien
5	894.5	89.6	597	2	Q9BQB8	Q9BQB8	homo sapien
6	851	85.3	620	2	Q96EY0	Q96EY0	homo sapien
7	733	73.4	606	2	Q6GMX2	Q6GMX2	homo sapien
8	713	71.4	613	2	Q8WUK1	Q8WUK1	homo sapien
9	698.5	70.0	597	2	Q96BB9	Q96BB9	homo sapien
10	572	57.3	465	2	Q6GMX6	Q6GMX6	homo sapien
11	553.5	55.5	476	2	Q6GMX1	Q6GMX1	homo sapien
12	530.5	53.2	576	2	Q6P4I8	Q6P4I8	homo sapien
13	527.5	52.9	477	2	Q6GMX7	Q6GMX7	homo sapien
14	512.5	51.4	613	2	Q8VCX7	Q8VCX7	mus musculus
15	492.5	49.3	478	2	Q72379	Q72379	homo sapien
16	490.5	49.1	496	2	Q96KX8	Q96KX8	homo sapien
17	485	48.6	473	2	Q8TC63	Q8TC63	homo sapien
18	484	48.5	614	2	Q7TMT6	Q7TMT6	mus musculus
19	475	47.6	478	2	Q6NYH3	Q6NYH3	homo sapien
20	475	47.6	492	2	Q72374	Q72374	homo sapien
21	474.5	47.5	476	2	Q6MZX7	Q6MZX7	homo sapien
22	465	46.6	150	2	Q95973	Q95973	homo sapien
23	461	46.2	146	1	HV21 HUMAN	HV21	homo sapien
24	460.5	46.1	479	2	Q9M22	Q9M22	mus musculus
25	442	44.3	116	2	Q723Y6	Q723Y6	homo sapien
26	433	43.4	454	1	MUC HUMAN	MUC	homo sapien
27	428.5	42.9	605	2	Q6GN83	Q6GN83	homo sapien
28	417.5	41.8	119	2	Q9UL73	Q9UL73	homo sapien
29	417	41.8	593	2	Q6TNM5	Q6TNM5	homo sapien
30	414.5	41.5	470	2	Q8PJA4	Q8PJA4	homo sapien
31	410.5	41.1	614	2	Q6DDQ7	Q6DDQ7	homo sapien

32	410	41.1	482	2	Q91X92	Q91X92	mus musculus
33	399	40.0	572	2	Q66IQ7	Q66IQ7	homo sapien
34	397	39.8	139	2	Q86SX2	Q86SX2	homo sapien
35	397	39.8	465	2	Q6PC4	Q6PC4	homo sapien
36	395.5	39.6	478	2	Q6PI81	Q6PI81	homo sapien
37	393	39.4	225	2	Q6PAF5	Q6PAF5	homo sapien
38	385	38.5	482	2	Q8KL72	Q8KL72	mus musculus
39	384.5	38.5	464	2	Q6MZU6	Q6MZU6	homo sapien
40	383.5	38.4	129	1	HV2F HUMAN	HV2F	homo sapien
41	383.5	38.4	466	2	Q6IN78	Q6IN78	homo sapien
42	383.5	38.4	480	2	Q6N094	Q6N094	homo sapien
43	383	38.4	473	2	Q6P055	Q6P055	homo sapien
44	383	38.4	493	2	Q6GMX2	Q6GMX2	homo sapien
45	380.5	38.1	472	2	Q6N089	Q6N089	homo sapien

#### ALIGNMENTS

#### RESULT 1

Q8WUX4 ID Q8WUX4 PRELIMINARY; PRT; 595 AA.  
AC Q8WUX4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RC SEQUENCE FROM N.A.  
RX TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC019235; AAL19235.2; -;  
DR PIR; G34964; G34964.  
DR HSSP; P01861; 1ADQ.  
DR Pfam; PF07654; Cl-set; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGL; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKS; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Query Match

90.2%; Score 900.5; DB 2; Length 595;

Best Local Similarity 89.8%; Pred. No. 2.3e-72;  
Matches 176; Conservative 2; Mismatches 11; Indels 7; Gaps 2;

Qy 1 SETLSLTCVAVYGGSGFYYSWIRQPGKLEWIGEHNSGTYNPNPSLKSRTVISVDT 60  
Db 41 SETLSLTCVAVYGGSGFYYSWIRQPGKLEWIGEHNSGTYNPNPSLKSRTVISVDT 100  
Qy 61 KNQFSLKLSVTAADTAIVYCAR-----GGTTVTFDAFDIWGQTMVTVSSGSASAPTL 114  
Db 101 KKQLSLKLSVNAADTAIVYCARVITRASPGTDGRY-GMDVWGQGTTVTVSSGSASAPTL 159  
Qy 115 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGKGYAAT 174  
Db 160 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGKGYAAT 219  
Qy 175 SQVLLPSKDVMOGTDE 190  
Db 220 SQVLLPSKDVMOGTDE 235

RESULT 2  
Q6GMX5 ID Q6GMX5 PRELIMINARY; PRT; 597 AA.  
AC Q6GMX5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073767; AAH73767.1; -.  
DR InterPro; IPR003599; IG-like.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 4.  
DR Pfam; PF00047; ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 4.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Hypothetical protein\_  
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;  
Query Match 90.2%; Score 900.5; DB 2; Length 597;  
Best Local Similarity 89.8%; Pred. No. 2.3e-72;  
Matches 176; Conservative 2; Mismatches 11; Indels 7; Gaps 2;

Qy 1 SETLSLTCVAVYGGSGFYYSWIRQPGKLEWIGEHNSGTYNPNPSLKSRTVISVDT 60  
Db 34 SETLSLTCVAVYGGSGFYYSWIRQPGKLEWIGEHNSGTYNPNPSLKSRTVISVDT 93  
Qy 61 KNQFSLKLSVTAADTAIVYCAR-----GGTTVTFDAFDIWGQTMVTVSSGSASAPTL 114  
Db 94 KKQLSLKLSVNAADTAIVYCARVITRASPGTDGRY-GMDVWGQGTTVTVSSGSASAPTL 152  
Qy 115 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGKGYAAT 174  
Db 153 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGKGYAAT 212  
Qy 175 SQVLLPSKDVMOGTDE 190  
Db 213 SQVLLPSKDVMOGTDE 228

RESULT 3  
Q9BU10 ID Q9BU10 PRELIMINARY; PRT; 597 AA.  
AC Q9BU10;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHM protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lymph;  
RC Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002963; AAH02963.1; -.  
DR HSP; P01861; IADQ.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 4.

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DR SMART: SM00406; IGV: 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match          90.2%; Score 900.5; DB 2; Length 597;
Best Local Similarity 89.8%; Pred. No. 2.3e-72;
Matches 176; Conservative 2; Mismatches 11; Indels 7; Gaps 2;

Qy 1 SETLSLTCVYGGSFSGYVSWIRQPPGKGLWIEGHNHSGSTNYNPSLKSRTVISVDT 60
Db 34 SETLSLTCVYGGSFSGYVSWIRQPPGKGLWIEGHNHSGSTNYNPSLKSRTVISVDT 93
Qy 61 KNQPSLKLSSVTAADTAVYCAR-----GGTTVTFDAFDWGGTWTVSSGSASAPTL 114
Db 94 KKQLSLKLSSVNAADTAVYCARVITRASPGTDGRY-GMDVWGQGTITTVSSGSASAPTL 152
Qy 115 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKGYAAT 174
Db 153 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKGYAAT 212
Qy 175 SQVLLPSKDVMOQGTDE 190
Db 213 SQVLLPSKDVMOQGTDE 228

RESULT 4
ID Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC017356; AAH17356.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01861; 1ADQ.
DR DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
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DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBFE CRC64;

Query Match          90.2%; Score 900.5; DB 2; Length 625;
Best Local Similarity 89.8%; Pred. No. 2.5e-72;
Matches 176; Conservative 2; Mismatches 11; Indels 7; Gaps 2;

Qy 1 SETLSLTCVYGGSFSGYVSWIRQPPGKGLWIEGHNHSGSTNYNPSLKSRTVISVDT 60
Db 41 SETLSLTCVYGGSFSGYVSWIRQPPGKGLWIEGHNHSGSTNYNPSLKSRTVISVDT 100
Qy 61 KNQPSLKLSSVTAADTAVYCAR-----GGTTVTFDAFDWGGTWTVSSGSASAPTL 114
Db 101 KKQLSLKLSSVNAADTAVYCARVITRASPGTDGRY-GMDVWGQGTITTVSSGSASAPTL 159
Qy 115 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKGYAAT 174
Db 160 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKGYAAT 219
Qy 175 SQVLLPSKDVMOQGTDE 190
Db 220 SQVLLPSKDVMOQGTDE 235

RESULT 5
ID Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC006180; AAH06180.1; -.
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DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAPAD50A6375851 CRC64;

Query Match      89.6%; Score 894.5; DB 2; Length 597;
Best Local Similarity 89.3%; Pred. No. 8.1e-72;
Matches 175; Conservative 2; Mismatches 12; Indels 7; Gaps 2;

Qy 1 SETLSLTCVYGGSGFYGSWIRQPGKGLWIGINHSSTNYNPSLKSRTVISVDT 60
Db 34 SETLSLTCVYGGSGFYGSWIRQPGKGLWIGINHSSTNYNPSLKSRTVISVDT 93
Qy 61 KNQFSLKLSVTAADTAIVYCAR-----GGTTVTFDAFDWGGTMTVTVSSGSASAPTL 114
Db 94 KKQLSLKLSVNAADTAIVYCARVITRASPTGDRY-GMDVWGQGTTVTVSSGSASAPTL 152
Qy 115 PPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGKYAAT 174
Db 153 PPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGKYAAT 212
Qy 175 SQVLLPSKDVMOQGTDE 190
Db 213 SQVLLPSKDVMOQGTDE 228

RESULT 6
Q96EY0
ID Q96EY0 PRELIMINARY; PRT; 620 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.;
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01820; IG7J.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match      85.3%; Score 851; DB 2; Length 620;
Best Local Similarity 87.9%; Pred. No. 6.9e-68;
Matches 167; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

Qy 1 SETLSLTCVYGGSGFYGSWIRQPGKGLWIGINHSSTNYNPSLKSRTVISVDT 60
Db 41 SETLSLTCVYGGSGFYGSWIRQPGKGLWIGIRYTSSTNYNPSLKSRTVISVDT 100
Qy 61 KNQFSLKLSVTAADTAIVYCARGGTTVTFDAFDWGGTMTVTVSSGSASAPTLFPLVSC 120
Db 101 KNQFSLKLSVTAADTAIVYCARQWELPTVGLFYWGQGLTVTVSSGSASAPTLFPLVSC 160
Qy 121 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGKYAATSOVLLP 180
Db 161 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGKYAATSOVLLP 220
Qy 181 SKDVMOQGTDE 190
Db 221 SKDVMOQGTDE 230

RESULT 7
Q6GMV2
ID Q6GMV2 PRELIMINARY; PRT; 606 AA.
AC Q6GMV2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
```



RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
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RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC015760; AAH15760.1; -;  
DR PIR; S05271; S05271.  
DR PIR; S24260; S24260.  
DR HSP; P01861; IADQ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E263D9 CRC64;

Query Match 70.08; Score 698.5; DB 2; Length 597;  
Best Local Similarity 73.18; Pred. No. 3.4e-54;  
Matches 141; Conservative 16; Mismatches 31; Indels 5; Gaps 3;  
QY 3 TSLTCAVYGGSGFYWSWIRQPPGKLEWIGIINHS-GSTWYNPSLKSRTVISVDTSK 61  
DB 36 SLRLSCAAGFSFSSYAMWVRQAPGKLEWVSAGSGGTYADSVKGRFTISRDNSR 95  
QY 62 NQFSLKLSVTAADTAVYYCA---RG-GTTVTDFPIWGQGTMTVTVSSGSASAPTLFPL 117  
DB 96 DTLYLQWNSLRADTAVYYCAKDPGRYSASGNTYREDYWGQGLTVTVSSGSASAPTLFPL 155  
QY 118 VSCNSPDSSTSSVAVGCLAQDFLPSITPSWKYKNNSDISSTRGFPSPVLRGGKYAATSQV 177  
DB 156 VSCNSPDSSTSSVAVGCLAQDFLPSITPSWKYKNNSDISSTRGFPSPVLRGGKYAATSQV 215  
QY 178 LLPSKDVMOQTDE 190  
DB 216 LLPSKDVMOQTDE 228

RESULT 10  
Q6GMX6 PRELIMINARY; PRT; 465 AA.  
ID Q6GMX6  
AC Q6GMX6  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
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RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073766; AAH73766.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
KW Hypothetical protein.  
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;  
Query Match 57.33; Score 572; DB 2; Length 465;  
Best Local Similarity 62.7%; Pred. No. 6e-43;  
Matches 116; Conservative 18; Mismatches 43; Indels 8; Gaps 4;  
QY 1 SETLSITCAVYGGSGFYWSWIRQPPGKLEWIGIINHS-GSTWYNPSLKSRTVISVDTS 60  
DB 34 SETLSITCTVSGSGISGYWSWIRQAPGKLEWIGRIYTSSTWYNPSLKSRTVMSVDTS 93  
QY 61 KNQFSLKLSVTAADTAVYYCARGTTVDFADPIWGQGTMTVTVSSGSASAPTLFPLVSC 120  
DB 94 KNQFSLKLSVTAADTAVYYCARG---RPTYFDYWGQGLTVTVSSASTKGPVFFLAPS 149  
QY 121 ENSPSPDSTSSVAVGCLAQDFLPSITPSWKYKNNSDISSTRGFPSPVLR-GGKYAATSQVLL 179  
DB 150 SKSTSG-GTAALGCLVVDYFPEPTVSW--NSGALTSGVHTFFAVLQSSGLYSLSVVTV 206  
QY 180 PSKDV 184  
DB 207 PSSSL 211

RESULT 11  
Q6GMX1 PRELIMINARY; PRT; 476 AA.  
ID Q6GMX1  
AC Q6GMX1  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.





AC Q6GMX7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullanby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
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 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RP "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073765; AAH73765.1; -.  
 DR InterPro; IPR003599; Ig-like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; C1-set; 2.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00409; Ig; 4.  
 DR SMART; SM00407; IGc1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;  
 Query Match 52.9%; Score 527.5; DB 2; Length 477;  
 Best Local Similarity 58.5%; Pred. No. 6.2e-39;  
 Matches 113; Conservative 22; Mismatches 43; Indels 15; Gaps 7;  
 Qy 1 SETLSLTCVAVYGGSGFYVSWIRQPPGKLEWIGI-NHSGSTYVNSPSLSKRVTSVDTSS 60  
 Db 34 SETLSLTCVAVYGGSGFYVSWIRQPPGKLEWIGI-NHSGSTYVNSPSLSKRVTSVDTSS 93  
 Qy 61 KNQSLKLSVTAADTAVVYCARGGTTVTPD-AFDINGQGTMTVTVSSGSASAPTLPLVLS 119  
 Db 94 KNQSLKLSVTAADTAVVYCARGGTTVTPD-AFDINGQGTMTVTVSSGSASAPTLPLVLS 149  
 Qy 120 KNSPSTSSVAVGCLAQDFLPD---SITFSWKYKNSDISSTGRFP--SVLRGGKYAAT 174  
 Db 150 LDSTPQD-GNVVAVCLVQGFPPQPLSVTWSESGN----VTARNFPSPQDASGLDLYTS 204  
 Qy 175 SQVLLPSKDVNQ 187  
 Db 205 SQTLPATQCPDG 217

RESULT 14  
 O8VCX7 PRELIMINARY; PRT; 613 AA.  
 ID Q8VCX7  
 AC Q8VCX7;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Igh-6 protein.  
 GN Name=Igh-6;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
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 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
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 RA Jones S.J., Marra M.A.;  
 RP "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RX Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018315; AAH18315.1; -.  
 DR PIR; C30562; C30562.  
 DR HSP; P01751; Ia6W.  
 DR MGD; MGI:96448; Igh-6.  
 DR GO; GO:0019815; C:B-cell receptor complex; IDA.  
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.  
 DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.  
 DR GO; GO:0003823; P:antigen binding; IDA.  
 DR GO; GO:0030333; P:antigen processing; IDA.  
 DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.  
 DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.  
 DR GO; GO:0050871; P:positive regulation of B-cell activation; IDA.  
 DR GO; GO:0030890; P:positive regulation of B-cell proliferation; IDA.  
 DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.  
 DR Pfam; PF07654; C1-set; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 51.4%; Score 512.5; DB 2; Length 613;  
 Best Local Similarity 52.6%; Pred. No. 1.9e-37;  
 Matches 100; Conservative 34; Mismatches 51; Indels 5; Gaps 3;  
 Qy 3 TSLTCAVYGGSGFYVSWIRQPPGKLEWIGI-NHSGSTYVNSPSLSKRVTSVDTSS 61  
 Db 36 SVKISCATGYTFSSYVWIKVQPPGKLEWIGI-NHSGSTYVNSPSLSKRVTSVDTSS 95  
 Qy 62 NQFSLKLSVTAADTAVVYCARGGTTVTPD-AFDINGQGTMTVTVSSGSASAPTLPLVLS 121

Search completed: March 8, 2005, 06:35:52  
Job time : 70.9554 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 88.0892 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-33

Perfect score: 998

Sequence: 1 SETLSLTCVVGSGFSGYY.....YAATSQVLLPSKDVNQGTDE 190

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: geneseqp1980s.\*

2: geneseqp1990s.\*

3: geneseqp2000s.\*

4: geneseqp2001s.\*

5: geneseqp2002s.\*

6: geneseqp2003as.\*

7: geneseqp2003bs.\*

8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	998	100.0	190	2	AY34304 Igm antib
2	919	92.1	205	2	AY34299 Igm antib
3	898	90.0	202	2	AY34303 Igm antib
4	880.5	88.2	197	2	AY34300 Igm antib
5	720	72.1	596	4	AAM23924 Human EST
6	717	71.8	223	2	AY08598 Anti-huma
7	712.5	71.4	228	8	ADL70776 Anti-TNPa
8	711	71.2	223	8	ADL70773 Anti-TNPa
9	693.5	69.5	266	8	ADF69305 Human lun
10	689	69.0	588	2	AAW71880 Anti-huma
11	689	69.0	588	3	AB112917 Anti-huma
12	686	68.7	595	3	ADM05427 Human pro
13	678.5	68.0	627	7	ADP97370 Human imm
14	675	67.6	588	2	AAW71881 Anti-huma
15	675	67.6	588	3	AB112918 Anti-huma
16	673.5	67.5	199	2	AY34302 Igm antib
17	673.5	67.5	203	2	AY34301 Igm antib
18	666	66.7	533	7	ADB65070 Human pro
19	662.5	66.4	570	8	ADR19329 Chimeric
20	656	65.7	571	8	ADP84970 Chimeric
21	655	65.6	569	8	ADR19330 Chimeric
22	634.5	63.6	450	6	ABP96294 4A5-3.1.1
23	624	62.5	229	7	ADJ32128 Human int
24	623	62.4	223	7	ADJ32112 Human int
25	620.5	62.2	462	3	AA266884 Human imm

26	617.5	61.9	453	6	ABP96295
27	616.5	61.8	230	7	ADJ32118 Human int
28	599.5	60.1	472	2	AAR93166
29	590	59.1	537	3	RAY96290 Human IGF
30	584.5	58.6	466	7	ADE28479 Human ant
31	581.5	58.3	466	7	ADE28471 Human ant
32	579.5	58.1	580	6	AAO30915
33	575	57.6	580	6	AAO30913
34	570.5	57.2	466	7	ADE28419 Human ant
35	564.5	56.6	464	7	ADE28411 Human ant
36	560.5	56.2	446	8	ADK52356 Human ant
37	556	55.7	221	7	ADJ32126 Human int
38	553	55.4	473	4	AB36206 Human imm
39	551	55.2	241	8	ADS84467 Human ant
40	551	55.2	241	8	ADR68609 Human ant
41	547	54.8	241	8	ADS84432 Human ant
42	547	54.8	241	8	ADR68574 Human ant
43	540	54.1	239	8	ADS84461 Human ant
44	540	54.1	239	8	ADR68603 Human ant
45	539	54.0	241	8	ADS84449 Human ant

## ALIGNMENTS

RESULT 1  
AAY34304  
ID AAY34304 standard; protein; 190 AA.  
XX  
AC AAY34304;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE Igm antibody CEM 13.5 heavy chain sequence.  
XX  
KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
OS Homo sapiens.  
XX  
PN WO9945031-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 03-MAR-1999; 99WO-US004583.  
XX  
PR 03-MAR-1998; 98US-00034607.  
XX  
PR 03-FEB-1999; 99US-00244253.  
XX  
(ABGE-) ABGENIX INC.  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX  
WPI; 1999-540816/45.  
XX  
N-PSDB; AAZ20405.  
PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX  
Claim 60; Fig 29; 245pp; English.  
CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the Igm Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
 XX  
 SQ Sequence 190 AA;  
 Query Match 100.0%; Score 998; DB 2; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-63;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SETLSLTCAYVGSFSGYYSWIRQPPGKLEWIGEHSGSTNPNPSLKSRTIISVDTS 60  
 |||||  
 DB 1 SETLSLTCAYVGSFSGYYSWIRQPPGKLEWIGEHSGSTNPNPSLKSRTIISVDTS 60  
 |||||  
 QY 61 KNQPSLKLSSVTAADTAVVYCARGGTTVTFDAFIMGQGTMTVTSSGSASAPTLFPLVSC 120  
 |||||  
 DB 61 KNQPSLKLSSVTAADTAVVYCARGGTTVTFDAFIMGQGTMTVTSSGSASAPTLFPLVSC 120  
 |||||  
 QY 121 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVSLRGKGYAATSQVLLP 180  
 |||||  
 DB 121 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVSLRGKGYAATSQVLLP 180  
 |||||  
 QY 181 SKDVMQGTDE 190  
 |||||  
 DB 181 SKDVMQGTDE 190  
 |||||  
 RESULT 2  
 AAY34299  
 ID AAY34299 standard; protein; 205 AA.  
 XX  
 AC AAY34299;  
 XX  
 DT 19-NOV-1999 (first entry)  
 XX  
 DE Igm antibody CEM 10.1 C3 heavy chain sequence.  
 XX  
 KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 150 /label= unknown  
 FT /note= "encoded by TYC"  
 FT  
 XX  
 PN WO9945031-A2.  
 XX  
 PD 10-SEP-1999.  
 XX  
 PF 03-MAR-1999; 99WO-US004583.  
 XX  
 PR 03-MAR-1998; 98US-00034607.  
 PR 03-FEB-1999; 99US-00244253.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;  
 XX  
 DR WPI; 1999-540816/45.  
 DR N-PSDB; AAZ20400.  
 XX  
 XX New monoclonal antibody, used for treating e.g. graft versus host  
 PT disease, cancers, autoimmune diseases and inflammatory diseases.  
 PT  
 PS Claim 60; Fig 24; 245pp; English.  
 XX  
 CC This sequence represents the heavy chain of an antibody of the invention.  
 CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
 CC complement and a variable region that binds to the epitope on CD147 bound

CC by the Igm MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
 CC can selectively kill activated T-cells, activated B-cells or resting or  
 CC activated monocytes. The products and methods can be used for treating  
 CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
 CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
 CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
 CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
 XX  
 SQ Sequence 205 AA;  
 Query Match 92.1%; Score 919; DB 2; Length 205;  
 Best Local Similarity 93.2%; Pred. No. 1.2e-57;  
 Matches 179; Conservative 3; Mismatches 8; Indels 2; Gaps 1;  
 QY 1 SETLSLTCAYVGSFSGYYSWIRQPPGKLEWIGEHSGSTNPNPSLKSRTIISVDTS 60  
 |||||  
 DB 6 SETLSLTCAYVGSFSGYYSWIRQPPGKLEWIGEHSGSTNPNPSLKSRTIISVDTS 65  
 |||||  
 QY 61 KNQPSLKLSSVTAADTAVVYCARGGTTVTFDAF--DIWGGTMTVTSSGSASAPTLFPLV 118  
 |||||  
 DB 66 KNQPSLKLSSVTAADTAVVYCARGTTEYYYYYGMVGGGTTVTSSGSASAPTLFPLV 125  
 |||||  
 QY 119 SCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVSLRGKGYAATSQVL 178  
 |||||  
 DB 126 SCENSPDSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVSLRGKGYAATSQVL 185  
 |||||  
 QY 179 LPSKDVMOGTDE 190  
 |||||  
 DB 186 LPSKDVMOGTDE 197  
 |||||  
 RESULT 3  
 AAY34303  
 ID AAY34303 standard; protein; 202 AA.  
 XX  
 AC AAY34303;  
 XX  
 DT 19-NOV-1999 (first entry)  
 XX  
 DE Igm antibody CEM 13.12 heavy chain sequence.  
 XX  
 KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 147 /label= unknown  
 FT /note= "encoded by TYC"  
 FT Misc-difference 151 /label= unknown  
 FT /note= "encoded by TYC"  
 FT  
 XX  
 PN WO9945031-A2.  
 XX  
 PD 10-SEP-1999.  
 XX  
 PF 03-MAR-1999; 99WO-US004583.  
 XX  
 PR 03-MAR-1998; 98US-00034607.  
 PR 03-FEB-1999; 99US-00244253.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 XX  
 XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;  
 XX  
 DR WPI; 1999-540816/45.  
 DR N-PSDB; AAZ20404.

XX New monoclonal antibody, used for treating e.g. graft versus host  
 PT disease, cancers, autoimmune diseases and inflammatory diseases.  
 XX  
 XX  
 PS Claim 60; Fig 28; 245pp; English.

XX This sequence represents the heavy chain of an antibody of the invention.  
 CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
 CC complement and a variable region that binds to the epitope on CD147 bound  
 CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
 CC can selectively kill activated T-cells, activated B-cells or resting or  
 CC activated monocytes. The products and methods can be used for treating  
 CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
 CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
 CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
 CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)

XX Sequence 202 AA;

Query Match 90.0%; Score 898; DB 2; Length 202;

Best Local Similarity 92.1%; Pred. No. 3.6e-56;

Matches 176; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

Qy 2 ETLISLTCAVYGSFSGYVMSWIRPPGKLEWIGETINHSSTNPNPSLKSRVTISVDTSK 61  
 Db 4 ETLISLTCAVYGSFSGYVMSWIRPPGKLEWIGETINHSSTNPNPSLKSRVTISVDTSK 63  
 Qy 62 NQPSLKLSSVTAADTAVYVCARGGTTVTDFAF--DIMGGQTMVTVSSGSASAPTLFPLVS 119  
 Db 64 NQPSLKLSSVTAADTAVYVCARGAAEYVYVYGGMDVMGQGTITVSSGSASAPTLFPLVS 123  
 Qy 120 CENSPTSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFPSVLRGGKYAATSQVLL 179  
 Db 124 CENSPTSSTSSVAVGCLAQDFLPDXITTFKWKYKNNSDISSTRGPFPSVLRGGKYAATSQVLL 183  
 Qy 180 PSKDVMOQTDE 190  
 Db 184 PSKDVMOQTDE 194

RESULT 4

AAY34300  
 ID AAY34300 standard; protein; 197 AA.

AC AAY34300;

XX 19-NOV-1999 (first entry)

XX IGM antibody CEM 10.1 G10 heavy chain sequence.

XX Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
 KW organ transplant rejection disease; lymphoma; pancreatic disease;  
 KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Homo sapiens.

OS WO9945031-A2.

PN 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

DR N-PSDB; AAZ20401.

XX New monoclonal antibody, used for treating e.g. graft versus host  
 PT disease, cancers, autoimmune diseases and inflammatory diseases.  
 XX

PS Claim 60; Fig 25; 245pp; English.

XX This sequence represents the heavy chain of an antibody of the invention.  
 CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
 CC complement and a variable region that binds to the epitope on CD147 bound  
 CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
 CC can selectively kill activated T-cells, activated B-cells or resting or  
 CC activated monocytes. The products and methods can be used for treating  
 CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
 CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
 CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
 CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)

XX Sequence 197 AA;

Query Match 88.2%; Score 880.5; DB 2; Length 197;

Best Local Similarity 90.6%; Pred. No. 6.1e-55;

Matches 173; Conservative 3; Mismatches 12; Indels 3; Gaps 2;

Qy 1 SETLSLTCAVYGSFSGYVMSWIRPPGKLEWIGETINHSSTNPNPSLKSRVTISVDTS 60  
 Db 5 SETLSLTCTVYSGSISYYVNWIRPPGKLEWIGETINHSSTNPNPSLKSRVTISVDTS 64  
 Qy 61 KNQPSLKLSSVTAADTAVYVCARG-GTTVTDFADIMGGQTMVTVSSGSASAPTLFPLVS 119  
 Db 65 KNQPSLKLSSVTAADTAVYVCARDRGVAT--GFDYMGQGTITVSSGSASAPTLFPLVS 122  
 Qy 120 CENSPTSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFPSVLRGGKYAATSQVLL 179  
 Db 123 CENSPTSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFPSVLRGGKYAATSQVLL 182  
 Qy 180 PSKDVMOQTDE 190  
 Db 183 PSKDVMOQTDE 193

RESULT 5

AAM23924

ID AAM23924 standard; protein; 596 AA.

AC AAM23924;

XX 12-OCT-2001 (first entry)

XX Human EST encoded protein SEQ ID NO: 1449.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
 KW gene therapy; nutrition.

XX Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US002687.

XX 25-JAN-2000; 2000US-00491404.

XX 17-JUL-2000; 2000US-00617746.

XX 03-AUG-2000; 2000US-00631451.

XX 15-SEP-2000; 2000US-00663870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;







Qy 62 NQFSLKLSVTAADTAVYTCARGTTVTDFADINWGQGTWTVTVSSGSASAPTLPLVSC 121  
Db 77 NTLYLQWNSLRAEDTAVYTCARSDGL---AFDIWGQGTWTVTVSSGSASAPTLPLVSC 133  
Qy 122 NSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQVLLPS 181  
Db 134 NSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQVLLPS 193  
Qy 182 KDVNMQGTDE 190  
Db 194 KDVNMQGTDE 202  
RESULT 9  
ADF69305  
ID ADF69305 standard; protein; 266 AA.  
XX ADF69305;  
XX 26-FEB-2004 (first entry)  
XX Human lung specific protein sequence SEQ ID NO:62.  
XX human; lung specific nucleic acid; lung specific protein; lung cancer;  
KW cytostatic; gene therapy.  
XX Homo sapiens.  
XX WO2003102137-A2.  
XX 11-DEC-2003.  
XX 30-MAY-2003; 2003WO-US016810.  
XX 31-MAY-2002; 2002US-0385301P.  
XX (DIAD-) DIADEXUS INC.  
XX Chen S, Macina RA, Sun Y, Liu C, Turner LR;  
XX WPI; 2004-053457/05.  
XX New human lung specific nucleic acid, useful for preparing a composition  
PT for diagnosing or treating lung cancer.  
XX Claim 11; SEQ ID NO 62; 221pp; English.  
XX The present invention describes a human lung specific nucleic acid  
CC molecule. Also described: (1) a method for determining the presence of a  
CC lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising  
CC the nucleic acid molecule; (3) a host cell comprising the vector; (4) a  
CC method for producing a polypeptide encoded by the nucleic acid molecule;  
CC (5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody  
CC or its fragment that specifically binds to the polypeptide; (7) a method  
CC for determining the presence of a lung specific protein in a sample; (8)  
CC a method for diagnosing and monitoring the presence and metastases of  
CC lung cancer in a patient; (9) a kit for detecting a risk of cancer or  
CC presence of cancer in a patient comprising a means for determining the  
CC presence the nucleic acid molecule or polypeptide in a sample of a  
CC patient; (10) a method of treating a patient with lung cancer; and (11) a  
CC vaccine comprising the polypeptide or the nucleic acid encoding the  
CC polypeptide. Human LSNA molecules and related proteins have cytostatic  
CC activity, and can be used in gene therapy. They are useful for preparing  
CC a composition for diagnosing or treating lung cancer. The present  
CC sequence represents a human lung specific protein, which is used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 266 AA;  
Query Match 69.5%; Score 693.5; DB 8; Length 266;  
Best Local Similarity 72.6%; Pred. No. 1.6e-41;  
Matches 138; Conservative 16; Mismatches 35; Indels 1; Gaps 1;  
XX

Qy 2 ETLSLTCANVYGSGFSGYVWSWIRQPPGKGLIEWIGBINHSGS-TNYPNLSKSRVTISVDT 60  
Db 27 ESLKISCKSGSYFTSYWIGVQRQMPGKLEWGLIYPGDSIDTRYSPFQQTIVISADKS 86  
Qy 61 KNQFSLKLSVTAADTAVYTCARGTTVTDFADINWGQGTWTVTVSSGSASAPTLPLVSC 120  
Db 87 ISTAYLQWNSLRAEDTAVYTCARPIAVAGHYFDYWGQGTWTVTVSSGSASAPTLPLVSC 146  
Qy 121 ENSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQVLLP 180  
Db 147 ENSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQVLLP 206  
Qy 181 SKDVNMQGTDE 190  
Db 207 SKDVNMQGTDE 216  
RESULT 10  
AAW71880  
ID AAW71880 standard; protein; 588 AA.  
XX AAW71880;  
XX AC AAW71880;  
XX 18-JAN-1999 (first entry)  
XX Anti-human Fas humanised antibody CH11 heavy chain HmuH.  
XX Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;  
KW autoimmune disease; rheumatoid arthritis; therapy; human;  
KW antibody engineering.  
XX Homo sapiens.  
XX Synthetic.  
XX Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= sig\_peptide  
FT Protein 20..588  
FT /label= Mat\_protein  
FT Region 50..54  
FT /label= CDR1  
FT /note= "complementarity determining region 1 from CH11  
FT heavy chain"  
FT Region 69..84  
FT /label= CDR2  
FT /note= "complementarity determining region 2 from CH11  
FT heavy chain"  
FT Region 118..124  
FT /label= CDR3  
FT /note= "complementarity determining region 3 from CH11  
FT heavy chain"  
XX EP866131-A2.  
XX 23-SEP-1998.  
XX 20-MAR-1998; 98EP-00302113.  
XX 21-MAR-1997; 97JP-00067938.  
XX (SANY ) SANKYO CO LTD.  
XX Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;  
XX WPI; 1998-482965/42.  
XX N-PSDB; AAV61363.  
XX Production of anti-Fas protein humanised antibodies - for use in inducing  
PT apoptosis on Fas expressing cells in the treatment of auto:immune  
XX diseases, especially rheumatoid arthritis.  
XX Claim 21; Page 105-107; 187pp; English.  
XX





FT Region 118..124  
 FT /label= CDR3  
 FT /note= "complementarity determining region 3 from CH11  
 heavy chain"  
 XX  
 PN EP866131-A2.  
 XX  
 PD 23-SEP-1998.  
 XX  
 PF 20-MAR-1998; 98EP-00302113.  
 XX  
 PR 21-MAR-1997; 97JP-00067938.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;  
 XX  
 DR WPI; 1998-482965/42.  
 DR N-PSDB; AAV61364.  
 XX  
 PT Production of anti-Fas protein humanised antibodies - for use in inducing  
 PT apoptosis on Fas expressing cells in the treatment of auto-immune  
 PT diseases, especially rheumatoid arthritis.  
 XX  
 PS Claim 22; Page 111-113; 187pp; English.  
 XX  
 CC This is the amino acid sequence of a humanised anti-Fas antibody CH11  
 CC heavy chain, designated HmuM. HmuM is based on the heavy chain (see  
 CC AA71888) of murine anti-human Fas monoclonal antibody CH11. The  
 CC humanised sequence was designed following selection of donor residues  
 CC from CH11 to be grafted onto acceptor molecule 21.28\*CL. 2 Heavy chain  
 CC sequences (see AA71880-81) have been designed, and each can be used in  
 CC combination with any of 4 light chain sequences (see AA71876-79) to  
 CC provide novel, claimed humanised CH11 IgM antibodies that lack a J chain.  
 CC These humanised anti-human Fas antibodies are capable of inducing  
 CC apoptosis in cells expressing Fas (e.g. synovocytes) and are useful in  
 CC the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA  
 CC sequences encoding the humanised antibodies are claimed, as are vectors  
 CC such as pHmuM1-1 including the HmuM nucleotide sequence (see AAV61364),  
 CC and host cells such as Escherichia coli pHmuM1-1 (FERM BP-5864)  
 XX  
 SQ Sequence 588 AA;  
 Query Match 67.6%; Score 675; DB 2; Length 588;  
 Best Local Similarity 69.3%; Pred. No. 7.6e-40;  
 Matches 131; Conservative 22; Mismatches 30; Indels 6; Gaps 2;  
 QY 3 TSLTCAVYGGSFSGYWSWIRPPGKLEWIGEI-NHSGSTNYNPSLKSRVTISVDTSK 61  
 Db 36 SVKVSCKASGYFTFDYNNHWKQAHGKSLWVGYYIPYNGGTGYNQKPKSKATITVDNSA 95  
 QY 62 NQFSLKLSSTVAADTAVVYCARGGTTVTDFADIWGQGTMTVTVSSGSASAPTLPLVSC 121  
 Db 96 STAYMELSLSESDTAVYCAR-----SYIAMDYWGQGTITVTVSSGSASAPTLPLVSC 150  
 QY 122 NSPSTSSVAVGCLAQDPLPDSITFSWKYKXNSDISSTRGPPSVLRGGKYAATSOVLPS 181  
 Db 151 NSPSTSSVAVGCLAQDPLPDSITFSWKYKXNSDISSTRGPPSVLRGGKYAATSOVLPS 210  
 QY 182 KDVMOGTDE 190  
 Db 211 KDVMOGTDE 219  
 RESULT 15  
 AAB12918  
 ID AAB12918 standard; protein; 588 AA.  
 AC AAB12918;  
 XX  
 AC AAB12918;  
 XX  
 DT 16-NOV-2000 (first entry)  
 XX  
 DE Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #88.

XX  
 KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
 KW immunosuppression; autoimmune disease; treatment; rheumatism;  
 KW anti-Fas antibody.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2000154149-A.  
 XX  
 PD 06-JUN-2000.  
 XX  
 PF 17-SEP-1999; 99JP-00263984.  
 XX  
 PR 18-SEP-1998; 98JP-00264598.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2000-454476/40.  
 DR N-PSDB; AAA78272.  
 XX  
 PT Anti-human Fas humanizing antibody-containing antirheumatic agents.  
 XX  
 PS Claim 1; Page 80-81; 109pp; Japanese.  
 XX  
 CC The present invention relates to antirheumatic agents which comprise as  
 CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
 CC does not include a J segment, has apoptosis inducing activity, and  
 CC consists of a light and heavy chain polypeptide produced synthetically.  
 CC The agents of the invention exhibit antirheumatic and immunosuppressive  
 CC activity and can be used to treat autoimmune diseases, especially  
 CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
 CC binding properties. Included in the invention are nucleotide sequences of  
 CC the IgM light and heavy chains (see AAA78267-A78272) and the  
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
 CC AA78202-A78206) and protein sequences (see AAB12908-B12910). Also  
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
 CC chains used in the invention are represented by sequences AAA78213-  
 CC A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AAA78277-A78318 and AAA78335-  
 CC A78337, while humanised anti-Fas Ig DNA sequencing primers are  
 CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer  
 CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in  
 CC the production of the agent of the invention  
 XX  
 SQ Sequence 588 AA;  
 Query Match 67.6%; Score 675; DB 3; Length 588;  
 Best Local Similarity 69.3%; Pred. No. 7.6e-40;  
 Matches 131; Conservative 22; Mismatches 30; Indels 6; Gaps 2;  
 QY 3 TSLTCAVYGGSFSGYWSWIRPPGKLEWIGEI-NHSGSTNYNPSLKSRVTISVDTSK 61  
 Db 36 SVKVSCKASGYFTFDYNNHWKQAHGKSLWVGYYIPYNGGTGYNQKPKSKATITVDNSA 95  
 QY 62 NQFSLKLSSTVAADTAVVYCARGGTTVTDFADIWGQGTMTVTVSSGSASAPTLPLVSC 121  
 Db 96 STAYMELSLSESDTAVYCAR-----SYIAMDYWGQGTITVTVSSGSASAPTLPLVSC 150  
 QY 122 NSPSTSSVAVGCLAQDPLPDSITFSWKYKXNSDISSTRGPPSVLRGGKYAATSOVLPS 181  
 Db 151 NSPSTSSVAVGCLAQDPLPDSITFSWKYKXNSDISSTRGPPSVLRGGKYAATSOVLPS 210  
 QY 182 KDVMOGTDE 190  
 Db 211 KDVMOGTDE 219  
 Search completed: March 8, 2005, 06:17:15  
 Job time : 89.0892 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 100.828 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-33

Perfect score: 998

Sequence: 1 SEILSLTCAVYGSFSGCYW.....YAATSVQLFSDVMQGTDE 190

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:\*
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  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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  - 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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  - 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686	68.7	595	15	US-10-108-260A-4112
2	678.5	68.0	627	13	US-10-047-542-47
3	666	66.7	533	15	US-10-104-047-3224
4	624	62.5	229	10	US-09-972-656-82
5	623	62.4	223	10	US-09-972-656-66
6	616.5	61.8	230	10	US-09-972-656-72
7	584.5	58.6	466	15	US-10-292-088-86
8	581.5	58.3	466	15	US-10-292-088-70
9	579.5	58.1	580	14	US-10-310-719-37
10	575	57.6	580	14	US-10-310-719-35
11	570.5	57.2	466	15	US-10-292-088-30
12	564.5	56.6	464	15	US-10-292-088-22
13	556	55.7	221	10	US-09-972-656-80
14					Sequence 4112, Ap
15					Sequence 47, Appl
16					Sequence 3224, Ap
17					Sequence 82, Appl
18					Sequence 66, Appl
19					Sequence 86, Appl
20					Sequence 72, Appl
21					Sequence 86, Appl
22					Sequence 70, Appl
23					Sequence 37, Appl
24					Sequence 35, Appl
25					Sequence 30, Appl
26					Sequence 22, Appl

14	555.5	55.7	179	15	US-10-309-762-171	Sequence 171, App
15	551	55.2	241	16	US-10-684-109-106	Sequence 106, App
16	547	54.8	241	16	US-10-684-109-71	Sequence 71, Appl
17	540	54.1	239	16	US-10-684-109-100	Sequence 100, App
18	539	54.0	241	16	US-10-684-109-88	Sequence 88, Appl
19	526	52.7	173	15	US-10-309-762-173	Sequence 173, App
20	521.5	52.3	193	15	US-10-264-049-4331	Sequence 4331, Ap
21	518	51.9	119	14	US-10-078-958-3	Sequence 3, Appli
22	515.5	51.7	172	14	US-10-153-382-21	Sequence 21, Appl
23	515	51.6	152	9	US-09-187-693-68	Sequence 68, Appl
24	512.5	51.4	125	15	US-10-371-942-110	Sequence 110, App
25	512	51.3	235	16	US-10-684-109-112	Sequence 112, App
26	511.5	51.3	254	10	US-09-880-748-1659	Sequence 1659, Ap
27	511.5	51.3	254	15	US-10-293-418-1659	Sequence 1659, Ap
28	511	51.2	122	15	US-10-360-828-63	Sequence 63, Appl
29	511	51.2	229	9	US-09-974-449-37	Sequence 37, Appl
30	509.5	51.1	120	14	US-10-078-958-4	Sequence 4, Appli
31	509	51.0	250	14	US-10-194-975-110	Sequence 110, App
32	504.5	50.6	487	9	US-09-800-729-145	Sequence 145, App
33	504.5	50.6	487	11	US-09-833-245-2194	Sequence 2194, Ap
34	504	50.5	249	10	US-09-880-748-1321	Sequence 1321, Ap
35	504	50.5	249	15	US-10-293-418-1321	Sequence 1321, Ap
36	504	50.5	253	10	US-09-880-748-1333	Sequence 1333, Ap
37	504	50.5	253	15	US-10-293-418-1333	Sequence 1333, Ap
38	499.5	50.1	476	9	US-09-758-173-12	Sequence 12, Appl
39	499.5	50.1	476	9	US-09-948-429B-12	Sequence 12, Appl
40	499.5	50.1	476	13	US-10-124-905-12	Sequence 12, Appl
41	499.5	50.1	476	14	US-10-124-807-12	Sequence 12, Appl
42	499.5	50.1	476	14	US-10-291-532-12	Sequence 12, Appl
43	497.5	49.8	250	10	US-09-880-748-1413	Sequence 1413, Ap
44	497.5	49.8	250	15	US-10-293-418-1413	Sequence 1413, Ap
45	496.5	49.7	476	9	US-09-758-173-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-10-108-260A-4112  
; Sequence 4112, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA  
; FILE REFERENCE: HI-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4112  
; LENGTH: 595  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-108-260A-4112

Query Match 68.7%; Score 686; DB 15; Length 595;

Best Local Similarity 71.6%; Pred. No. 5.9e-44;

Matches 136; Conservative 17; Mismatches 35; Indels 2; Gaps 2;

Qy	3	TLISITCAVYGSFSGCYWMTROPPGKGLWIGWIGHSSTN-YNPSLKSRVTISVDTSK 61
Db	37	SLRLSCAASGFTFSNFAMHWVROAPGKGLVSTVSISSNGROKYYGESVKGRTISRDSK 96
Qy	62	NQFSLKSLSVTAADTAVYVYCARGGTTVTFFD-AFDWQGTMTVTVSSGSASAPTLPPLVSC 120
Db	97	NTLFLQWGLREDDTAVYVYCARGHSDYHYGVQVWQGTITVTVSSGSASAPTLPPLVSC 156
Qy	121	ENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGKGYAATSQVLLP 180
Db	157	ENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGKGYAATSQVLLP 216
Qy	181	SKDVMQGTDE 190

Db 217 SKDVMQGTDE 226

RESULT 2  
US-10-047-542-47  
; Sequence 47, Application US/10047542  
; Publication No. US20020168367A1  
; GENERAL INFORMATION:  
; APPLICANT: LARICK, JAMES W.  
; APPLICANT: WYCOFF, KEITH L.  
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
; FILE REFERENCE: 030905.0004.C1P1  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: PCT/US01/13932  
; PRIOR FILING DATE: 2001-04-28  
; PRIOR APPLICATION NUMBER: 60/200,298  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 627  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-047-542-47

Query Match 68.0%; Score 678.5; DB 13; Length 627;  
Best Local Similarity 66.7%; Pred. No. 2.3e-43;  
Matches 134; Conservative 20; Mismatches 34; Indels 13; Gaps 2;

Qy 3 TSLTCAVYGGFSGYVSWIRPPGKGLWIG- INHSGSTNPNPGLKSRVTISVDTSK 61  
Db 36 SVKSCASGGTFSYAISWIRAPGGGLEWGGIIPGTANYAQFQGRVITADEST 95

Qy 62 NQFSLKLSVTAADTAVYVCARGGTTTFDA-----FDINGQGTMTVSSGSA 109  
Db 96 STAYMELSLRLSEDTAVYCAKTIIGLGYSSGWYPNSDYVYGGMDVWGQGTMTVSSGSA 155

Qy 110 SAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSSTRGFPSPVLRG 169  
Db 156 SAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSSTRGFPSPVLRG 215

Qy 170 KYAATSOVLLPSPKDVMOGTDE 190  
Db 216 KYAATSOVLLPSPKDVMOGTDE 236

RESULT 3  
US-10-104-047-3224  
; Sequence 3224, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA  
; FILE REFERENCE: HI-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3224  
; LENGTH: 533  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3224

Query Match 66.7%; Score 666; DB 15; Length 533;  
Best Local Similarity 70.5%; Pred. No. 1.7e-42;  
Matches 134; Conservative 13; Mismatches 41; Indels 2; Gaps 1;

Qy 3 TSLTCAVYGGFSGYVSWIRPPGKGLWIG- INHSGSTNPNPGLKSRVTISVDTSKN 62

Db 36 SLRLSCAASGFDVSSNYSWVRQSPGKGPSEWATMYGGCTTYAESVKGRFTVSRDGSQN 95

Qy 63 QPSLKLSVTAADTAVYVCARGGTTV--TFDAFDINGQGTMTVSSGSAASAPTLFPLVSC 120  
Db 96 TLYLEMSLSLRPDDTAVYVCVRDHRNYADTSPYGRKWGGTLVTVSSGSAASAPTLFPLVSC 155

Qy 121 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSSTRGFPSPVLGGKYAATSQVLLP 180  
Db 156 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSSTRGFPSPVLGGKYAATSQVLLP 215

Qy 181 SKDVMQGTDE 190  
Db 216 SKDVMQGTDE 225

RESULT 4  
US-09-972-656-82  
; Sequence 82, Application US/09972656  
; Publication No. US2003009647A1  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Tsai, Mei-Mei  
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
; TITLE OF INVENTION: Neutralizing Activity  
; FILE REFERENCE: A-799  
; CURRENT APPLICATION NUMBER: US/09/972,656  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 82  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-656-82

Query Match 62.5%; Score 624; DB 10; Length 229;  
Best Local Similarity 64.9%; Pred. No. 1.1e-39;  
Matches 124; Conservative 19; Mismatches 38; Indels 10; Gaps 4;

Qy 1 SETLSLTCAVYGGFSGYVSWIRPPGKGLWIG- INHSGSTNPNPGLKSRVTISVDTKS 60  
Db 15 SETLSLTCAVYGGFSGYVSWIRPPGKGLWIG- INHSGSTNPNPGLKSRVTISVDTKS 74

Qy 61 KNQFSLKLSVTAADTAVYVCARGGTTTFDA-----FDINGQGTMTVSSGSAASAPTL 114  
Db 75 KNQFSLKLSVTAADTAVYVCARGGTTTFDA-----FDINGQGTMTVSSGSAASAPTL 134

Qy 115 FPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSSTRGFPSPVL- GGYAA 173  
Db 135 FPLAPSSKSTSG-GTAALGCLVKDYRPPETVSM--NSGALTSGVHTFPAVLQSSGLYSL 191

Qy 174 TSQVLLPSPKDV 184  
Db 192 SSVVTVSPSSL 202

RESULT 5  
US-09-972-656-66  
; Sequence 66, Application US/09972656  
; Publication No. US2003009647A1  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Tsai, Mei-Mei  
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
; TITLE OF INVENTION: Neutralizing Activity  
; FILE REFERENCE: A-799  
; CURRENT APPLICATION NUMBER: US/09/972,656  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 66  
; LENGTH: 223



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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-656-66

Query Match      62.4%; Score 623; DB 10; Length 223;
Best Local Similarity 66.5%; Pred. No. 1.3e-39;
Matches 123; Conservative 17; Mismatches 41; Indels 4; Gaps 3;

Qy 1 SETLSLTCVAVGGSGFYGYSWIRQPPGKGLEWIGEINHSNSTYNNPSLKSRTVISDVS 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
15 SETLSLTCVAVGGSGFYGYSWIRQPPGKGLEWIGEINHSNSTYNNPSLKSRTVISDVS 74
Qy 61 KNQFSLKLSVTAADTAVVYCARGGTTVPDAPDWGGTMTVTVSSGSASAPTLFPLVSC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
75 KNQFSLKLSVTAADTAVVYCARGRNRWRFDYGGQTLTVSSASTKGPSVFPPLAPS 134
Qy 121 ENSPDSSTSSVAVGCLAQDFLPSITFSWKYKNSDISSTRGFPFSLVR-GGKYAATSOVLL 179
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
135 SKSTSG-GTAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVTV 191
Qy 180 PSKDV 184
Db ||||| :
192 PSSSL 196

RESULT 6
US-09-792-656-72
; Sequence 72, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-656-72

Query Match      61.8%; Score 616.5; DB 10; Length 230;
Best Local Similarity 64.6%; Pred. No. 4.2e-39;
Matches 124; Conservative 19; Mismatches 38; Indels 11; Gaps 5;

Qy 1 SETLSLTCVAVGGSGFYGYSWIRQPPGKGLEWIGEINHSNSTYNNPSLKSRTVISDVS 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
15 SETLSLTCVAVGGSGFYGYSWIRQPPGKGLEWIGEINHSNSTYNNPSLKSRTVISDVS 74
Qy 61 KNQFSLKLSVTAADTAVVYCARG-GTTVTF-----DAPDWGGTMTVTVSSGSASAPT 113
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
75 KNQFSLKLSVTAADTAVVYCARDKGRITTFGVVGSAGFDYGGQTLTVSSASTKGPS 134
Qy 114 LFPLVSCNSPDSSTSSVAVGCLAQDFLPSITFSWKYKNSDISSTRGFPFSLVR-GGKYA 172
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
135 VFPLAPSSKSTSG-GTAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLYS 191
Qy 173 ATSOVLLPSKDV 184
Db ||||| :
192 LSSVTVPPSSSL 203

RESULT 7
US-10-292-088-86
; Sequence 86, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
```

```
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-86

Query Match      58.6%; Score 584.5; DB 15; Length 466;
Best Local Similarity 63.8%; Pred. No. 2.3e-36;
Matches 118; Conservative 20; Mismatches 42; Indels 5; Gaps 4;

Qy 1 SETLSLTCVAVGGSGFYGYSWIRQPPGKGLEWIGEINHSNSTYNNPSLKSRTVISDVS 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 SETLSLTCVSGSGIRGYYSWIRQPPGKGLEWIGIYVYSGSTYNNPSLKSRTVISDVS 93
Qy 61 KNQFSLKLSVTAADTAVVYCAR-GGTTVTFDAPDWGGTMTVTVSSGSASAPTLFPLVS 119
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
94 KNQFSLKLSVTAADTAVVYCARRGGLYGDYGFAPWGQGTTLTVSSASTKGPSVFPPLAP 153
Qy 120 CENSPDSTSSVAVGCLAQDFLPSITFSWKYKNSDISSTRGFPFSLVR-GGKYAATSOVL 178
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
154 CSRSTSG-GTAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVTV 210
Qy 179 LPKSD 183
Db ||||| :
211 VPSSN 215

RESULT 8
US-10-292-088-70
; Sequence 70, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-70

Query Match      58.3%; Score 581.5; DB 15; Length 466;
Best Local Similarity 63.2%; Pred. No. 3.9e-36;
Matches 117; Conservative 21; Mismatches 42; Indels 5; Gaps 4;

Qy 1 SETLSLTCVAVGGSGFYGYSWIRQPPGKGLEWIGEINHSNSTYNNPSLKSRTVISDVS 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 SETLSLTCVSGSGIRGYYSWIRQPPGKGLEWIGIYVYSGSTYNNPSLKSRTVISDVS 93
Qy 61 KNQFSLKLSVTAADTAVVYCAR-GGTTVTFDAPDWGGTMTVTVSSGSASAPTLFPLVS 119
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
94 KNQFSLKLSVTAADTAVVYCARRGGLYGDYGFAPWGQGTTLTVSSASTKGPSVFPPLAP 153
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```
RESULT 12
US-10-292-088-22
; Sequence 22, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-22

Query Match      56.6%; Score 564.5; DB 15; Length 464;
Best Local Similarity 61.4%; Pred. No. 7.5e-35;
Matches 113; Conservative 21; Mismatches 45; Indels 5; Gaps 4;

Qy 1 SETLSLTCAVYGGSPGSGYVSWIRQPPGKGLWEGINHSSTNNPSLKSRTVISVDT 60
Db 34 SETLSLTCTVSGGSISSYVWIRQPPGKGLWEGIRVTSSTNNPSLKSRTVISVDT 93

Qy 61 KNQFSLKSSVTAADTAVYVCARGTTVTDFADPWGQGTMTVTSVSSGSASAPTLFPLV 179
Db 94 KNQFSLKSSVTAADTAVYVCARDGLYRGY-GMDVWGQGTMTVTSVSSASTKGPSVFPAPC 152

Qy 121 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-GGKYAATSOVL 179
Db 153 SRSTSE-STAAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVV 209

Qy 180 PSKD 183
Db 210 PSSN 213

RESULT 13
US-09-972-656-80
; Sequence 80, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Wei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-80

Query Match      55.7%; Score 556; DB 10; Length 221;
Best Local Similarity 62.0%; Pred. No. 1.6e-34;
Matches 116; Conservative 18; Mismatches 43; Indels 10; Gaps 5;

Qy 1 SETLSLTCAVYGGSPGSGYVSWIRQPPGKGLWEGINHSSTNNPSLKSRTVISVDT 58
Db 15 SETLSLTCAVSGGSISSYVWIRQPPGKGLWEGIYHSGSTYNNPSLKSRTVISVDT 74
```

```
Qy 59 TSKNQFSLKSSVTAADTAVYVCARGTTVTDFADPWGQGTMTVTSVSSGSASAPTLFPLV 118
Db 75 RSKNQFSLKSSVTAADTAVYVCARG---DWGYFDYWGQGTTLVTSSASTKGPSVFPPLA 130

Qy 119 SCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-GGKYAATSOV 177
Db 131 PSSKSTSG-GTAAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSV 187

Qy 178 LLPSKDV 184
Db 188 TVPSSSL 194

RESULT 14
US-10-309-762-171
; Sequence 171, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-171

Query Match      55.7%; Score 555.5; DB 15; Length 179;
Best Local Similarity 63.7%; Pred. No. 1.4e-34;
Matches 109; Conservative 17; Mismatches 38; Indels 7; Gaps 3;

Qy 1 SETLSLTCAVYGGSPGSGYVSWIRQPPGKGLWEGINHSSTNNPSLKSRTVISVDT 60
Db 9 SETLSLTCTVSGGSISSYVWIRQPPGKGLWEGIYHSGSTYNNPSLKSRTVISVDT 68

Qy 61 KNQFSLKSSVTAADTAVYVCAR---GGTTVTDFADPWGQGTMTVTSVSSGSASAPTLFP 116
Db 69 KNQFSLKLTSTVTAADTAVYVCARDQHSVSVYVYVYVYVYVYVYVYVYVYVYVYVYV 128

Qy 117 LVSCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR 167
Db 129 LAPCSRSTSE-STAAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQ 176

RESULT 15
US-10-684-109-106
; Sequence 106, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-684-109-106

Query Match          55.2%; Score 551; DB 16; Length 241;
Best Local Similarity 60.8%; Pred. No. 4.1e-34;
Matches 113; Conservative 22; Mismatches 41; Indels 10; Gaps 5;

Qy 1 SETLSLTCAVYGGSFSGYMSWIRQPPGKGLEWIGEINHSGSTNYPNPKSRVTISV-D 58
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
36 SETLSLACTVSGGSIISRYMSWIRQPPGKGLEWIGYVSGSYNPNPKSRVTISVASP 95
Qy 59 TSKNQPSLKLSSVTAADTAVYVCARGGTTVTFDAFDIWGGTMYTVSSGSAAPLFLV 118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
96 TSKNQPSLKLSSVTAADTAVYVCARDKLGIG- ---DYWGQGLTVTVSSASTKGPSVFPLA 151
Qy 119 SCENSPSDTSSVAVGCLAQDPLPDSITFSWKYKNNSDISSTRGPPSVLR-GGKYAATSQV 177
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
152 PCSRSTSE-STALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSV 208
Qy 178 LLPSKD 183
Db :||| :
209 TVPSSN 214
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Search completed: March 8, 2005, 07:05:54  
Job time : 100.828 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 20.8917 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-33  
Perfect score: 998  
Sequence: 1 SETLSUTCAVYGGSFSGYYW.....YAATSQVLLPSKDVQMGTDE 190

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	599.5	60.1	472	3	US-08-793-450-8
2	553	55.4	473	3	US-09-049-672A-4
3	515.5	51.7	172	4	US-09-472-087-7
4	515.5	51.7	172	4	US-09-472-087-7
5	509	51.0	832	3	US-08-630-820-7
6	509	51.0	832	4	US-09-273-453-7
7	504.5	50.6	487	4	US-09-800-729-145
8	499.5	50.1	476	3	US-08-487-550-12
9	499.5	50.1	476	4	US-09-526-098-12
10	499.5	50.1	476	4	US-09-383-916-12
11	496.5	49.7	476	3	US-08-487-550-4
12	496.5	49.7	476	4	US-09-526-098-4
13	496.5	49.7	476	4	US-09-383-916-4
14	495	49.6	139	4	US-09-203-768A-2
15	492.5	49.3	467	3	US-08-523-894-8
16	492.5	49.3	467	3	US-08-523-894-10
17	492.5	49.3	467	3	US-08-523-894-12
18	490.5	49.1	219	3	US-09-460-384-37
19	480.5	48.1	123	3	US-08-793-450-4
20	474	47.5	429	4	US-09-372-425A-6
21	472	47.0	467	4	US-08-030-175-42
22	469	47.0	467	4	US-08-030-175-41
23	466	46.7	118	3	US-09-025-769B-25
24	466	46.7	118	4	US-09-490-070A-25
25	466	46.7	118	4	US-09-490-153-25
26	466	46.7	118	4	US-09-490-324-25
27	466	46.7	447	4	US-09-372-425A-2

28	460	46.1	120	4	US-09-424-840B-20	Sequence 20, Appl
29	456.5	45.7	229	2	US-08-887-352B-20	Sequence 20, Appl
30	456.5	45.7	229	3	US-09-109-207C-20	Sequence 20, Appl
31	456.5	45.7	229	3	US-09-296-005-20	Sequence 20, Appl
32	456.5	45.7	229	4	US-09-920-171-20	Sequence 20, Appl
33	456.5	45.7	229	4	US-09-716-028-20	Sequence 20, Appl
34	456.5	45.7	229	4	US-10-113-996-20	Sequence 20, Appl
35	456.5	45.7	233	2	US-08-887-352B-25	Sequence 25, Appl
36	456.5	45.7	233	3	US-09-109-207C-25	Sequence 25, Appl
37	456.5	45.7	233	3	US-09-296-005-25	Sequence 25, Appl
38	456.5	45.7	233	4	US-09-920-171-25	Sequence 25, Appl
39	456.5	45.7	233	4	US-09-716-028-25	Sequence 25, Appl
40	456.5	45.7	233	4	US-10-113-996-25	Sequence 25, Appl
41	456.5	45.7	451	2	US-08-887-352B-14	Sequence 14, Appl
42	456.5	45.7	451	2	US-08-887-352B-16	Sequence 16, Appl
43	456.5	45.7	451	3	US-08-466-151-65	Sequence 65, Appl
44	456.5	45.7	451	3	US-09-109-207C-14	Sequence 14, Appl
45	456.5	45.7	451	3	US-09-109-207C-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-793-450-8  
; Sequence 8, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHABBIH, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/793,450  
; APPLICATION NUMBER: 03-MAR-1997  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 472 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-793-450-8

Query Match 60.1%; Score 599.5; DB 3; Length 472;  
Best Local Similarity 63.2%; Pred No. 5.7e-46;  
Matches 122; Conservative 17; Mismatches 37; Indels 17; Gaps 5;

Qy		1	SETLSLTCAVYGGSPGYYWSWIRPPCKGLEWIGEINHGSGTWNPNPSLKSRVTISVDTS	60
			:	
			:	
			:	
Dd		34	SETLSLTCVYGGSPGYYWSWIRPPCKGLEWIGEINHGSGTWNPNPSLKSRVTISVDTS	93
			:	
			:	
			:	
Qy		61	KNOFSLKLSVTAADTAIVYICARG-----GTTVTFDAPDIHQGTWTMTVSSGSASAP	112
			:	
			:	
			:	
Dd		94	KNOFSLKLNSVTAADTAIVYCACAPEYKWKYHG-----DWDFDPWGQGTTVTVSSASTKGP	148
			:	
			:	
			:	
Qy		113	TLPPLVCSNPSDSTSSVAVGCLAQDFLPDSITTSWKYKNNSDISSTRGRPPSVLR-GGKY	171
			:   :	:
			:   :	:
			:   :	:
Dd		149	SVPFLAPSCKSTSG-GTAALGCLVKDYPPPTVSW--NSGALTSGVHTFPFVQLQSGLY	205
			:   :	:
			:   :	:
Qy		172	AATSQVLFLPKDV	184
			:   :	:
			:   :	:
Dd		206	SLSGVTVTPSSSL	218

RESULT 2  
 US-09-049-672A-4  
 Sequence 4, Application US/09049672A  
 Patent No. 6135941  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Lal, Preeti  
 APPLICANT: Tang, Y. Tom  
 APPLICANT: Yue, Henry  
 APPLICANT: Au-Young, Janice  
 APPLICANT: Corley, Neil C.  
 APPLICANT: Guegler, Karl J.  
 APPLICANT: Baughn, Mariah R.  
 TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
 NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/049,672A  
 FILING DATE: HEREWITH  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cerrone, Michael C  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0497 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 473 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: PANCUT01  
 CLONE: 1513264  
 US-09-049-672A-4

Query Match 55.4%; Score 553; DB 3; Length 473;  
Best Local Similarity 60.1%; Pred. No. 8.9e-42;

	Matches	116;	Conservative	20;	Mismatches	41;	Indels	16;	Gaps	67;
Qy	1	SETLSLTCAYVGGFS--GYYSWIRPPGKGLEWIGEINHSGSTNYNPSLKSRTISVD	58							
Db	34	SETLSLTCAYVGGISITSGGYYSWIRPPGKLEWIGIYYSGSTLYNPSLKSRTISVD	93							
Qy	59	TSKNQPSLKLSSVTAADTAVYCA-----RGGTTVTDFADTWGQGTMTVTVSSGSASAP	112							
Db	94	TSKNQPSLKLSSVTAADTAVYCARDVGLRGNY-----GMDVMGQGTLTVTVSSASTKGP	149							
Qy	113	TLRPLVSCNSPDSSTSVAVGCLAQDPLPDSITFSWKYKKNDSITSSRGGPPSVLR--GQKY	171							
Db	150	SVFPLAPSSKSTSG-GTAALGCLVKDYFPFPVTVSW--NSGALTSGVHTTFAVLQSSGLY	206							
Qy	172	AATSQVLLPSPKDV	184							
Db	207	SLSSVTVTPSSSL	219							

```

RESULT 3
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN B.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      51.7%; Score 515.5; DB 4; Length 172;
Best Local Similarity 61.5%; Pred. No. 5.9e-39;
Matches 104; Conservative 20; Mismatches 38; Indels 7;

Qy      1 SETLSLTCVAVYGGSFs--GYTWSWIRQPPGKLEWIGEHSGSTNYNPSLKS
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      9 SQLSLSLTCVSGGSISSGGHYSWIRQHPGKLEWIGYIYIGNTVYNPSLKS
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy      59 TSKNQPSLKLSSVTAADTAVYTCARGGTTVTDFADPWGGTMTVTVSSGSAS
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      69 TSKNQPSLKLSSVTAADTAVYTCAR--DSGDYVIGDVMVGQGTTVTVSSASTKG
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy      119 SCENSPDSTSVAVGCLAQDFLPDSITFSWKYKNSDLSSTFGFPFVLRL
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      127 PCSRSTSE-STAAALGCLVKDYPFBPBTVSW--NSGALTSGVHTFFPAVLQ
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN B.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY

```



Query Match	51.0%;	Score 509;	DB 4;	Length 832;
Best Local Similarity	55.5%;	Pred. No. 1.7e-37;		
Matches 106; Conservative	27;	Mismatches 44;	Indels 14;	Gaps 7;
QY	1	SETLSLTCAYVGGSF-SGYTWSLRPPGKGLEWIGHSGSTNYNPSLKSRVTISVD	T 59	
Db	16	SQTLSLTCTVSGFTISSGSWHWRPGRGLEWIGYIQSGITNYNPSLKSRVTMLVD	T 75	
QY	60	SKNQFSKLSSVTAADTAVYYCAGGTGTVTD----	AFDIWGGQM--VTVSSGSASAPTL	114
Db	76	SKNQFSLRLSSVTAADTAVYYCAR-----EDYDHYWFDMVGQGSLVTVTSSASTKGP	SV 131	
QY	115	FPLVSCNSPDSTSSVAVGLCAQDFLPDSITFFSKYKNNSDISSTRGPPSVLR-GGKYAA	173	
Db	132	FPLAPCRSRTSG-TAALGCLVKDYFPFEPVIVSW--NSGALTGVHTFPVLQSSGLYS	L 188	
QY	174	TSQVLLSPSKDV	184	
Db	189	SSVTVTFSSSL	199	

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RESULT 7
US-09-800-729-145
; Sequence 145, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-145

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Query Match	50.6%	Score 504.5	DB 4	Length 487
Best Local Similarity	55.5%	Pred. No. 2.2e-37		
Matches 111	Conservative 23	Mismatches 47	Indels 19	Gaps 7
Qy	1	SETLSLTCVAVGGSGFS--GYWWSWIROPPCKGLEWIGSEINHSGSTNYPNLSKSRVTISVD	58	
Db	34	SETLSLTCVTSVGGSISSGGHWWSWIRQHPGKLEWIGYISVGYTYPNLSKSRVTISVD	93	
Qy	59	TSKNQFSLKLSVTAADTAVTYCA-----RGTTVTTFDAFDINGQGHVTVTVSSGSASAP	112	
Db	94	TSQNQFSLRLSSVTAADTAVTYCAKDRATRDRDGYQLEYRGFDYWGQGLLVTVSSASPTSP	153	
Qy	113	TLRPLVCSNCSPTSSVAVGCLAQDFLPD---SITFSWKYKNNSDISSTGFP--SVLR	167	
Db	154	KVFPL-SLDSTPQD-GNVVAVCLVQGFPPQBPFLSVTWSSESQN-----VTARFPPSQDAS	207	
Qy	168	GGKYAATSQVLLPSKDNVQMG	187	
Db	208	GDLYTSSQLTLPATQCPDG	227	

RESULT 8  
US-08-487-550-12  
; Sequence 12, Application US/08487550  
; Patent No. 6113898  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

```

; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 0127112-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-550-12

Query Match 50.1%; Score 499.5; DB 3; Length 476;
Best Local Similarity 55.2%; Pred. No. 5.9e-37; Indels 11; Gaps 6
Matches 106; Conservative 24; Mismatches 51;

QY 1 SETLSLTCAYVGSGFS-GYYWSWIRQPPGKLEWIGEI-NHSGSTNYPNPSLKSRVTISVD 58
Db 34 SETLSLTCAYVGSGISGGYGMWIRQPPGKLEWIGSYSSGNTYYNPSLKSVTISTD 93
QY 59 TSKNQFSLKLSGVTAADTAVYVCARGGT-----TTFDAFDIWGGGTWTVSSGASAPT 113
Db 94 TSKNQFSLKLSMTAADTAVYVCVRDLFSVVGMYNNWFDVWPGVLTVTVSSASTKGPS 153
QY 114 LFLVLCSENPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSVLR-GGKYA 172
Db 154 VFPLAPSSKSTSG-GTAAALGCLVKDYPPEPVTVSW--NSGALTSGVHTFPFVAVLQSSGLYS 210
QY 173 ATSOVLPLSKDV 184
Db 211 LSSVTVFPSSL 222

RESULT 9
US-09-526-098-12
; Sequence 12, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF.
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:

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RESIN.T 9

US-09-52

: Sequen

; Patent

GENERAL

APP

TIT

; TIT

TIT ;

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; NUM

COR ;

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2

COM:



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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-526-098-12

Query Match          50.1%; Score 499.5; DB 4; Length 476;
Best Local Similarity 55.2%; Pred. No. 5.9e-37;
Matches 106; Conservative 24; Mismatches 51; Indels 11; Gaps 6;

Qy 1 SETLSLTCVYGGSFSGYVWSWIRPPGKGLEWIGEI-NHSGSTNNPNSLKSRVTISVD 58
Db 34 SETLSLTCVSGGSGISGGYWGIRPPGKGLEWIGSFYSSGNTYNNPSLKSVQVTISTD 93
Qy 59 TSKNQPSLKLSVTAADTAANYVCARGGT-----TVTFDAPDIWGQGTMTVYSSGSASAPT 113
Db 94 TSKNQPSLKLSMTAADTAANYVCVRDLRFVSVMVYNNWFDVWPGVLVTVYSSASTKGPS 153
Qy 114 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVSLR-GGKYA 172
Db 154 VFPLAPSKSTSG-GTAAIGCLVKDYFPEPTVSW--NSGALTSGVHTFFPAVLQSSGLYS 210
Qy 173 ATSOVLPLSKDV 184
Db 211 LSSVTVPSSSL 222

RESULT 10
US-09-383-916-12
; Sequence 12, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-383-916-12

Query Match          50.1%; Score 499.5; DB 4; Length 476;
Best Local Similarity 55.2%; Pred. No. 5.9e-37;
Matches 106; Conservative 24; Mismatches 51; Indels 11; Gaps 6;

Qy 1 SETLSLTCVYGGSFSGYVWSWIRPPGKGLEWIGEI-NHSGSTNNPNSLKSRVTISVD 58
Db 34 SETLSLTCVSGGSGISGGYWGIRPPGKGLEWIGSFYSSGNTYNNPSLKSVQVTISTD 93
Qy 59 TSKNQPSLKLSVTAADTAANYVCARGGT-----TVTFDAPDIWGQGTMTVYSSGSASAPT 113
Db 94 TSKNQPSLKLSMTAADTAANYVCVRDLRFVSVMVYNNWFDVWPGVLVTVYSSASTKGPS 153
Qy 114 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVSLR-GGKYA 172
Db 154 VFPLAPSKSTSG-GTAAIGCLVKDYFPEPTVSW--NSGALTSGVHTFFPAVLQSSGLYS 210
Qy 173 ATSOVLPLSKDV 184
Db 211 LSSVTVPSSSL 222

RESULT 11
US-08-487-550-4
; Sequence 4, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131

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TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-550-4

Query Match 49.7%; Score 496.5; DB 3; Length 476;  
Best Local Similarity 54.7%; Pred. No. 1.1e-36;  
Matches 105; Conservative 26; Mismatches 50; Indels 11; Gaps 7;  
QY 1 SETLSLTCVAVGSGFSG-YVWSWIRQPPGKLEWIGBHNHSG-STNNPSLKSRTVTSVD 58  
DB 34 SETLSRTCVVSGGSGISGYYTWTIRQTPGRGLEWIGHYNGGATTNNPSLKSRTVTSKD 93  
QY 59 TSKNQPSLKLSSVTAADTAVVYCARGG---TTVTDFAF-DIKQGTMTVTSSGSSASAPT 113  
DB 94 TSKNQPFNLNSVTDADTAVVYCARGPRDCTTICYGWVDVWGPGLVTVSSASTKGPS 153  
QY 114 LFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVSLR-GGKYA 172  
DB 154 VFPLAPSSKSTSG-GTAALGCLVKDYFPPEPTVYSW--NSGALTSGVHTFFPAVLQSSGLYS 210  
QY 173 ATSOVLPLSKDV 184  
DB 211 LSSVTVTPSSSL 222

RESULT 12  
US-09-526-098-4  
Sequence 4, Application US/09526098  
Patent No. 6492134  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/526,098  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
FILING DATE: 07-JUN-1995  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-550-4

LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-526-098-4  
Query Match 49.7%; Score 496.5; DB 4; Length 476;  
Best Local Similarity 54.7%; Pred. No. 1.1e-36;  
Matches 105; Conservative 26; Mismatches 50; Indels 11; Gaps 7;  
QY 1 SETLSLTCVAVGSGFSG-YVWSWIRQPPGKLEWIGBHNHSG-STNNPSLKSRTVTSVD 58  
DB 34 SETLSRTCVVSGGSGISGYYTWTIRQTPGRGLEWIGHYNGGATTNNPSLKSRTVTSKD 93  
QY 59 TSKNQPSLKLSSVTAADTAVVYCARGG---TTVTDFAF-DIKQGTMTVTSSGSSASAPT 113  
DB 94 TSKNQPFNLNSVTDADTAVVYCARGPRDCTTICYGWVDVWGPGLVTVSSASTKGPS 153  
QY 114 LFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVSLR-GGKYA 172  
DB 154 VFPLAPSSKSTSG-GTAALGCLVKDYFPPEPTVYSW--NSGALTSGVHTFFPAVLQSSGLYS 210  
QY 173 ATSOVLPLSKDV 184  
DB 211 LSSVTVTPSSSL 222  
RESULT 13  
US-09-383-916-4  
Sequence 4, Application US/09383916  
Patent No. 6709654  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/383,916  
FILING DATE: 26-AUG-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-383-916-4  
Query Match 49.7%; Score 496.5; DB 4; Length 476;



**This Page Blank (uspto)**

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.4472 Seconds  
(without alignments)  
1953.842 Million cells updates/sec

Title: US-09-784-950-34

Perfect score: 771  
Sequence: 1 LAVSLGERATINCKSSQSVL.....VCLLNFPYKQVQVKV 147

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	646	83.8	216	2 JEO241	Ig kappa chain Am3
2	611	79.2	240	2 S06084	Ig kappa chain pre
3	597.5	77.5	215	2 JEO242	Ig kappa chain NIG
4	582	75.5	214	2 S68212	Ig kappa chain (Ma
5	575.5	74.6	215	2 JEO244	Ig kappa chain NIG
6	575	74.6	220	2 A31790	Ig kappa chain V r
7	565.5	73.3	215	2 A23746	Ig kappa chain V-I
8	544.5	70.6	215	2 JEO243	Ig kappa chain NIG
9	527	68.4	120	2 S51147	antibody light cha
10	521	67.6	114	1 K4HULN	Ig kappa chain V-I
11	520	67.4	113	2 S4002	Ig kappa chain V r
12	515	66.8	134	2 S49531	anti-Sm antibody v
13	512	65.4	129	2 S40347	Ig kappa chain - h
14	508.5	66.0	219	2 PC4203	Ig kappa chain (mo
15	504	65.4	134	1 K4HU17	Ig kappa chain pre
16	502	65.1	113	2 S30520	Ig kappa chain V r
17	502	65.1	113	2 S34003	Ig kappa chain V r
18	501.5	65.0	225	2 S37484	Ig kappa chain - m
19	499.5	64.8	219	2 S25028	Ig kappa chain - m
20	498.5	64.7	133	1 K4HUJ1	Ig kappa chain pre
21	496.5	64.4	138	2 A53261	Ig kappa chain pre
22	496.5	64.4	217	2 S42772	Ig kappa chain - m
23	496	64.3	113	2 S30523	Ig kappa chain V-J
24	496	64.3	114	2 S44119	Ig kappa chain V-J
25	494	64.1	210	2 A56169	Ig kappa chain V r
26	494	64.1	218	2 JC5810	monoclonal antibod
27	493.5	64.0	219	2 S38865	Ig kappa chain - m
28	493	63.9	114	2 S44116	Ig kappa chain V-J
29	491	63.7	218	2 S68241	Ig kappa chain V r

RESULT 1

JEO241

Ig kappa chain Am37 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JEO241

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, I.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A:Description: Structure relationship of kappatype light chains with AL amyloidosis: Mult

A:Reference number: JEO241

A:Accession: JEO241

A:Molecule type: protein

A:Residues: 1-216 <Ali>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 646; DB 2; Length 216;

Best Local Similarity 88.4%; Pred. No. 3.6e-45;

Matches 129; Conservative 7; Mismatches 6; Indels 4; Gaps 3;

Qy	1	LAVSLGERATINCKSSQSVLYSFNNKNVLANVYQKQGPQPKLLIYWASTRESGVDRFRSG	60
Db	11	LAVSLGERATINCKSSQSVLY--NSKNFLAVYQKQPGQ-PKLLI-WANVRESGVDRFRSG	66
Qy	61	SGSGTDFLTITSSLQAEADVAVYQOYVSTPRTFGQTKVEIKRTVAAPSVFIFPPSDEQ	120
Db	67	SGVGTDFLTITSNLQAEADVAVYQOYVSTPRTFGQTKVEIKRTVAAPSVFIFPPSDEQ	126
Qy	121	LKSGTASVCLLNFPYKQVQVKV	146
Db	127	LKSGTASVCLLNFPYKQVQVKV	152

RESULT 2

S06084

Ig kappa chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000

C:Accession: S06084

R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.

A:Reference number: S06084; MUID:90016888; PMID:2508067

A:Accession: S06084

A:Molecule type: mRNA

A:Residues: 1-240 <CRO>

A:Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-240/Product: Ig kappa chain #status predicted <MAT>

F:153-222/Domain: immunoglobulin homology <IMM>

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Query Match 79.2%; Score 611; DB 2; Length 240;
Best Local Similarity 77.4%; Pred. No. 2.7e-42;
Matches 113; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAQQKPGQPKLLIYWASTRESGVDPDRFG 60
Db 31 LAVSAGETVTITINCKSSQSLFSGNQKNYLAQQKPGQSPKLLIYWASTRQSGVDPDRFG 90
Qy 61 SGSGTDFLTITSSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIIPPSEDEQ 120
Db 91 SGSGTDFLTITSSVQAEADLAIYCLQYETPTFGAGTKLEIKRADAAPTIVSIFPPSTEQ 150
Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 151 LATGASVVCVCLMNNFYPRDISVWKI 176

RESULT 3
Ig kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A;Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 597.5; DB 2; Length 215;
Best Local Similarity 79.5%; Pred. No. 2.9e-41;
Matches 116; Conservative 11; Mismatches 14; Indels 5; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAQQKPGQPKLLIYWASTRESGVDPDRFG 60
Db 11 LLSLFGERTATLSCRSQSV-----SNLYLAQQKPGQAPSLIYDASSRATGIPDRFG 65
Qy 61 SGSGTDFLTITSSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIIPPSEDEQ 120
Db 66 SGSGTDFLTITISGLEPDEFAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIIPPSEDEQ 125
Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 126 LKSGTASVVCVCLMNNFYPREAKVQWKV 151

RESULT 4
Ig kappa chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C;Accession: S68212
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:749816
A;Accession: S68212
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-214 <TAK>
A;Cross-references: EMBL:D29668
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 75.5%; Score 582; DB 2; Length 214;
Best Local Similarity 74.0%; Pred. No. 5.2e-40;
Matches 108; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAQQKPGQPKLLIYWASTRESGVDPDRFG 60
```

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Db 11 LAMSVGQKVTMSCKSSQSLNRSRQKNYLAQQKPGQSPKLLIYVFASITRESGVDPDRFG 70
Qy 61 SGSGTDFLTITSSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIIPPSEDEQ 120
Db 71 SGSGTDFLTITSTVQAEADLADYFCQGHYSTPTFGGGTKLEIKRADAAPTIVSIFPPSEQ 130
Qy 121 LKSGTASVVCVCLMNNFYPREAKVQWKV 146
Db 131 LTSGASVVCVCLMNNFYPKDINVKWI 156

RESULT 5
Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Te
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 575.5; DB 2; Length 215;
Best Local Similarity 78.2%; Pred. No. 1.7e-39;
Matches 115; Conservative 12; Mismatches 13; Indels 7; Gaps 2;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAQQKPGQPKLLIYWASTRESGVDPDRFG 60
Db 11 LSVSPGERATLSCRSQSV-----HSNLYLAQQKPGQAPALLIYRATGIPARFG 64
Qy 61 SGSGTDFLTITSSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIIPPSEDE 119
Db 65 SGSGTDFLTITSSLOAEDFALYCCQYVSTPRTFGGQTKVEIKRTVAAPSVFIIPPSEDE 124
Qy 120 QLSGTASVVCVCLMNNFYPREAKVQWKV 146
Db 125 QLSGTASVVCVCLMNNFYPREAKVQWKV 151

RESULT 6
Ig kappa chain V region (17/9) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: A31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an ant
A;Reference number: A92686; MUID:89034213; PMID:3182835
A;Accession: A31790
A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:M23626; GB:J04061; NID:G533234; PIDN:AAA39162.1; PID:G533235
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 575; DB 2; Length 220;
Best Local Similarity 72.6%; Pred. No. 2e-39;
Matches 106; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAQQKPGQPKLLIYWASTRESGVDPDRFG 60
Db 11 LTVAGEKVTMSCTSSQSLFNSGKQKNYLAQQKPGQPKLLIYWASTRESGVDPDRFG 70
Qy 61 SGSGTDFLTITSSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIIPPSEDEQ 120
```







A:Molecule type: mRNA  
A:Residues: 1-134 <MAR>  
A>Note: the sequence was determined from the differentiated gene  
A>Note: the authors translated the codon TGC for residue 76 as Trp  
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-134/Product: Ig kappa chain V-IV region (B17) #status predicted <MAT>  
F:21-43/Region: framework 1  
F:36-116/Domain: immunoglobulin homology <IMM>  
F:44-60/Region: complementarity-determining 1  
F:61-75/Region: framework 2  
F:76-82/Region: complementarity-determining 2  
F:83-114/Region: framework 3  
F:115-121/Region: complementarity-determining 3  
F:122-134/Region: framework 4  
F:43-114/Disulfide bonds: #status predicted

Query Match 65.4%; Score 504; DB 1; Length 134;  
Best Local Similarity 93.3%; Pred. No. 6.4e-34;  
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLYWASTRESGVDRPFG 60  
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLYWASTRESGVDRPFG 90

Qy 61 SGSGTDFTLTISSLQAEADVAVYCOQYVSTPRTFGQGTKEIKR 104  
Db 91 SGSGTDFTLTISSLQAEADVAVYCOQYVSTPRTFGQGTKEIKR 134

Search completed: March 8, 2005, 06:39:28  
Job time : 11.4972 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 54.8971 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-34

Perfect score: 771

Sequence: 1 LAVALGERATINCKSSQSVL.....VVCLLNNFYPREAKVQWKVI 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	587.5	76.2	235	2	Q6GMV9	Q6gm9v homo sapien
2	586	76.0	236	2	Q6PIT5	Q6pit5 homo sapien
3	586	76.0	240	2	Q6PIH6	Q6pih6 homo sapien
4	585.5	75.9	239	2	Q8NEK0	Q8nek0 homo sapien
5	582	75.5	234	2	Q7Z473	Q7z473 homo sapien
6	581	75.4	236	2	Q6PIL8	Q6pil8 homo sapien
7	577	74.8	236	2	Q6PIH7	Q6pih7 homo sapien
8	574.5	74.5	239	2	Q6P491	Q6p491 homo sapien
9	573.5	74.4	235	2	Q6PJF2	Q6pjf2 homo sapien
10	573	74.3	236	2	Q6GMW1	Q6gmw1 homo sapien
11	571	74.1	236	2	Q6GMX8	Q6gmx8 homo sapien
12	569	73.8	236	2	Q7Z3Y4	Q7z3y4 homo sapien
13	567	73.5	236	2	Q6P5S8	Q6p5s8 homo sapien
14	565.5	73.3	235	2	Q6GMW0	Q6gmw0 homo sapien
15	562.5	73.0	239	2	Q8TCD0	Q8tcd0 homo sapien
16	561	72.8	236	2	Q6GMX0	Q6gmx0 homo sapien
17	555	72.0	236	2	Q6GMX9	Q6gmx9 homo sapien
18	551	71.5	236	2	Q6PIH4	Q6pih4 homo sapien
19	521	67.6	114	1	KV4A_HUMAN	P01625 homo sapien
20	517	67.1	134	1	KV4C_HUMAN	P06314 homo sapien
21	501	65.0	238	2	Q6GJS7	Q6gjs7 mus musculus
22	498.5	64.7	133	1	KV4B_HUMAN	P06313 homo sapien
23	495	64.2	241	2	Q63ZX4	Q63zx4 mus musculus
24	493.5	64.0	219	2	Q6SZC0	Q6szc0 mus musculus
25	475	61.6	236	2	Q7ITS9	Q7itc9 mus musculus
26	474	61.5	121	1	KV4D_HUMAN	P06312 homo sapien
27	473.5	61.4	243	2	Q6NTU5	Q6ntu5 xenopus lae
28	471	61.1	237	2	Q7SZ36	Q7sz36 xenopus lae
29	457	59.3	109	1	KV4D_HUMAN	P83593 homo sapien
30	414	53.7	255	2	Q6KB05	Q6kb05 mus musculus
31	394.5	51.2	129	1	KV3L_HUMAN	P18135 homo sapien

32	386.5	50.1	109	1	KV3B_HUMAN	P01620 homo sapien
33	385.5	50.0	109	1	KV3D_HUMAN	P01622 homo sapien
34	383.5	49.7	109	2	Q9UL78	Q9ul78 homo sapien
35	381.5	49.5	109	1	KV3E_HUMAN	P01623 homo sapien
36	378	49.0	108	2	Q9UL70	Q9ul70 homo sapien
37	378	49.0	108	2	Q9UL79	Q9ul79 homo sapien
38	376	48.8	108	1	KV1M_HUMAN	P01605 homo sapien
39	374.5	48.6	109	1	KV3G_HUMAN	P04206 homo sapien
40	374.5	48.6	129	1	KV3H_HUMAN	P04207 homo sapien
41	374.5	48.6	129	1	KV3M_HUMAN	P18136 homo sapien
42	373.5	48.4	109	1	KV3F_HUMAN	P01624 homo sapien
43	371	48.1	99	2	Q9JL74	Q9jl74 mus musculus
44	369	47.9	149	1	KV5A_MOUSE	P01633 mus musculus
45	363.5	47.1	117	1	KV2E_HUMAN	P06309 homo sapien

#### ALIGNMENTS

#### RESULT 1

ID	Q6GMV9	PRELIMINARY;	PRT;	235 AA.
AC	Q6GMV9;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DB	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RX	MEDLINE=32388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uadin T.B., Tohiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Ioquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnrerch A., Schein J.E.,			
RT	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
[2]				
RC	TISSUE=Spleen;			
RA	Strausberg R.;			
DR	EMBL; BC073793; AAH73793.1; -			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003006; IG MHC.			
DR	InterPro; IPR003596; IG v.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	Pfam; PF00047; IG; 2.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			

KW Hypothetical protein.  
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 76.2%; Score 587.5; DB 2; Length 235;  
Best Local Similarity 76.7%; Pred. No. 4.8e-50;  
Matches 112; Conservative 16; Mismatches 13; Indels 5; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFSG 60  
Db 31 LLSLFGGERALSQRSQSV-----NSKYLAWYQKQPGQAPRLMYASIRATGIPDRFSG 85  
Qy 61 SGSCTDFTLTISSLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120  
Db 86 SGSCTDFTLTISRLSESDFALYCCQYGTSTLTGGTKEIKRTVAAPSVFIPPPSDEQ 145  
Qy 121 LKSGTASVCLLNFFYPREAKVQWKV 146  
Db 146 LKSGTASVCLLNFFYPREAKVQWKV 171

RESULT 2  
Q6PIH6 PRELIMINARY; PRT; 236 AA.  
ID Q6PITS  
AC Q6PITS;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC029444; AAH29444.1; --  
DR HSSP; P01607; 1AR2  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG ci.  
DR InterPro; IPR003006; IG MHC.  
DR InterPro; IPR003596; IG v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGci; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEE8351 CRC64;

Query Match 76.0%; Score 586; DB 2; Length 236;  
Best Local Similarity 78.1%; Pred. No. 6.8e-50;  
Matches 114; Conservative 10; Mismatches 16; Indels 6; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFSG 60  
Db 33 LLSLFGGERALTICRASQGI-----SSALAWYQKQPGPKLLIYDASTWESGVPSRFSG 86  
Qy 61 SGSCTDFTLTISSLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120  
Db 87 SGSCTDFTLTISSLQEPDFATFYCCQYKSYPRIFGGTTLTKRTVAAPSVFIPPPSDEQ 146  
Qy 121 LKSGTASVCLLNFFYPREAKVQWKV 146  
Db 147 LKSGTASVCLLNFFYPREAKVQWKV 172

RESULT 3  
Q6PIH6 PRELIMINARY; PRT; 240 AA.  
ID Q6PIH6  
AC Q6PIH6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC034142; AAH34142.1; --  
DR HSSP; P01837; 1KB5.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG ci.  
DR InterPro; IPR003006; IG MHC.  
DR InterPro; IPR003596; IG v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGci; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 2.

DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;  
  
Query Match 76.0%; Score 586; DB 2; Length 240;  
Best Local Similarity 78.2%; Pred. No. 6,9e-50;  
Matches 115; Conservative 11; Mismatches 19; Indels 2; Gaps 2;  
  
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESSGVDPDRFSG 60  
Db 31 LSVTPGEPASISCRSSQSLHLS-NGYNYFDWYLRKPGQSPOLLIIYWGNSRASGVDPDRFSG 89  
Qy 61 SGSCTDFTLTSSLOAEDVAVYCCQYYST-PRPFGQGTKEIKRTVAAPSVFIPPSPDE 119  
Db 90 SGSCTDFTLKISRVEADGVYVCMQALQTPPTFGQGTKEIKRTVAAPSVFIPPSPDE 149  
Qy 120 QKSGTASVVCLLNNFYPREAKVQWKV 146  
Db 150 QKSGTASVVCLLNNFYPREAKVQWKV 176  
  
RESULT 4  
Q8NEKO PRELIMINARY; PRT; 239 AA.  
ID Q8NEKO  
AC Q8NEKO; 22, Created  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C.,  
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley D.N., Sodergren E.J., Lu X., Gibbs S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC030814; AAH30814.1; -.  
DR PIR; S23638; S23638.  
DR PIR; S34091; S34091.  
DR PIR; S40342; S40342.  
DR PIR; S40357; S40357.  
DR HSSP; P01834; I172.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR

DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;  
  
Query Match 75.9%; Score 585.5; DB 2; Length 239;  
Best Local Similarity 78.1%; Pred. No. 7,7e-50;  
Matches 114; Conservative 12; Mismatches 19; Indels 1; Gaps 1;  
  
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESSGVDPDRFSG 60  
Db 31 LSVTPGEPASISCRSSQSLHLS-DCYNYLDWYLRKPGQSPOLLIIYWGNSRASGVDPDRFSG 89  
Qy 61 SGSCTDFTLTSSLOAEDVAVYCCQYYST-PRPFGQGTKEIKRTVAAPSVFIPPSPDEQ 120  
Db 90 SGSCTDFTLKISRVEADGVYVCMQGLQTPPTFGQGTKEIKRTVAAPSVFIPPSPDEQ 149  
Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146  
Db 150 LKSGTASVVCLLNNFYPREAKVQWKV 175  
  
RESULT 5  
Q7Z473 PRELIMINARY; PRT; 234 AA.  
ID Q7Z473  
AC Q7Z473;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C.,  
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC056256; AAH56256.1; -.  
DR HSSP; P01834; I1HEZ.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IGv; 1.

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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match
Best Local Similarity 75.5%; Score 582; DB 2; Length 234;
Matches 112; Conservative 12; Mismatches 15; Indels 6; Gaps 1;

QY 2 AVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRSGS 61
DB 32 SASGTRDVTITCRASQSI-----GSLAWYQKPGKAPOLLIIYAANSTLQSGVPSRFGS 85
QY 62 GSGTDFTLTSSLOAEDVAVYCCQYVSTPTFGQGTVEIKRTVAAPSFIIPPSPDEQL 121
DB 86 ASGTDFTLSICLOSEDPATYCCQYTYPTWTFQGTVEIKRTVAAPSFIIPPSPDEQL 145
QY 122 KSGTASVVCLLNFPYPREAKVQWKV 146
DB 146 KSGTASVVCLLNFPYPREAKVQWKV 170

RESULT 6
Q6PIL8 PRELIMINARY; PRT; 236 AA.
AC Q6PIL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032451; AAH32451.1; -.
DR HSSP; P01837; 1KC0.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG ci.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IG; 2.

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DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match
Best Local Similarity 75.4%; Score 581; DB 2; Length 236;
Matches 112; Conservative 17; Mismatches 12; Indels 6; Gaps 2;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 60
DB 31 LSLSPERATLSRASQSL-----SSSYLAWYQKPGQAPRLIIYGVSRRATGIDPRFG 85
QY 61 SSGTDFTLTSSLOAEDVAVYCCQYVSTPTFGQGTVEIKRTVAAPSFIIPPSPDE 119
DB 86 SSGTDFTLTSSLOAEDVAVYCCQYVSTPTFGQGTVEIKRTVAAPSFIIPPSPDE 145
QY 120 QKSGTASVVCLLNFPYPREAKVQWKV 146
DB 146 QKSGTASVVCLLNFPYPREAKVQWKV 172

RESULT 7
Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RC Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG ci.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.

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[illegible]



DR PIR; S40374; S40374.  
 DR PIR; S42267; S42267.  
 DR PIR; S42268; S42268.  
 DR HSSP; P01834; 1172.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein\_  
 SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 73.0%; Score 562.5; DB 2; Length 239;  
 Best Local Similarity 74.0%; Pred. No. 1.5e-47;  
 Matches 108; Conservative 17; Mismatches 20; Indels 1; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKYNLYAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 60  
 Db 31 LPVTIGQPASISCRSTQSLVYSDGN-TYLNWFQORPGQSPRRLIYKVSNRDSGVDPDRFSG 89

Qy 61 SGSGTDFTLTSSLQAEADVAVVYCOQYVSTPRTFGQGTKEIKETVAAPSVFIPPSDEQ 120  
 Db 90 SGSGTDFTLKITRVEADVGVFCQGTHTWESTFGQGTKEIKETVAAPSVFIPPSDEQ 149

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146  
 Db 150 LKSGTASVVCLLNNFYPREAKVQWKV 175

Search completed: March 8, 2005, 06:35:53  
 Job time : 55.8971 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 68.1532 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-34

Perfect score: 771

Sequence: 1 LAVSLGRATINCKSSQSVL.....VCLLNFFYPREAKVQWKVI 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	771	100.0	147	2 AAY34314	Aay34314 Igm antib
2	747	96.9	211	5 ABP43134	Abp43134 Human ova
3	743	96.4	179	8 ADK52434	Adk52434 Human ant
4	737	95.6	240	4 AAU00815	Aau00815 Human Imm
5	736	95.5	163	8 ADK52394	Adk52394 Human ant
6	735	95.3	149	2 AAY34311	Aay34311 Igm antib
7	735	95.3	220	8 ADK52314	Adk52314 Human ant
8	734	95.2	159	8 ADK52406	Adk52406 Human ant
9	731	94.8	173	8 ADK52430	Adk52430 Human ant
10	731	94.8	220	8 ADK52386	Adk52386 Human ant
11	730	94.7	171	8 ADK52422	Adk52422 Human ant
12	730	94.7	220	8 ADK52334	Adk52334 Human ant
13	729	94.6	159	8 ADK52382	Adk52382 Human ant
14	729	94.6	163	8 ADK52310	Adk52310 Human ant
15	726	94.2	220	8 ADK52362	Adk52362 Human ant
16	724	93.9	163	8 ADK52346	Adk52346 Human ant
17	724	93.9	163	8 ADK52306	Adk52306 Human ant
18	724	93.9	163	8 ADK52326	Adk52326 Human ant
19	723	93.8	154	8 ADK52342	Adk52342 Human ant
20	722	93.6	159	8 ADK52302	Adk52302 Human ant
21	722	93.6	264	5 ABP43142	Abp43142 Human ova
22	721	93.5	158	8 ADK52378	Adk52378 Human ant
23	721	93.5	240	2 AAY50161	Aay50161 Human res
24	719	93.3	163	8 ADK52398	Adk52398 Human ant
25	717	93.0	220	2 AAY08601	Aay08601 JP1112785

26	716	92.9	159	8	ADK52410	Adk52410 Human ant
27	716	92.9	220	8	ADK52298	Adk52298 Human ant
28	715	92.7	178	8	ADK52418	Adk52418 Human ant
29	714	92.6	163	8	ADK52338	Adk52338 Human ant
30	714	92.6	244	3	AAY96305	Aay96305 Human IGF
31	711.5	92.3	241	2	AAR28809	Aar28809 Vector pm
32	709	92.0	163	8	ADK52374	Adk52374 Human ant
33	708	91.8	159	8	ADK52366	Adk52366 Human ant
34	706	91.6	166	7	ADD28248	Add28248 Human het
35	703.5	91.2	238	8	ADL23055	Adl23055 Humanised
36	703.5	91.2	238	8	ADS88804	Adse88804 Humanised
37	702	91.1	240	5	AAE27927	Aae27927 Human CC4
38	702	91.1	240	6	ABB82836	Abb82836 Antibody
39	696	90.3	173	8	ADK52438	Adk52438 Human ant
40	695	90.1	149	8	ADK52402	Adk52402 Human ant
41	688	89.2	240	8	ADJ65029	Adj65029 Plasmid p
42	674	87.4	242	4	AAU80338	Aau80338 Human mil
43	674	87.4	242	4	AAU97949	Aau97949 HMF61 Fab
44	674	87.4	242	4	AAU80039	Aau80039 HMF61 Fab
45	669	86.8	154	6	ABO04851	Abo04851 Human epi

## ALIGNMENTS

### RESULT 1

AAY34314  
ID AAY34314 standard; protein; 147 AA.  
XX  
AC AAY34314;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE Igm antibody CEM 13.5 kappa chain sequence.  
XX  
KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
OS Homo sapiens.  
XX  
PN WO9945031-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 03-MAR-1999; 99WO-US004583.  
XX  
PR 03-MAR-1998; 98US-00034607.  
XX  
PR 03-FEB-1999; 99US-00244253.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX  
DR WPI; 1999-540816/45.  
DR N-PSDB; AAZ20415.  
XX  
XX New monoclonal antibody, used for treating e.g. graft versus host  
FT disease, cancer, autoimmune diseases and inflammatory diseases.  
PS  
XX Claim 61; Fig 29; 245pp; English.  
CC This sequence represents the kappa chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the Igm MAB ABX-CBL, providing that the antibody is not CBL. The MAB  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
 CC  
 SQ Sequence 147 AA;

Query Match 100.0%; Score 771; DB 2; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 4e-53;  
 Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 60  
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 DB 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 60  
 |||||

QY 61 SSGSGTDFTLTSSIQAEADVAVVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120  
 |||||  
 DB 61 SSGSGTDFTLTSSIQAEADVAVVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120  
 |||||

QY 121 LKSGTASVCLLNFFYPREAKVQWKVI 147  
 |||||  
 DB 121 LKSGTASVCLLNFFYPREAKVQWKVI 147  
 |||||

RESULT 2  
 ABP43134  
 ID ABP43134 standard; protein; 211 AA.  
 AC ABP43134;  
 XX  
 XX 22-AUG-2002 (first entry)  
 DT  
 XX Human ovarian antigen HVVBK13, SEQ ID NO:4266.  
 DE  
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200200677-A1.  
 PN  
 XX  
 XX 03-JAN-2002.  
 PD  
 XX  
 XX 07-JUN-2001; 2001WO-US018569.  
 PF  
 XX  
 XX 07-JUN-2000; 2000US-0209467P.  
 PR  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX  
 XX Birse CE, Rosen CA;  
 PI  
 XX WPI; 2002-147878/19.  
 DR  
 XX N-PSDB; ABQ56211.  
 DR  
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
 PT cancer), immune disorders, cardiovascular disorders and neurological  
 PT diseases.  
 XX  
 XX Claim 11; SEQ ID NO 4266; 2922pp; English.  
 PS  
 XX  
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use

CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g. congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 211 AA;

Query Match 96.9%; Score 747; DB 5; Length 211;  
 Best Local Similarity 96.8%; Pred. No. 4.5e-51;  
 Matches 141; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 60  
 |||||  
 DB 35 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRYGG 94  
 |||||

QY 61 SSGSGTDFTLTSSIQAEADVAVVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120  
 |||||  
 DB 95 SSGSGTDFTLTSSIQAEADVAVVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 154  
 |||||

QY 121 LKSGTASVCLLNFFYPREAKVQWKV 146  
 |||||  
 DB 155 LKSGTASVCLLNFFYPREAKVQWKV 180  
 |||||

RESULT 3  
 ADK52434  
 ID ADK52434 standard; protein; 179 AA.  
 XX  
 XX ADK52434;  
 AC  
 XX  
 XX 20-MAY-2004 (first entry)  
 DT  
 XX Human anti-MCP-1 variable region light chain #35.  
 DE  
 XX  
 XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
 KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;  
 KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;  
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
 KW anti-MCP-1; heavy chain; light chain.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2004016769-A2.  
 PN  
 XX  
 XX 26-FEB-2004.  
 PD  
 XX  
 XX 19-AUG-2003; 2003WO-US026232.  
 PF  
 XX  
 XX 19-AUG-2002; 2002US-0404802P.  
 PR  
 XX  
 XX (ABGE-) ABGENIX INC.  
 PA  
 XX Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
 PI Bhakta S;

XX WPI; 2004-203794/19.  
 DR N-PSDB; ADK52433.  
 XX  
 PT New human monoclonal antibody that binds to monocyte chemo-attractant  
 PT protein-1 and is immobilized on an insoluble matrix, useful for  
 PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
 PT rheumatoid arthritis or psoriasis.  
 XX  
 PS Claim 2; SEQ ID NO 140; 154pp; English.  
 XX  
 CC The present invention relates to a human monoclonal antibody that binds  
 CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
 CC for the preparation of a medicament useful for treating neoplastic or  
 CC inflammatory conditions. The neoplastic disease is selected from breast  
 CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer or prostate cancer. The inflammatory condition is  
 CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
 CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
 CC antibodies are also useful for diagnosing the above diseases. It is also  
 CC useful for the determining the level of MCP-1 and MCP-1 family members in  
 CC patient samples. The present sequence represents a human anti-MCP-1  
 CC variable region light chain sequence.  
 XX  
 SQ Sequence 179 AA;

Query Match 96.4%; Score 743; DB 8; Length 179;  
 Best Local Similarity 96.6%; Pred. No. 7.8e-51;  
 Matches 141; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDFSG 60  
 Db 27 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDFSG 86  
 Qy 61 SGSGTDFTLTSSLAQEDVAVYVCOQYVSTPTFGQTKVEIKRTVAAPSVFIPPSDEQ 120  
 Db 87 SGSGTDFTLTSSLAQEDVAVYVCOQYVSTPTFGQTKVEIKRTVAAPSVFIPPSDEQ 146  
 Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146  
 Db 147 LKSGTASVVCLLNNFYPREAKVQWKV 172

RESULT 4  
 AAU00815  
 ID AAU00815 standard; protein; 240 AA.  
 XX  
 AC AAU00815;  
 XX  
 DT 01-JUN-2001 (first entry)  
 XX  
 DE Human Immunoglobulin superfamily, IgSF, protein #1.  
 XX  
 KW Human; Immunoglobulin superfamily protein; IgSF; Immune response;  
 KW inflammatory response; cell-cell interaction; cell-surface recognition;  
 KW neural disorder; immune system disorder; muscular disorder;  
 KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;  
 KW cardiovascular disorder; renal disorder; proliferative disorder; cancer;  
 KW common variable adhesion deficiency syndrome; AIDS; SCID;  
 KW acquired immunodeficiency syndrome; anaemia; rheumatoid arthritis;  
 KW Alzheimer's disease; Crohn's disease; liver cancer; leukaemia;  
 KW Hodgkin's lymphoma; Parkinson's disease; Huntington's disease; dementia;  
 KW arteriosclerosis; stroke; diabetes mellitus; Addison's disease;  
 KW urticaria; severe combined immunodeficiency; antibody.  
 OS Homo sapiens.  
 XX  
 FH Location/Qualifiers  
 FT Key 52..58  
 FT Region /label= Immunogenic\_epitope  
 FT Region 63..70  
 FT /label= Immunogenic\_epitope

Region 79..90  
 /label= Immunogenic\_epitope  
 Region 118..126  
 /label= Immunogenic\_epitope  
 Region 146..154  
 /label= Immunogenic\_epitope  
 Domain 160..240  
 /label= Immunoglobulin\_like\_domain  
 Region 183..199  
 /label= Immunogenic\_epitope  
 Region 209..215  
 /label= Immunogenic\_epitope  
 Region 233..240  
 /label= Immunogenic\_epitope  
 WO200118176-A1.  
 15-MAR-2001.  
 29-AUG-2000; 2000WO-US023662.  
 03-SEP-1999; 99US-0152248P.  
 (HUMA-) HUMAN GENOME SCI INC.  
 (NIJ/) NI J.  
 Young PE, Ruben SM, Shi Y;  
 WPI; 2001-203084/20.  
 N-PSDB; AAS00145.  
 Isolated nucleic acid molecule encoding a human secreted protein is used  
 in preventing, treating or ameliorating a medical condition.  
 Claim 11; Page 237; 247pp; English.  
 The sequence is a Human Immunoglobulin superfamily, IgSF, protein, a  
 diverse family of proteins involved in cell-cell interactions, cell-  
 surface recognition, intercellular communication and immune and  
 inflammatory responses. Polypeptides and antibodies directed to  
 polypeptides of the present invention are useful to provide immunological  
 probes for differential identification of tissues. Antibodies can be used  
 to assay levels of polypeptides encoded by polynucleotides of the  
 invention. Polypeptides of the present invention can be used to treat or  
 prevent diseases or conditions such as neural disorders, immune system  
 disorders, muscular disorders, reproductive disorders, gastrointestinal  
 disorders, proliferative disorders, cardiovascular disorders, renal  
 conditions. Polynucleotides of the invention are also useful in treating  
 the above disorders. Examples of the disorders include common variable  
 adhesion deficiency syndrome, acquired immunodeficiency syndrome (AIDS),  
 anaemia, rheumatoid arthritis, Alzheimer's disease, Crohn's disease,  
 liver cancer, leukaemia, Hodgkin's lymphoma, Parkinson's disease,  
 Huntington's disease, dementia, arteriosclerosis, stroke, diabetes  
 mellitus, Addison's disease, urticaria, severe combined immunodeficiency  
 (SCID). Many more examples of diseases and disorders are given in the  
 specification  
 Sequence 240 AA;

Query Match 95.6%; Score 737; DB 4; Length 240;  
 Best Local Similarity 95.9%; Pred. No. 3.1e-50;  
 Matches 140; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDFSG 60  
 Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDFSG 90  
 Qy 61 SGSGTDFTLTSSLAQEDVAVYVCOQYVSTPTFGQTKVEIKRTVAAPSVFIPPSDEQ 120  
 Db 91 SGSGTDFTLTSSLAQEDVAVYVCOQYVSTPTFGQTKVEIKRTVAAPSVFIPPSDEQ 150  
 Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146

Db 151 LKSGTASVCLNNFYPRKQVQWK 176  
|||||

RESULT 5  
ADK52394  
ID ADK52394 standard; protein; 163 AA.

XX AC ADK52394;

XX DT 20-MAY-2004 (first entry)

XX DE Human anti-MCP-1 variable region light chain #25.

XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;  
KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.

XX OS Homo sapiens.

XX PN W02004016769-A2.

XX PD 26-FEB-2004.

XX PF 19-AUG-2003; 2003WO-US026232.

XX PR 19-AUG-2002; 2002US-0404802P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;

XX DR WPI; 2004-203794/19.

XX DR N-PSDB; ADK52393.

XX PT New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.

XX PS Claim 2; SEQ ID NO 100; 154pp; English.

XX CC The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.

XX SQ Sequence 163 AA;

Query Match 95.5%; Score 736; DB 8; Length 163;  
Best Local Similarity 95.9%; Pred. No. 2.5e-50;  
Matches 140; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPKLLIYWASTRESGVDFRFSG 60

Db 11 LAVSLGERATINCKSSQSVLYSSNNENFLAWYQKPGPKLLIYWASTRESGVDFRFSG 70

Qy 61 SGSGTDTLTISLQAEADVAVYQCYYSPTRTFGQTKVEIKRTVAAPSVFIIPPSDEQ 120

Db 71 SGSGTDTLTISLQAEADVAVYQCYYSNTPWTFGQTKVEIKRTVAAPSVFIIPPSDEQ 130

Qy 121 LKSGTASVCLNNFYPRKQVQWK 146  
Db 131 LKSGTASVCLNNFYPRKQVQWK 156  
|||||

RESULT 6  
AAV34311

ID AAV34311 standard; protein; 149 AA.

XX AC AAV34311;

XX DT 19-NOV-1999 (first entry)

XX DE IGM antibody CEM 10.12 F3 kappa chain sequence.

XX KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.

XX PN W09945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;

XX DR WPI; 1999-540816/45.

XX DR N-PSDB; AAZ20412.

XX PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 61; Fig 26; 245pp; English.

XX CC This sequence represents the kappa chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the Igm Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)

XX SQ Sequence 149 AA;

Query Match 95.3%; Score 735; DB 2; Length 149;  
Best Local Similarity 97.2%; Pred. No. 2.8e-50;  
Matches 141; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPKLLIYWASTRESGVDFRFSG 60

Db 3 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPKLLIYWASTRESGVDFRFSG 62

Qy 61 SGSGTDTLTISLQAEADVAVYQCYYSPTRTFGQTKVEIKRTVAAPSVFIIPPSDEQ 120

Db 63 SGSGTDTLTISLQAEADVAVYQCYYSPTRTFGQTKVEIKRTVAAPSVFIIPPSDEQ 122

Qy 121 LKSGTASVCLNNFYPRKQVQWK 145

Db 123 LKSGTASVCLNNFYPRKQVQWK 147  
|||||



RESULT 7  
ADK52314  
ID ADK52314 standard; protein; 220 AA.

AC ADK52314;

XX 20-MAY-2004 (first entry)

XX Human anti-MCP-1 variable region light chain #5.

XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;  
KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.

XX Homo sapiens.

XX WO2004016769-A2.

XX 26-FEB-2004.

XX 19-AUG-2003; 2003WO-US026232.

XX 19-AUG-2002; 2002US-0404802P.

XX (ABGE-) ABGENIX INC.

XX Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;

XX WPI; 2004-203794/19.

XX N-PSDB; ADK52313.

XX New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.

XX Claim 2; SEQ ID NO 20; 154pp; English.

XX The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.

XX Sequence 220 AA;

Query Match 95.3%; Score 735; DB 8; Length 220;  
Best Local Similarity 96.6%; Pred. No. 4.1e-50;  
Matches 141; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFSG 60

Db 11 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFSG 70

Qy 61 SGSGTDFTLTSSLAQEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPSDEQ 120

Db 71 SGSGTDFTLTSSLAQEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPSDEQ 130

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146

|||||

Db 131 LKSGTASVVCLLNNFYPREAKVQWKV 156

RESULT 8

ADK52406

XX ADK52406 standard; protein; 159 AA.

XX ADK52406;

XX 20-MAY-2004 (first entry)

XX Human anti-MCP-1 variable region light chain #28.

XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;  
KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.

XX Homo sapiens.

XX WO2004016769-A2.

XX 26-FEB-2004.

XX 19-AUG-2003; 2003WO-US026232.

XX 19-AUG-2002; 2002US-0404802P.

XX (ABGE-) ABGENIX INC.

XX Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;

XX WPI; 2004-203794/19.

XX N-PSDB; ADK52405.

XX New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.

XX Claim 2; SEQ ID NO 112; 154pp; English.

XX The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.

XX Sequence 159 AA;

Query Match 95.2%; Score 734; DB 8; Length 159;  
Best Local Similarity 96.6%; Pred. No. 3.5e-50;  
Matches 141; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFSG 60

Db 11 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFSG 70

Qy 61 SGSGTDFTLTSSLAQEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPSDEQ 120

Db 71 SGSGTDFTLTSSLAQEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPSDEQ 130

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146

Db 131 LKSGTASVWCLNNFYPREAKVQWKV 156  
|||||

RESULT 9  
ADK52430  
ID ADK52430 standard; protein; 173 AA.

XX AC ADK52430;

XX DT 20-MAY-2004 (first entry)

XX DE Human anti-MCP-1 variable region light chain #34.

XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;  
KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.

XX OS Homo sapiens.

XX PN WO2004016769-A2.

XX PD 26-FEB-2004.

XX PF 19-AUG-2003; 2003WO-US026232.

XX PR 19-AUG-2002; 2002US-0404802P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;

XX DR WPI; 2004-203794/19.

XX DR N-PSDB; ADK52429.

XX PT New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.

XX PS Claim 2; SEQ ID NO 136; 154pp; English.

XX CC The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.

XX SQ Sequence 173 AA;

Query Match 94.8%; Score 731; DB 8; Length 173;  
Best Local Similarity 95.2%; Pred. No. 6.6e-50;  
Matches 139; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60  
Db 26 LAVSLGERAAINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 85

Qy 61 SGSCTDFTLTSSLOAEDVAVYCOQYVSTPRTFGQTKVEIKETVAAPSVFIPPSDEQ 120

Db 86 SGSCTDFTLTSSLOAEDVAVYCOQYVSTPRTFGQTKVEIKETVAAPSVFIPPSDEQ 145

Qy 121 LKSGTASVWCLNNFYPREAKVQWKV 146  
Db 146 LKSGTASVWCLNNFYPREAKVQWKV 171

RESULT 10  
ADK52386

ID ADK52386 standard; protein; 220 AA.

XX AC ADK52386;

XX DT 20-MAY-2004 (first entry)

XX DE Human anti-MCP-1 variable region light chain #23.

XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;  
KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;  
KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
KW anti-MCP-1; heavy chain; light chain.

XX OS Homo sapiens.

XX PN WO2004016769-A2.

XX PD 26-FEB-2004.

XX PF 19-AUG-2003; 2003WO-US026232.

XX PR 19-AUG-2002; 2002US-0404802P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;

XX DR WPI; 2004-203794/19.

XX DR N-PSDB; ADK52385.

XX PT New human monoclonal antibody that binds to monocyte chemo-attractant  
PT protein-1 and is immobilized on an insoluble matrix, useful for  
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
PT rheumatoid arthritis or psoriasis.

XX PS Claim 2; SEQ ID NO 92; 154pp; English.

XX CC The present invention relates to a human monoclonal antibody that binds  
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
CC for the preparation of a medicament useful for treating neoplastic or  
CC inflammatory conditions. The neoplastic disease is selected from breast  
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer or prostate cancer. The inflammatory condition is  
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
CC antibodies are also useful for diagnosing the above diseases. It is also  
CC useful for the determining the level of MCP-1 and MCP-1 family members in  
CC patient samples. The present sequence represents a human anti-MCP-1  
CC variable region light chain sequence.

XX SQ Sequence 220 AA;

Query Match 94.8%; Score 731; DB 8; Length 220;  
Best Local Similarity 95.2%; Pred. No. 8.4e-50;  
Matches 139; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60  
Db 11 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 70

Qy 61 SGSCTDFTLTSSLOAEDVAVYCOQYVSTPRTFGQTKVEIKETVAAPSVFIPPSDEQ 120

Db 71 SGSCTDFTLTSSLOAEDVAVYCOQYVSTPRTFGQTKVEIKETVAAPSVFIPPSDEQ 130



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Qy 121 LKSGTASVWCLNNFYPREAKVQMKV 146
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Db 131 LKSGTASVWCLNNFYPREAKVQMKV 156
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RESULT 13
ADK52382
ID ADK52382 standard; protein; 159 AA.
XX
AC ADK52382;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region light chain #22.
XX
KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN WO2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52381.
XX
XX New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
PS Claim 2; SEQ ID NO 88; 154pp; English.
XX
XX The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX
SQ Sequence 159 AA;
XX
Query Match 94.6%; Score 729; DB 8; Length 159;
Best Local Similarity 95.9%; Pred. No. 8.8e-50;
Matches 140; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGOPPKLLIYWASTRESGVDPDRFSG 60
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Qy 121 LKSGTASVWCLNNFYPREAKVQMKV 146
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Db 131 LKSGTASVWCLNNFYPREAKVQMKV 156
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
ADK52310
ID ADK52310 standard; protein; 163 AA.
XX
AC ADK52310;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region light chain #4.
XX
KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN WO2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52309.
XX
XX New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
PS Claim 2; SEQ ID NO 16; 154pp; English.
XX
XX The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX
SQ Sequence 163 AA;
XX
Query Match 94.6%; Score 729; DB 8; Length 163;
Best Local Similarity 95.2%; Pred. No. 9e-50;
Matches 139; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGOPPKLLIYWASTRESGVDPDRFSG 60
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Db 11 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGOPPKLLIYWASTRESGVDPDRFSG 70
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[illegible]

**RESULT 15**

ADK52362  
ID ADK52362 standard; protein; 220 AA.

AC ADK52362;

DT 20-MAY-2004 (first entry)

DE Human anti-MCP-1 variable region light chain #17.

monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
 KW  
 Anti-rheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;  
 KW  
 Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;  
 KW  
 inflammatory condition; cancer; arthritis; multiple sclerosis;  
 KW  
 anti-MCP-1; heavy chain; light chain.  
 KW

OS Homo sapiens.

PN WO2004016769-A2.

PD 26-FEB-2004.

PF 19-AUG-2003;

PR 19-AUG-2002: 2002US-0404802P.

PA (ABGE-) ABGENIX INC.

PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
PI Bhakta S;

DR WPI; 2004-203794/19.

XX  
XX  
:1067CVMW,1993-N

PT A new human monoclonal antibody that binds to monocyte chemo-attractant protein-1 and is immobilized on an insoluble matrix, useful for diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer, rheumatoid arthritis or psoriasis.

PS Claim 2; SEQ ID NO 68; 154pp; English.

The present invention relates to a human monoclonal antibody that binds to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful for the preparation of a medicament useful for treating neoplastic or inflammatory conditions. The neoplastic disease is selected from breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma, stomach cancer, endometrial cancer, kidney cancer, colon cancer, pancreatic cancer or prostate cancer. The inflammatory condition is selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease or multiple sclerosis. The antibodies are also useful for diagnosing the above diseases. It is also useful for the determining the level of MCP-1 and MCP-1 family members in patient samples. The present sequence represents a human anti-MCP-1 variable region light chain sequence.

Sequence 220 AA;

Query Match 94.2%; Score 726; DB 8; Length 220;

Best Local Similarity 95.2%; Pred. No. 2.1e-49;

Matches 139; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINC KSSQSVLYSFNNKNYLAWYQOKPGQPKLLIYWASTRESGVDFRFG 60

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 78.009 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-34

Perfect score: 771

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Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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  - 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
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  - 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	96.9	211	15	US-10-264-049-4266 Sequence 4266, Ap
2	737	95.6	240	9	US-09-799-514-8 Sequence 8, Appli
3	722	93.6	264	15	US-10-264-049-4274 Sequence 4274, Ap
4	721	93.5	240	9	US-09-301-593-36 Sequence 36, Appl
5	721	93.5	240	14	US-10-159-006-36 Sequence 36, Appl
6	696.5	90.3	165	15	US-10-384-743-26 Sequence 26, Appl
7	688	89.2	240	16	US-10-630-406-8 Sequence 8, Appli
8	677.5	87.9	239	9	US-09-249-011A-22 Sequence 22, Appl
9	674	87.4	239	9	US-09-825-012-9 Sequence 9, Appli
10	674	87.4	242	10	US-09-819-266-26 Sequence 26, Appl
11	667	86.5	220	9	US-09-995-693-1 Sequence 1, Appli
12	667	86.5	220	14	US-10-232-408-1 Sequence 1, Appli
13	662	85.9	153	9	US-09-187-693-62 Sequence 62, Appl

14	656	85.1	220	9	US-09-301-593-17 Sequence 17, Appl
15	656	85.1	220	14	US-10-159-006-17 Sequence 17, Appl
16	656	85.1	240	9	US-09-301-593-28 Sequence 28, Appl
17	656	85.1	240	14	US-10-159-006-28 Sequence 28, Appl
18	653	84.7	220	9	US-09-917-410-5 Sequence 5, Appli
19	645	83.7	218	15	US-10-449-566-102 Sequence 102, App
20	641	83.1	218	15	US-10-449-566-119 Sequence 119, App
21	638	82.7	218	14	US-10-171-452A-39 Sequence 39, Appl
22	638	82.7	218	14	US-10-171-452A-57 Sequence 57, Appl
23	638	82.7	218	15	US-10-353-708-39 Sequence 39, Appl
24	638	82.7	218	15	US-10-353-708-57 Sequence 57, Appl
25	638	82.7	218	16	US-10-731-984-4 Sequence 4, Appli
26	638	82.7	218	16	US-10-731-984-28 Sequence 28, Appl
27	638	82.7	238	14	US-10-171-452A-38 Sequence 38, Appl
28	638	82.7	238	14	US-10-171-452A-56 Sequence 56, Appl
29	638	82.7	238	15	US-10-353-708-38 Sequence 38, Appl
30	638	82.7	238	15	US-10-353-708-56 Sequence 56, Appl
31	638	82.7	238	16	US-10-731-984-3 Sequence 3, Appli
32	638	82.7	238	16	US-10-731-984-27 Sequence 27, Appl
33	637	82.6	218	15	US-10-449-566-98 Sequence 98, Appl
34	628	81.5	218	14	US-10-171-452A-45 Sequence 45, Appl
35	628	81.5	218	14	US-10-171-452A-51 Sequence 51, Appl
36	628	81.5	218	15	US-10-353-708-45 Sequence 45, Appl
37	628	81.5	218	15	US-10-353-708-51 Sequence 51, Appl
38	628	81.5	218	16	US-10-731-984-12 Sequence 12, Appl
39	628	81.5	218	16	US-10-731-984-20 Sequence 20, Appl
40	628	81.5	238	14	US-10-171-452A-44 Sequence 44, Appl
41	628	81.5	238	14	US-10-171-452A-50 Sequence 50, Appl
42	628	81.5	238	15	US-10-353-708-44 Sequence 44, Appl
43	628	81.5	238	15	US-10-353-708-50 Sequence 50, Appl
44	628	81.5	238	16	US-10-731-984-11 Sequence 11, Appl
45	628	81.5	238	16	US-10-731-984-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1  
US-10-264-049-4266  
; Sequence 4266, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA133P1  
; CURRENT APPLICATION NUMBER: US/10/264,049  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/18569  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 4266  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (5) \_FEATURE  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-10-264-049-4266

Query Match	Best Local Similarity	96.9%	Score 747;	DB 15;	Length 211;
Matches 141;	Conservative	3;	Mismatches	2;	Indels 0; Gaps 0;
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Db 95 SSGSTDFTLTSSQAEDVAVYCCQYNTPTRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 154  
Qy 121 LKSGTASVCLNNFYPREAKVQWKV 146  
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RESULT 2  
US-09-799-514-8  
; Sequence 8, Application US/09799514  
; Patent No. US20020065220A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ant  
; CURRENT APPLICATION NUMBER: US/09/799,514  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: PCT/US00/23662  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: 60/152,248  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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Query Match 95.6%; Score 737; DB 9; Length 240;  
Best Local Similarity 95.9%; Pred. No. 8.3e-49;  
Matches 140; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60  
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 90  
Qy 61 SSGSTDFTLTSSQAEDVAVYCCQYNTPTRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120  
Db 91 SSGSTDFTLTSSQAEDVAVYCCQYNTPTRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 150  
Qy 121 LKSGTASVCLNNFYPREAKVQWKV 146  
Db 151 LKSGTASVCLNNFYPREAKVQWKV 176  
RESULT 3  
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; Sequence 4274, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA133P1  
; CURRENT APPLICATION NUMBER: US/10/264,049  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/18569  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 4274  
; LENGTH: 264  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
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; LOCATION: (163)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (201)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
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; LOCATION: (215)  
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; LOCATION: (226)  
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; LOCATION: (258)  
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; LOCATION: (263)  
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US-10-264-049-4274  
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Best Local Similarity 94.5%; Pred. No. 1.3e-47;  
Matches 138; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60  
Db 35 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 94  
Qy 61 SSGSTDFTLTSSQAEDVAVYCCQYNTPTRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120  
Db 95 SSGSTDFTLTSSQAEDVAVYCCQYNTPTRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 154  
Qy 121 LKSGTASVCLNNFYPREAKVQWKV 146  
Db 155 LKSGTASVCLNNFYPREAKVQWKV 180  
RESULT 4  
US-09-301-593-36  
; Sequence 36, Application US/09301593A  
; Publication No. US20020052480A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652.1890001  
; CURRENT APPLICATION NUMBER: US/09/301,593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0



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; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-36

Query Match          93.5%; Score 721; DB 9; Length 240;
Best Local Similarity 94.5%; Pred. No. 1.4e-47;
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGQPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGQPPKLLIYWASTRESGVDPDRFSG 90

Qy 61 SGSGTDFTLTSSLOAEDVAVYQYQYSTRPTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
Db 91 SGFGTDFTLTSSLOAEDVAVYQYQYSTRPTFGQTKVEIKRTVAAPSVFIPPPSDEQ 150

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 151 LKSGTASVVCLLNNFYPREAKVQWKV 176

RESULT 5
US-10-159-006-36
; Sequence 36, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John B.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saidanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-36

Query Match          93.5%; Score 721; DB 14; Length 240;
Best Local Similarity 94.5%; Pred. No. 1.4e-47;
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGQPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGQPPKLLIYWASTRESGVDPDRFSG 90

Qy 61 SGSGTDFTLTSSLOAEDVAVYQYQYSTRPTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
Db 91 SGFGTDFTLTSSLOAEDVAVYQYQYSTRPTFGQTKVEIKRTVAAPSVFIPPPSDEQ 150

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 151 LKSGTASVVCLLNNFYPREAKVQWKV 176

RESULT 6
US-10-364-743-26
; Sequence 26, Application US/10364743
; Publication No. US20040009178A1
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; GENERAL INFORMATION:
; APPLICANT: Bowdich, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 165
; TYPE: PRT
; ORGANISM: human
US-10-364-743-26

Query Match          90.3%; Score 696.5; DB 15; Length 165;
Best Local Similarity 91.1%; Pred. No. 7.3e-46;
Matches 133; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGQPPKLLIYWASTRESGVDPDRFSG 60
Db 13 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGQPPKLLIYWASTRESGVDPDRFSG 71

Qy 61 SGSGTDFTLTSSLOAEDVAVYQYQYSTRPTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
Db 72 SGSGTDFTLTSSLOAEDVAVYQYQYSTRPTFGQTKVEIKRTVAAPSVFIPPPSDEQ 131

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 132 LKSGTASVVCLLNNFYPREAKVQWKV 157

RESULT 7
US-10-630-406-8
; Sequence 8, Application US/10630406
; Publication No. US20040105855A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Ganguly, Subinay
; APPLICANT: Abraham, Ralph
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Rillema, Jill
; APPLICANT: Thorne, Barbara
; APPLICANT: Shuford, Walter W.
; APPLICANT: Muttler, Robert S.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: D0288 NP
; CURRENT APPLICATION NUMBER: US/10/630,406
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/399,646
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-630-406-8

Query Match          89.2%; Score 688; DB 16; Length 240;
Best Local Similarity 91.8%; Pred. No. 4.6e-45;
Matches 134; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGQPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGQPPKLLIYWASTRESGVDPDRFSG 90
```



```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,693
; FILING DATE: 29-NOV-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/952,235
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-995-693-1

;
; Query Match 86.5%; Score 667; DB 9; Length 220;
; Best Local Similarity 84.2%; Pred. No. 1.7e-43;
; Matches 123; Conservative 15; Mismatches 8; Indels 0; Gaps 0;
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Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAAYQKPGQPKLLIYWASTRESGVDPDRFG 60
Db 11 LTVSVGEKVTVCSSQSLLYTSQKNYLAAYQKPGQPKLLIYWASTRESGVDPDRFG 70

Qy 61 SGSGTDFLTITSSQAEADVAVYCOQYVSTRTGQGTKEIKRTVAAPSVFIPTPSDEQ 120
Db 71 SGSGTDFLTITSSQAEADVAVYCOQYVSTRTGQGTKEIKRTVAAPSVFIPTPSDEQ 130

Qy 121 LKSGTASVCLLNFPYKPAKQVQKV 146
Db 131 LKSGTASVCLLNFPYKPAKQVQKV 156

RESULT 12
US-10-232-408-1
; Sequence 1, Application US/102332408
; Publication No. US20030118587A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,408
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/669,971
; FILING DATE: 05-Jul-2001
; APPLICATION NUMBER: US/08/952,235
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/460368
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-232-408-1

;
; Query Match 86.5%; Score 667; DB 14; Length 220;
; Best Local Similarity 84.2%; Pred. No. 1.7e-43;
; Matches 123; Conservative 15; Mismatches 8; Indels 0; Gaps 0;
;
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAAYQKPGQPKLLIYWASTRESGVDPDRFG 60
Db 11 LTVSVGEKVTVCSSQSLLYTSQKNYLAAYQKPGQPKLLIYWASTRESGVDPDRFG 70

Qy 61 SGSGTDFLTITSSQAEADVAVYCOQYVSTRTGQGTKEIKRTVAAPSVFIPTPSDEQ 120
Db 71 SGSGTDFLTITSSQAEADVAVYCOQYVSTRTGQGTKEIKRTVAAPSVFIPTPSDEQ 130

Qy 121 LKSGTASVCLLNFPYKPAKQVQKV 146
Db 131 LKSGTASVCLLNFPYKPAKQVQKV 156

RESULT 13
US-09-187-693-62
; Sequence 62, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; Growth Factor Receptor
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: SeqSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(153)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-187-693-62

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Query Match 85.1%; Score 662; DB 9; Length 153;  
Best Local Similarity 90.3%; Pred. No. 2.9e-43;  
Matches 130; Conservative 2; Mismatches 10; Indels 2; Gaps 1;  
  
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 60  
Db 7 LAVSLGERATINCKSSQSVLYSGKNQNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 66  
  
Qy 61 SSGTDTFTLTSSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120  
Db 67 SSGRTDFTLTSSLOAEDVAVFCHQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 126  
  
Qy 121 LKSGTASVVCCLNNFY--PREAKV 142  
Db 127 LKSGTASVVCCLNNLYRKPRTKV 150

RESULT 14  
US-09-301-593-17  
; Sequence 17, Application US/09301593A  
; Publication No. US20020052480A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652.1890001  
; CURRENT APPLICATION NUMBER: US/09/301.593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-301-593-17

Query Match 85.1%; Score 656; DB 9; Length 220;  
Best Local Similarity 84.2%; Pred. No. 1.2e-42;  
Matches 123; Conservative 13; Mismatches 10; Indels 0; Gaps 0;  
  
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 60  
Db 11 LAVSVGEKVTMSCKSSQSVLYSRNQNYLAWFQKPGQSPKLLIFWASTRESGVDPDRFTG 70  
  
Qy 61 SSGTDTFTLTSSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120  
Db 71 SSGTDTFTLTSSLOAEDLAVYDCQYVSYPLTFGAGTKLELKRVAAPSVFIPPPSDEQ 130  
  
Qy 121 LKSGTASVVCCLNNFYPREAKVQMKV 146  
Db 131 LKSGTASVVCCLNNFYPREAKVQMKV 156

RESULT 15  
US-10-159-006-17  
; Sequence 17, Application US/10159006  
; Publication No. US20030143229A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saldanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility

; FILE REFERENCE: 0652.1890002  
; CURRENT APPLICATION NUMBER: US/10/159,006  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US 09/301,593  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: EP 98107925.4  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: US 60/086,049  
; PRIOR FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-159-006-17

Query Match 85.1%; Score 656; DB 14; Length 220;  
Best Local Similarity 84.2%; Pred. No. 1.2e-42;  
Matches 123; Conservative 13; Mismatches 10; Indels 0; Gaps 0;  
  
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 60  
Db 11 LAVSVGEKVTMSCKSSQSVLYSRNQNYLAWFQKPGQSPKLLIFWASTRESGVDPDRFTG 70  
  
Qy 61 SSGTDTFTLTSSLOAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120  
Db 71 SSGTDTFTLTSSLOAEDLAVYDCQYVSYPLTFGAGTKLELKRVAAPSVFIPPPSDEQ 130  
  
Qy 121 LKSGTASVVCCLNNFYPREAKVQMKV 146  
Db 131 LKSGTASVVCCLNNFYPREAKVQMKV 156

Search completed: March 8, 2005, 07:05:55  
Job time : 79.009 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.1636 Seconds  
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678.897 Million cell updates/sec

Title: US-09-784-950-34

Perfect score: 771

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	721	93.5	240	4	US-09-301-593-36
2	711.5	92.3	241	2	US-07-916-098A-56
3	677.5	87.9	239	4	US-09-627-896B-22
4	667	86.5	220	3	US-08-952-235-1
5	667	86.5	220	4	US-09-669-971-1
6	656	85.1	220	4	US-09-301-593-17
7	656	85.1	240	4	US-09-301-593-28
8	635	82.4	239	3	US-08-812-586-29
9	635	82.4	239	4	US-09-535-832A-30
10	601	78.0	214	4	US-09-472-087-71
11	598.5	77.6	235	4	US-09-472-087-14
12	598.5	77.6	235	4	US-09-472-087-65
13	597	77.4	226	4	US-09-456-090A-74
14	597	77.4	226	4	US-09-453-234-74
15	596	77.3	226	4	US-09-456-090A-86
16	596	77.3	226	4	US-09-453-234-86
17	595	77.2	224	4	US-09-456-090A-82
18	595	77.2	224	4	US-09-456-090A-88
19	595	77.2	224	4	US-09-456-090A-90
20	595	77.2	224	4	US-09-453-234-82
21	595	77.2	224	4	US-09-453-234-88
22	595	77.2	224	4	US-09-453-234-90
23	595	77.2	226	4	US-09-456-090A-80
24	595	77.2	226	4	US-09-453-234-80
25	593	76.9	226	4	US-09-456-090A-50
26	593	76.9	226	4	US-09-453-234-50
27	591	76.7	224	4	US-09-456-090A-36

28	591	76.7	224	4	US-09-453-234-36	Sequence 36, Appl
29	590	76.5	226	4	US-09-456-090A-38	Sequence 38, Appl
30	590	76.5	226	4	US-09-453-234-38	Sequence 38, Appl
31	589	76.4	146	4	US-09-472-087-21	Sequence 21, Appl
32	589	76.4	146	4	US-09-472-087-93	Sequence 93, Appl
33	589	76.4	226	4	US-09-456-090A-42	Sequence 42, Appl
34	589	76.4	226	4	US-09-453-234-42	Sequence 42, Appl
35	588	76.3	218	2	US-08-887-352B-13	Sequence 13, Appl
36	588	76.3	218	3	US-08-466-151-9	Sequence 9, Appl
37	588	76.3	218	3	US-09-109-207C-13	Sequence 13, Appl
38	588	76.3	218	3	US-09-296-005-13	Sequence 13, Appl
39	588	76.3	218	3	US-08-466-163B-9	Sequence 9, Appl
40	588	76.3	218	4	US-09-920-171-13	Sequence 13, Appl
41	588	76.3	218	4	US-09-802-096-9	Sequence 9, Appl
42	588	76.3	218	4	US-09-802-077-9	Sequence 9, Appl
43	588	76.3	218	4	US-09-716-028-13	Sequence 13, Appl
44	588	76.3	218	4	US-10-113-996-13	Sequence 13, Appl
45	587	76.1	218	5	PCT-US96-13152-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-301-593-36  
; Sequence 36, Application US/09301593A  
; Patent No. 6455677  
; GENERAL INFORMATION:  
; APPLICANT: Park, John E.  
; APPLICANT: Garin-Chesa, Pilar  
; APPLICANT: Bamberger, Uwe  
; APPLICANT: Leger, Olivier  
; APPLICANT: Saidanha, Jose W.  
; APPLICANT: Rettig, Wolfgang J.  
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility  
; FILE REFERENCE: 0652.1830001  
; CURRENT APPLICATION NUMBER: US/09/301.593A  
; CURRENT FILING DATE: 1999-04-29  
; EARLIER APPLICATION NUMBER: EP 98107925.4  
; EARLIER FILING DATE: 1998-04-30  
; EARLIER APPLICATION NUMBER: US 60/086,049  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-301-593-36

Query Match 93.5%; Score 721; DB 4; Length 240;  
Best Local Similarity 94.5%; Pred. No. 3.3e-62;  
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy	1	LAVSLGERATINCKSSQSVLYSFNNKYLAWYQKPGPKLLIYWASTRESGVDPDRFG 60
Db	31	LAVSLGERATINCKSSQSVLYSFNNKYLAWYQKPGPKLLIYWASTRESGVDPDRFG 90
Qy	61	SGSGTDTLTISLQAEADVYVYCOQYVSTPRTGQGTKEIKETVAAPSVEIFPPSDEQ 120
Db	91	SGFGTDTLTISLQAEADVYVYCOQYVSTPRTGQGTKEIKETVAAPSVEIFPPSDEQ 150
Qy	121	LKSGTASVVCLLNNFYPREAKVQWKV 146
Db	151	LKSGTASVVCLLNNFYPREAKVQWKV 176

RESULT 2  
US-07-916-098A-56  
; Sequence 56, Application US/07916098A  
; Patent No. 5871732  
; GENERAL INFORMATION:  
; APPLICANT: BURKLY, LINDA C.

APPLICANT: CHISHOLM, PATRICIA L.  
APPLICANT: THOMAS, DAVID W.  
APPLICANT: ROSA, MARGARET D.  
APPLICANT: ROSA, JOSEPH J.  
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
STREET: 10 SOUTH WACKER DRIVE  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: U.S.A.  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
FILING DATE: July 24, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/08843  
FILING DATE: No. 5871732ember 27, 1991  
CLASSIFICATION: 424  
APPLICATION NUMBER: 07/618,542  
FILING DATE: No. 5871732ember 27, 1990  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: JOHN J. MC DONNELL  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,310-G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 715-1000  
TELEFAX: (312) 715-1234  
TELEX: 910/221-5317  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-916-098A-56

Query Match 92.3%; Score 711.5; DB 2; Length 241;  
Best Local Similarity 94.5%; Pred. No. 2.8e-61;  
Matches 138; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPQPKLLIYWASTRESGVDRFSG 60  
Db 33 LAVSLGERATINCKSSGSLYSTQKNYLAWYQKQPQPKLLIYWASTRESGVDRFSG 92

Qy 61 SSGSTDFTLTSSLAEDVAVYCCQYVSTRTFGQTKVEIKRTVAAPSVFIPPSDEQ 120  
Db 93 SSGSTDFTLTSSLAEDVAVYCCQYVSY-RTEGRGKLEIKRTVAAPSVFIPPSDEQ 151

Qy 121 LKSGTASVCLNNFYPREAKVQKV 146  
Db 152 LKSGTASVCLNNFYPREAKVQKV 177

RESULT 3  
US-09-627-896B-22  
Sequence 22, Application US/09627896B  
Patent No. 6827934  
GENERAL INFORMATION:  
APPLICANT: CO, MAN SUNG  
APPLICANT: VASQUEZ, MAXIMILIANO  
APPLICANT: CARRENO, BEATRIZ  
APPLICANT: CELNIKER, ABBIE CHERYL  
APPLICANT: COLLINS, MARY

APPLICANT: GOLDMAN, SAMUEL  
APPLICANT: GRAY, GARY S.  
APPLICANT: KNIGHT, ANDREA  
APPLICANT: O'HARA, DENISE  
APPLICANT: RUP, BONITA  
APPLICANT: VELDMAN, GEBTRUIDA M.  
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS  
TITLE OF INVENTION: OF TREATMENT THEREWITH  
FILE REFERENCE: 08702.0081-01000  
CURRENT APPLICATION NUMBER: US/09/627,896B  
CURRENT FILING DATE: 2000-07-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Mus sp.  
FEATURE:  
OTHER INFORMATION: 3D1 light chain  
US-09-627-896B-22

Query Match 87.9%; Score 677.5; DB 4; Length 239;  
Best Local Similarity 91.1%; Pred. No. 5.4e-58;  
Matches 133; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPQPKLLIYWASTRESGVDRFSG 60  
Db 31 LAVSLGERATINCKSSQSLNSRTRENYLAWYQKQPQPKLLIYWASTRESGVDRFSG 90

Qy 61 SSGSTDFTLTSSLAEDVAVYCCQYVSTRTFGQTKVEIKRTVAAPSVFIPPSDEQ 120  
Db 91 SSGSTDFTLTSSLAEDVAVYCCSQSYNL-YTFGQGTKEIKRTVAAPSVFIPPSDEQ 149

Qy 121 LKSGTASVCLNNFYPREAKVQKV 146  
Db 150 LKSGTASVCLNNFYPREAKVQKV 175

RESULT 4  
US-08-952-235-1  
Sequence 1, Application US/08952235  
Patent No. 6207152  
GENERAL INFORMATION:  
APPLICANT: Schwall, Ralph H.  
APPLICANT: Tabor, Kelly H.  
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
TITLE OF INVENTION: Antagonists and Uses Thereof  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/952,235  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/460368  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P0938P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 220 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-952-235-1

Query Match 86.5%; Score 667; DB 3; Length 220;  
Best Local Similarity 84.2%; Pred. No. 5.1e-57;  
Matches 123; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAAYQKPGQPKLLIYWASTRESGVDPDRFG 60  
DB 11 LTVSVGEKVTVCSSQSLLYTSQKNYLAAYQKPGQPKLLIYWASTRESGVDPDRFG 70

QY 61 SGSGTDFLTITSSLOAEDVAVYQYVSTRTFGQTKVEIKRTVAAPSFIIPPDSDEQ 120  
DB 71 SGSGTDFLTITSVKADDLAVYQYVYVPTWTEGGGKLEIKRTVAAPSFIIPPDSDEQ 130

QY 121 LKSGTASVCLNNFYPREAKVQWKV 146  
DB 131 LKSGTASVCLNNFYPREAKVQWKV 156

RESULT 5  
US-09-669-971-1  
Sequence 1, Application US/09669971  
Patent No. 6468529  
GENERAL INFORMATION:  
APPLICANT: Schwall, Ralph H.  
Tabor, Kelly H.  
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor  
Antagonists and Uses Thereof  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/669,971  
FILING DATE: 05-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/952,235  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/460368  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P0938P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 220 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-669-971-1

Query Match 86.5%; Score 667; DB 4; Length 220;  
Best Local Similarity 84.2%; Pred. No. 5.1e-57;

Matches 123; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAAYQKPGQPKLLIYWASTRESGVDPDRFG 60  
DB 11 LTVSVGEKVTVCSSQSLLYTSQKNYLAAYQKPGQPKLLIYWASTRESGVDPDRFG 70

QY 61 SGSGTDFLTITSSLOAEDVAVYQYVSTRTFGQTKVEIKRTVAAPSFIIPPDSDEQ 120  
DB 71 SGSGTDFLTITSVKADDLAVYQYVYVPTWTEGGGKLEIKRTVAAPSFIIPPDSDEQ 130

QY 121 LKSGTASVCLNNFYPREAKVQWKV 146  
DB 131 LKSGTASVCLNNFYPREAKVQWKV 156

RESULT 6  
US-09-301-593-17  
Sequence 17, Application US/09301593A  
Patent No. 6455677  
GENERAL INFORMATION:  
APPLICANT: Park, John E.  
APPLICANT: Garin-Chesa, Pilar  
APPLICANT: Bamberger, Uwe  
APPLICANT: Leger, Olivier  
APPLICANT: Saldanha, Jose W.  
APPLICANT: Rettig, Wolfgang J.  
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
FILE REFERENCE: 0652.1890001  
CURRENT APPLICATION NUMBER: US/09/301,593A  
CURRENT FILING DATE: 1999-04-29  
EARLIER APPLICATION NUMBER: EP 98107925.4  
EARLIER FILING DATE: 1998-04-30  
EARLIER APPLICATION NUMBER: US 60/086,049  
EARLIER FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 220  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-301-593-17

Query Match 85.1%; Score 656; DB 4; Length 220;  
Best Local Similarity 84.2%; Pred. No. 5.9e-56;  
Matches 123; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAAYQKPGQPKLLIYWASTRESGVDPDRFG 60  
DB 11 LTVSVGEKVTVCSSQSLLYTSQKNYLAAYQKPGQPKLLIYWASTRESGVDPDRFG 70

QY 61 SGSGTDFLTITSSLOAEDVAVYQYVSTRTFGQTKVEIKRTVAAPSFIIPPDSDEQ 120  
DB 71 SGSGTDFLTITSVKADDLAVYQYVYVPTWTEGGGKLEIKRTVAAPSFIIPPDSDEQ 130

QY 121 LKSGTASVCLNNFYPREAKVQWKV 146  
DB 131 LKSGTASVCLNNFYPREAKVQWKV 156

RESULT 7  
US-09-301-593-28  
Sequence 28, Application US/09301593A  
Patent No. 6455677  
GENERAL INFORMATION:  
APPLICANT: Park, John E.  
APPLICANT: Garin-Chesa, Pilar  
APPLICANT: Bamberger, Uwe  
APPLICANT: Leger, Olivier  
APPLICANT: Saldanha, Jose W.  
APPLICANT: Rettig, Wolfgang J.  
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility  
FILE REFERENCE: 0652.1890001  
CURRENT APPLICATION NUMBER: US/09/301,593A

	Best Local Similarity	86.3%;	Pred. No.	7.1e-54;	
	Matches	126;	Conservative	6;	Mismatches 14; Indels 0; Gaps 0;
Qy	1	LAVSLGERATINCKSSOSVLYSFNNKNYLA	WYQQKPGQP	PKLLIYWASTRESGV	PDRESG 60
Dd	30	LAVSLGERATINCKSSOSVLYSNNKNYLA	WYQQKPGQA	PRLLIYDASSRATG	IPDRFSG 89
Qy	61	SGSGTDFTLTISSIQABDVAVYYCQYYSTPRTFGQGTKEIKRTVAAPS	VFIPPPSDEQ	120	
Dd	90	SGSGTDFTLTISSLRPEDFAVYYGQYGSPLTFGGGTKEIKRTVAAPS	VFIPPPSDEQ	149	
Qy	121	LKSGTASVCLLNFPY	PREAKVQWKV	146	
Dd	150	LKEITASVVGILLNFPY	PREAKVQWKV	175	
 RESULT 9					
US-09-535-832A-30					
; Sequence 30, Application US/09535832A					
; Patent No. 6537769					
; GENERAL INFORMATION:					
; APPLICANT: Tilson, Martin David					
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated					
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and					
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof					
; FILE REFERENCE: 53862-AZ					
; CURRENT APPLICATION NUMBER: US/09/535,832A					
; CURRENT FILING DATE: 2000-03-28					
; NUMBER OF SEQ ID NOS: 57					
; SOFTWARE: PatentIn Ver. 2.1					
; SEQ ID NO 30					
; LENGTH: 239					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-09-535-832A-30					
 Query Match 82.4%; Score 635; DB 4; Length 239;					
Best Local Similarity 86.3%; Pred. No. 7.1e-54;					
Matches 126; Conservative 6; Mismatches 14; Indels 0; Gaps 0;					
Qy	1	LAVSLGERATINCKSSOSVLYSFNNKNYLA	WYQQKPGQP	PKLLIYWASTRESGV	PDRESG 60
Dd	30	LAVSLGERATINCKSSOSVLYSNNKNYLA	WYQQKPGQA	PRLLIYDASSRATG	IPDRFSG 89
Qy	61	SGSGTDFTLTISSIQABDVAVYYCQYYSTPRTFGQGTKEIKRTVAAPS	VFIPPPSDEQ	120	
Dd	90	SGSGTDFTLTISSLRPEDFAVYYGQYGSPLTFGGGTKEIKRTVAAPS	VFIPPPSDEQ	149	
Qy	121	LKSGTASVCLLNFPY	PREAKVQWKV	146	
Dd	150	LKEITASVVGILLNFPY	PREAKVQWKV	175	
 RESULT 10					
US-09-472-087-71					
; Sequence 71, Application US/09472087					
; Patent No. 6682736					
; GENERAL INFORMATION:					
; APPLICANT: HANSON, DOUGLAS C.					
; APPLICANT: NEVEU, MARK J.					
; APPLICANT: MUELLER, EILEEN E.					
; APPLICANT: HANKE, JEFFREY H.					
; APPLICANT: GILMAN, STEVEN C.					
; APPLICANT: DAVIS, C. GEOFFREY					
; APPLICANT: CORVALAN, JOSE R.					
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4					
; FILE REFERENCE: ABX-PF1					
; CURRENT APPLICATION NUMBER: US/09/472,087					
; CURRENT FILING DATE: 1999-12-23					
; PRIOR APPLICATION NUMBER: 60/113,647					
; PRIOR FILING DATE: 1998-12-23					
; NUMBER OF SEQ ID NOS: 147					
; SOFTWARE: PatentIn Ver. 2.1					

Query Match 82.4%; Score 635; DB 3; Length 239;



```
; SEQ ID NO 71
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-71

Query Match      78.0%; Score 601; DB 4; Length 214;
Best Local Similarity 79.5%; Pred. No. 1.2e-50;
Matches 116; Conservative 10; Mismatches 14; Indels 6; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 11 LSAVSGRVTTITCRASQSI-----NSYLDWYQKPGKAPKLLIYAASSLSQSGVPSRFSG 64

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 65 SGSGTDFTLTISLQEPEDFAVYCCQYYSPTPTFGPGTKVEIKRTVAAPSVFIPPPSDEQ 124

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 125 LKSGTASVVCLLNNFYPREAKVQWKV 150

RESULT 11
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-14

Query Match      77.6%; Score 598.5; DB 4; Length 235;
Best Local Similarity 78.8%; Pred. No. 2.4e-50;
Matches 115; Conservative 15; Mismatches 11; Indels 5; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LSLSPGERATLSCRASQSISSP-----LAWYQORPGQAPRLLIYGASSRATGIPDRFSG 85

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 86 SGSGTDFTLTISLQEPEDFAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 145

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 146 LKSGTASVVCLLNNFYPREAKVQWKV 171

RESULT 12
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-14

Query Match      77.6%; Score 598.5; DB 4; Length 235;
Best Local Similarity 78.8%; Pred. No. 2.4e-50;
Matches 115; Conservative 15; Mismatches 11; Indels 5; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LSLSPGERATLSCRASQSISSP-----LAWYQORPGQAPRLLIYGASSRATGIPDRFSG 85

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 86 SGSGTDFTLTISLQEPEDFAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 145

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 146 LKSGTASVVCLLNNFYPREAKVQWKV 171

RESULT 13
US-09-456-090A-74
; Sequence 74, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-456-090A-74

Query Match      77.4%; Score 597; DB 4; Length 226;
Best Local Similarity 78.9%; Pred. No. 3.2e-50;
Matches 116; Conservative 15; Mismatches 10; Indels 6; Gaps 2;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 11 LSLSPGERATLSCRASQGV-----SSSYLAWYQOKPGQAPRLLIYGASSRATGIPDRFSG 65

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDE 119
Db 66 SGSGTDFTLTISLQEPEDFAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDE 125

Qy 120 QKSGTASVVCLLNNFYPREAKVQWKV 146
Db 126 QKSGTASVVCLLNNFYPREAKVQWKV 152
```

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; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match      77.6%; Score 598.5; DB 4; Length 235;
Best Local Similarity 78.8%; Pred. No. 2.4e-50;
Matches 115; Conservative 15; Mismatches 11; Indels 5; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LSLSPGERATLSCRASQSISSP-----LAWYQORPGQAPRLLIYGASSRATGIPDRFSG 85

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 86 SGSGTDFTLTISLQEPEDFAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 145

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 146 LKSGTASVVCLLNNFYPREAKVQWKV 171

RESULT 13
US-09-456-090A-74
; Sequence 74, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-456-090A-74

Query Match      77.4%; Score 597; DB 4; Length 226;
Best Local Similarity 78.9%; Pred. No. 3.2e-50;
Matches 116; Conservative 15; Mismatches 10; Indels 6; Gaps 2;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQOKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 11 LSLSPGERATLSCRASQGV-----SSSYLAWYQOKPGQAPRLLIYGASSRATGIPDRFSG 65

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDE 119
Db 66 SGSGTDFTLTISLQEPEDFAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDE 125

Qy 120 QKSGTASVVCLLNNFYPREAKVQWKV 146
Db 126 QKSGTASVVCLLNNFYPREAKVQWKV 152
```



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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.5893 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-35

Perfect score: 803

Sequence: 1 NPQTLTLCTFGSFLITR.....SESTALGLVLYKDFPFPVT 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Pir1.\*
- 2: Pir2.\*
- 3: Pir3.\*
- 4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	507.5	63.2	124	2 A49002	Ig heavy chain V r
2	461.5	57.5	374	2 S69339	Ig heavy chain V r
3	452	56.3	138	2 S31513	Ig heavy chain - h
4	430	53.5	119	2 S18555	Ig heavy chain V r
5	412.5	51.4	472	2 S31459	Ig gamma-1 chain -
6	412	51.3	121	1 GIHURH	Ig heavy chain V-I
7	411	51.2	121	2 A36005	Ig heavy chain V r
8	409	50.9	220	2 A49444	Ig gamma-1 heavy c
9	407	50.7	125	1 MHUUMC	Ig heavy chain V-I
10	391.5	48.8	470	2 S22080	Ig heavy chain pre
11	390.5	48.6	118	2 S18556	Ig heavy chain V r
12	389	48.4	231	2 PC4155	Ig gamma-2b chain
13	375.5	46.8	241	2 S69131	Ig heavy chain (DO
14	373.5	46.5	122	2 S11740	Ig heavy chain pre
15	364.5	45.4	143	2 PT0174	Ig heavy chain V r
16	363.5	45.3	113	2 S26465	Ig heavy chain V r
17	361	45.0	96	2 S26923	Ig heavy chain pre
18	359.5	44.8	147	1 G2HUCS	Ig heavy chain pre
19	355	44.2	96	2 S26924	Ig heavy chain V r
20	353	44.0	107	2 A49442	Ig heavy chain V r
21	351.5	43.8	120	1 GIHUCO	Ig heavy chain V-I
22	348.5	43.4	220	2 S68211	Ig heavy chain (Ma
23	348.5	43.4	444	2 PC4346	monoclonal antibod
24	347	43.2	231	2 B23746	Ig Fab region IV-J
25	345	43.0	143	2 S23624	Ig heavy chain V r
26	339.5	42.3	116	2 S26328	Ig heavy chain V r
27	337	42.0	119	1 GIHUDW	Ig heavy chain V-I
28	335	41.7	96	2 S26922	Ig heavy chain V r
29	330	41.1	121	2 S09959	Ig heavy chain V r

30	330	41.1	592	2 S25705	Ig mu chain - shee
31	328.5	40.9	254	2 B31790	Ig heavy chain V r
32	325.5	40.5	568	2 A34891	Ig heavy chain pre
33	325	40.5	149	2 S30752	Ig heavy chain pre
34	325	40.5	213	2 S68213	Ig heavy chain (Ma
35	321.5	40.0	126	1 MHUOUU	Ig heavy chain V-I
36	319.5	39.8	548	2 S38864	Ig epsilon chain C
37	312.5	38.9	129	2 S44114	Ig heavy chain V r
38	309	38.5	144	1 G2MS14	Ig heavy chain pre
39	309	38.5	246	2 S38950	Ig gamma chain - m
40	309	38.5	446	2 S40295	Ig gamma-2a chain
41	307	38.2	221	2 S49220	Ig gamma-1 chain -
42	306.5	38.2	144	2 S11244	Ig gamma-2a chain
43	306.5	38.2	171	2 S23623	Ig heavy chain V r
44	304.5	37.9	474	1 G2MS11	Ig gamma-2b chain
45	304	37.9	103	2 B25913	Ig heavy chain pre

ALIGNMENTS

RESULT 1

A49002  
Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C:Accession: A49002  
R:Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.;  
Arthritis Rheum. 35, 900-904, 1992  
A:Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene  
A:Reference number: A49002; MUID:92352481; PMID:1322670  
A:Accession: A49002  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-124 <STU>  
A:Cross-references: GB:M90808; NID:G185515; PIDN:AA52989.1; PID:G567176  
A:Experimental source: EBV-transformed lymphoblastoid cell line SSH23  
A>Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBIIP:110262)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 63.2%; Score 507.5; DB 2; Length 124;  
Best Local Similarity 87.4%; Pred. No. 1.4e-38;

Matches 97; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Qy 2 PQTLTLCTFGSFLITRGVGVGWIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITK 61

Db 14 PTQTLTLCTFGSFLSTSGVGWIRQPPGKALEWLALYWNDDRYSPSLKSLRTITK 73

Qy 62 DTSKNQVLLTMTNMDPVDATYTCYCAHHFFDSSGYI-PFDSWGQGLTVSVSS 111

Db 74 DTSKNQVLLTMTNMDPVDATYTCYCAHWTVDSSGYLGFYWGQGLTVTVSS 124

RESULT 2

S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamlich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687; PMID:7744049  
A:Accession: S69339  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
R:Khamlich, A.A.  
submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664

A;Accession: S72664  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140, 'C', 142-374 <KH2>  
A;Cross-references: EMBL:X81695  
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 57.5%; Score 461.5; DB 2; Length 374;  
Best Local Similarity 58.9%; Pred. No. 6.2e-34;  
Matches 96; Conservative 12; Mismatches 30; Indels 25; Gaps 4;

QY 2 PQTLLTLCFSGFSILTRGVGDWIRQPPGKALQWLALIYWDDKRYSPSLKSRLTIITK 61  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 33 PTQTLLTLCFSGFSLSKSGVGVGWIRQPPGQALEWLALIFWDDDKRYSPLSRLTIITK 92  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 62 DTSKNQVLVTMTNMDPVDATYYCAHHFFDSSGY---YPDSDMGQGTLVSVSASTK--- 115  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 93 DTSKNQVLVTMTNMDPADTATYTCG---YSVVGQGYRFHSMGQGTLTVTVSSEPKCDK 149  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 116 -----GPSVFPELPACSRST--SESTAALGLVKD 142  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 150 THTCPAPPELLGGPSVFLFPKPCKDTLMISRTPEVTCVVVD 192  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3  
IG heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S31513  
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.  
submitted to the EMBL Data Library, December 1992  
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies in Sjögren's syndrome  
A;Reference number: S31509  
A;Accession: S31513  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-138 <CHA>  
A;Cross-references: EMBL:X69861; NID:g33084; PIDN:CAA49495.1; PID:g33085  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;30-114/Domain: immunoglobulin homology <IMM>

Query Match 56.3%; Score 452; DB 2; Length 138;  
Best Local Similarity 79.8%; Pred. No. 1.5e-33;  
Matches 87; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 2 PQTLLTLCFSGFSILTRGVGDWIRQPPGKALQWLALIYWDDKRYSPSLKSRLTIITK 61  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 29 PTQTLLTLCFSGFSLSKSGVGVGWIRQPPGKTLEWLALTYWDDDKRYSPLSRLTIITK 88  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 62 DTSKNQVLVTMTNMDPVDATYYCAHHFFDSSGYYPDPDSMGQGTLYSVS 110  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 89 DTSQNQVLVTMTNMDPVDATYYCAHRPGIAVTGNGFDYWGQGTLTVVS 137  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4  
S18555  
IG heavy chain V region precursor (VII-5) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 06-Jun-1997 #text\_change 21-Jul-2000  
C;Accession: S18555  
R;Shin, E.K.; Matsuda, F.; Nagaoaka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Higashiura, T.  
EMBO J. 10, 3641-3645, 1991  
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cloning and sequencing of the 3' terminal exon and intron  
A;Accession: S18555  
A;Molecule type: DNA  
A;Residues: 1-119 <SHI>  
A;Cross-references: EMBL:X62111; NID:g37839; PIDN:CAA44021.1; PID:g3980125  
C;Genetics:  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Mol. Immunol. 26, 841-850, 1989  
A1: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2  
A: Reference number: S06610; MUID: 90097956; PMID: 2513487



Search completed: March 8, 2005, 06:39:28  
Job time : 10.6393 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 55.644 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-35

Perfect score: 803

Sequence: 1 NPQTLTLTCTFSGSLITR.....SESTAALGCLVKDYFPEPVT 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	453	56.4	121	2 Q9UL96	Q9UL96 homo sapien
2	453	56.4	476	2 Q6GMX1	Q6GMX1 homo sapien
3	448.5	55.9	465	2 Q6GMX6	Q6GMX6 homo sapien
4	445	55.4	476	2 Q6WZX7	Q6WZX7 homo sapien
5	442.5	55.1	473	2 Q8TC63	Q8TC63 homo sapien
6	426.5	53.1	473	2 Q8P055	Q8P055 homo sapien
7	422.5	52.6	544	2 Q8PJ95	Q8PJ95 homo sapien
8	420	52.3	493	2 Q68CN4	Q68CN4 homo sapien
9	416	51.8	472	2 Q6N089	Q6N089 homo sapien
10	412	51.3	121	1 HV2E_HUMAN	Q6N093 homo sapien
11	412	51.3	121	1 HV2E_HUMAN	Q6N093 homo sapien
12	410	51.1	470	2 Q8PJ44	Q6PJ44 homo sapien
13	408	50.8	464	2 Q6MZU6	Q6MZU6 homo sapien
14	407	50.7	125	1 HV2D_HUMAN	P01817 homo sapien
15	403	50.2	466	2 Q6IN78	Q6IN78 homo sapien
16	403	50.2	482	2 Q7Z351	Q7Z351 homo sapien
17	401	49.9	480	2 Q6N094	Q6N094 homo sapien
18	397.5	49.5	465	2 Q6P6C4	Q6P6C4 homo sapien
19	396	49.3	478	2 Q6P181	Q6P181 homo sapien
20	392	48.8	521	2 Q6N4Y9	Q6N4Y9 homo sapien
21	391.5	48.8	473	2 Q6MZV7	Q6MZV7 homo sapien
22	389.5	48.5	475	2 Q6MZQ6	Q6MZQ6 homo sapien
23	385.5	48.0	475	2 Q6N095	Q6N095 homo sapien
24	383.5	47.8	518	2 Q6N030	Q6N030 homo sapien
25	378	47.1	466	2 Q6N096	Q6N096 homo sapien
26	378	47.1	470	2 Q7Z5W1	Q7Z5W1 homo sapien
27	375	46.7	492	2 Q7Z374	Q7Z374 homo sapien
28	373.5	46.5	481	2 Q6N097	Q6N097 homo sapien
29	365.5	45.5	469	2 Q7Z7P5	Q7Z7P5 homo sapien
30	364	45.3	208	2 Q8ZP87	Q8ZP87 homo sapien
31	359.5	44.8	147	1 HV2H_HUMAN	P04438 homo sapien

32	359.5	44.8	475	2 Q6GMW7	Q6GMW7 homo sapien
33	359.5	44.8	605	2 Q6GN83	Q6GN83 xenopus lae
34	358.5	44.6	118	2 Q811U5	Q811U5 mus musculus
35	357.5	44.5	496	2 Q6KXK8	Q6KXK8 homo sapien
36	357	44.5	480	2 Q6PJF1	Q6PJF1 homo sapien
37	354.5	44.1	147	2 Q9Y509	Q9Y509 homo sapien
38	351.5	43.8	120	1 HV2B_HUMAN	P01815 homo sapien
39	351.5	43.8	471	2 Q66K04	Q66K04 mus musculus
40	348.5	43.4	595	2 Q8WUX4	Q8WUX4 homo sapien
41	348.5	43.4	597	2 Q6GMX5	Q6GMX5 homo sapien
42	348.5	43.4	597	2 Q9BU10	Q9BU10 homo sapien
43	348.5	43.4	625	2 Q96AA6	Q96AA6 homo sapien
44	348	43.3	97	2 Q43234	Q43234 homo sapien
45	345.5	43.0	597	2 Q9BQ88	Q9BQ88 homo sapien

ALIGNMENTS

RESULT 1  
Q9UL96 PRELIMINARY; PRT; 121 AA.  
AC Q9UL96;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035018; AAD56254.1; -.  
DR HSSP; P01820; 1A7N  
DR InterPro; IPR007110; Ig-like.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 1.  
FT NON\_TER 1 121  
FT NON\_TER 121 121  
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match 56.4%; Score 453; DB 2; Length 121;

Best Local Similarity 80.9%; Pred. No. 2.2e-37;

Matches 89; Conservative 4; Mismatches 15; Indels 2; Gaps 2;

Qy	2	PQTTLTCTFSGSLTRGVGVNIRQPPGKALQWLAIYNDKRYSPSLKRLTITK	61
Db	14	PTQTLTCTFSGSLTSGMDVGVIRQPPGKALEWLIYDNDKRYSPSLKRLTITK	73

Qy 62 DTSKNQVLTWMDPVDATYTCYCAHFFDSSGGYYPFDSMGQGLTVSVSS 111

Db 74 DTSKNQVLTWMDPVDATYTCYCAHFFDSSGGYYPFDSMGQGLTVSVSS 121

RESULT 2

Q6GMX1 PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073773; AAH73773.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig.cl.
DR InterPro: IPR003006; Ig.MHC.
DR InterPro: IPR003596; Ig.v.
DR Pfam: PF07654; C1-set; 3.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 56.4%; Score 453; DB 2; Length 476;
Best Local Similarity 59.9%; Pred. No. 1.1e-36;
Matches 91; Conservative 17; Mismatches 40; Indels 4; Gaps 1;

Qy 2 PQTTLTCTFSGFLITRGVGDWIRQPPGKALQWLALIYWNDDKRYSPSLKSLRITK 61
Db 33 PSQFLSLTCTVSGGSISSGDIYVWIRQPPGKLEWIGIYIYSGTYPNPSLKSRTVLS 92
Qy 62 DTSKNQVLTMTNMDPVDATYTCYCAH----HFFDSSGYYPFDSWGQGLVSVSSASTKGP 117
Db 93 DTSKNQSLKXNSVTAADTAVYFCARAGVGSFSSWALDGNFNGQGTMTVSSASTKGP 152
Qy 118 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTV 149
Db 153 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTV 184

RESULT 3
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073766; AAH73766.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig.cl.
DR InterPro: IPR003006; Ig.MHC.
DR InterPro: IPR003596; Ig.v.
DR Pfam: PF07654; C1-set; 3.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 55.9%; Score 448.5; DB 2; Length 465;
Best Local Similarity 61.5%; Pred. No. 3.1e-36;
Matches 91; Conservative 15; Mismatches 35; Indels 7; Gaps 2;

Qy 2 PQTTLTCTFSGFLITRGVGDWIRQPPGKALQWLALIYWNDDKRYSPSLKSLRITK 61
Db 33 PSETLSLTCTVSGGSI--SGYVSWIRQPPAGKLEWIGRIYTGSTYNPNSLKSRTVMSV 90
Qy 62 DTSKNQVLTMTNMDPVDATYTCYCAHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 91 DTSKNQSLKXNSVTAADTAVYFCARGRFY-----FDYWGQGLTVSVSSASTKGPSVFP 145
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPTV 149
Db 146 LAPSSKSTSGTAAALGCLVKDYFPEPTV 173

RESULT 4
Q6GMX7 PRELIMINARY; PRT; 476 AA.
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFP686M24218.
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GN Name=DKFZp666M24218;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BX640824; CAB45900.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52420 MW; 0D3D1FFB5853958F CRC64;

Query Match 55.4%; Score 445; DB 2; Length 476;
Best Local Similarity 59.9%; Pred. No. 7.1e-36;
Matches 88; Conservative 18; Mismatches 37; Indels 4; Gaps 2;

Qy 5 TLTLTFCGSLITRGVGVDMIRQPGKALQWLALYWNDDKRYSPSLKSLRLTIKDT 64
Db 43 TSLTSCVDPDGLSDSSYGMIRQPGKGLWIGTVSYGTPTTSLKSLRLTIHVDPS 102

Qy 65 KNQVLTWMTNMDPVDATYYC-AHHFFDSSGYPPFDSWGOGTLVSVSSASTKGPSVF 122
Db 103 KSQIFLTLTSTAAADTAVYTCVRGGYSFASAPFF--WGQGAFTVSSASTKGPSVFPL 160

Qy 123 APCSRSTSESTAALGCLVKDYFPEPT 149
Db 161 APCSRSTSESTAALGCLVKDYFPEPT 187

RESULT 5
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGH4 protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC025985; AAH25985.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER BLUE; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 55.1%; Score 442.5; DB 2; Length 473;
Best Local Similarity 59.1%; Pred. No. 1.3e-35;
Matches 88; Conservative 18; Mismatches 38; Indels 5; Gaps 2;

Qy 2 PQTTLTCTFCGSLITRGVGVDMIRQPGKALQWLALYWNDDKRYSPSLKSLRLTIK 61
Db 40 PSVTLTSLTCTVSGDSVASSYVMGWVQRQPGKGLWIGTVSYGTPTTSLKSLRLTIK 99

Qy 62 DTSKNQVLTWMTNMDPVDATYYC-AHHFFDSSGYPPFDSWGOGTLVSVSSASTKGPSVF 120
Db 100 DMSSESYLKLDSTVTAADTAVYTCVRGGYSFASAPFF--WGQGAFTVSSASTKGPSVF 155

Qy 121 PLAPCSRSTSESTAALGCLVKDYFPEPT 149
Db 156 PLAPCSRSTSESTAALGCLVKDYFPEPT 184

RESULT 6
Q6P055 PRELIMINARY; PRT; 473 AA.
AC Q6P055
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Peripheral Nervous System;
RC Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 53.18; Score 426.5; DB 2; Length 473;
Best Local Similarity 56.34; Pred. No. 5e-34;
Matches 85; Conservative 22; Mismatches 39; Indels 5; Gaps 2;

QY 2 PQTTLTCTCFGSLITRGVGVDMIRQPGKALQWLALIYWNDD---KRYSPSLKSLT 58
DB 33 PGSLTSLCTSGSFTF--SGANLSWVRQAPGKLEWAVRQTEDDGCTTGYIAVGRFT 90

QY 59 ITKDTSKNQVLTMTNMPDVTATYCAHFFDSSGYYPFDSWGQGTILVSVSSASTKGPS 118
DB 91 VSRDSSRLTYLQMSDLRTDTAFYFCATGSMNTVGLTGFDSWGQGTILVSVSSASTKGPS 150

QY 119 VFPLAPCSRSTSESTAALGCLVKDYFPEPTV 149
DB 151 VFPLAPSKSTSGGTAALGCLVKDYFPEPTV 181

RESULT 7
Q6PJ95 ID Q6PJ95 PRELIMINARY; PRT; 544 AA.
AC Q6PJ95;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;

Query Match 52.84; Score 422.5; DB 2; Length 544;
Best Local Similarity 55.84; Pred. No. 1.5e-33;
Matches 87; Conservative 19; Mismatches 37; Indels 13; Gaps 4;

QY 2 PQTTLTCTCFGSLITRGVGVDMIRQPGKALQWLALIYWNDDKRYSPSLKSLTIT 60
DB 33 PGSLTSLCTSGSFTF--SNYGMHVRQAPGKLEWAVRQTEDDGCTTGYIAVGRFTIS 90

QY 61 KDTSKNQVLTMTNMPDVTATYCAHFFDSSGYYP-----FDSWGQGTILVSVSSAS 113
DB 91 RDNKNTLSLQMSLRLVADTAVYCAK---DQKPWYSNSWFLNFDNSWGRTILVTVSSAS 147

QY 114 TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTV 149
DB 148 TKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTV 183

RESULT 8
Q68CN4 ID Q68CN4 PRELIMINARY; PRT; 493 AA.
AC Q68CN4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKF2p686E23209 (Fragment).
GN Name=DKF2p686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Rectum tumor;
RC The German cDNA Consortium;
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749861; CAH18705.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
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DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS0835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 493 AA; 54117 MW; A1E4F5ED3FA8AB40 CRC64;  
Query Match 52.3%; Score 420; DB 2; Length 493;  
Best Local Similarity 55.3%; Pred. No. 2.3e-33;  
Matches 84; Conservative 19; Mismatches 43; Indels 6; Gaps 3;  
Qy 2 PQTTLTCTFSGFLITRGVGVDMIRQPPGKALQWLALIIYNNDDK-RYSPSLKSLRLTIT 60  
Db 56 PGKSVRLSCAASGFTF--YAMHWVRQSPGRLEWAVISYEGGKHVADSVKGRATIS 113  
Qy 61 KDTSKNQVLTMTNMDPVDITATYCAHHFFDSSGY---YPFDSWGQGLTVSVSSASTKGP 117  
Db 114 RDNSENKTVSLQSLGSLTDTGVYICARDFLPLSSWHTNYALDVMGQGTAVIVSSASTKGP 173  
Qy 118 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 174 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVT 205  
RESULT 9  
Q6N089 PRELIMINARY; PRT; 472 AA.  
AC Q6N089;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686P15220.  
GN Name=DKFZp686P15220;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640627; CAE45781.1; --  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig c1.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS0835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;  
Query Match 51.8%; Score 416; DB 2; Length 472;  
Best Local Similarity 54.5%; Pred. No. 5.6e-33;  
Matches 84; Conservative 19; Mismatches 39; Indels 12; Gaps 4;  
Qy 2 PQTTLTCTFSGFLITRGVGVDMIRQPPGKALQWLALIIYNNDDK-RYSPSLKSLRLTIT 60  
Db 33 PGRSLRLSCAASGFTF--DDYAMHWVRQAPGKLEWVSGISWNSGSIAYADSVKGRFTIS 90  
Qy 61 KDTSKNQVLTMTNMDPVDITATYTC-----AHHFFDSSGYYPFDSWGQGLTVSVSSASTK 115  
Db 114 RDNSENKTVSLQSLGSLTDTGVYICARDFLPLSSWHTNYALDVMGQGTAVIVSSASTKGP 173

Db 91 RDNGKNSLYQMNSLRADTALYYCAKEIGHNFFY-----YYGDMVGGGTTTVTVSSASTK 146  
Qy 116 GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 147 GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVT 180  
RESULT 10  
ID HV2E HUMAN STANDARD; PRT; 121 AA.  
AC P01818;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig heavy chain V-II region HE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=70114712; PubMed=5264153;  
RA Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;  
RT "Subgroups of amino acid sequences in the variable regions of immunoglobulin heavy chains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 64:997-1003 (1969).  
CC -I- MISCELLANEOUS: This gamma-1 chain was isolated from a myeloma protein.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR; A02093; GIHHE.  
DR HSSP; P01820; IATN.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS0835; IG LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin V region;  
KW Pyrolidone carboxylic acid.  
FT DOMAIN 1 120 Ig-like.  
FT MOD\_RES 1 121 Pyrolidone carboxylic acid.  
FT NON\_TER 121 121  
SQ SEQUENCE 121 AA; 13483 MW; 89A5082C273753B4 CRC64;  
Query Match 51.3%; Score 412; DB 1; Length 121;  
Best Local Similarity 70.4%; Pred. No. 2.8e-33;  
Matches 81; Conservative 9; Mismatches 13; Indels 12; Gaps 3;  
Qy 2 PQTTLTCTFSGFLITRGVGVDMIRQPPGKALQWLALIIYNNDDKRYSPSLKSLRLTIT 60  
Db 14 PTELTLTCTLSGLSLTDTGVAVGIRQPGRALEWLAWLLYWDKKRFSFLKSLRLTIT 73  
Qy 61 KDTSKNQVLTMTNMDPVDITATYCAHHFFDSSGYP-----FDSWGQGLTVSVSS 111  
Db 74 RDTSKNQVLTMTNMDPVDITATYTCVHR-----HPRTLAFVWGQGTAVIVSS 121  
RESULT 11  
Q6N093 PRELIMINARY; PRT; 417 AA.  
ID Q6N093  
AC Q6N093;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686I04196 (Fragment).  
GN Name=DKFZp686I04196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]



```
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 50.8%; Score 408; DB 2; Length 464;
Best Local Similarity 54.0%; Pred. No. 3.4e-32;
Matches 81; Conservative 22; Mismatches 39; Indels 8; Gaps 3;

Qy 2 PQTTLTCTSGSLITRGVGVWIRPPGKALQWLALI--YWNDDKRYSPSLKSLRLTITK 59
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 33 PGSLRLSCAASGFTF--SSYSMMWVRQAPGKLEWVSFSSRGSGSYEYVADSVKGRFTI 90
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 60 TKDTSKNQVLTWNTMDPVDVTATYCAHHFFDSSGYYPFDSWGQGLTVSVSSASTKGPSV 119
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 91 SRDNKNSLYLQMSLRARNTATYVYCARDL---GWFGLDYWGQGLTVTVSSASTKGPSV 146
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 120 FPLAPCSRSTSESTAALGCLVKDYFPEPTV 149
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 147 FPLAPCSRSTSESTVALGCLVKDYFPEPTV 176
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
ID HV2D HUMAN STANDARD; PRT; 125 AA.
AC P01817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG heavy chain V-II region MCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=81118242; PubMed=6780622;
RA Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,
RA Litman G.W.;
RT "Molecular basis for the temperature-dependent insolubility of
RT cryoglobulins. X. The amino acid sequence of the heavy chain variable
RT region of McE.";
RL J. Immunol. 126:1212-1216(1981).
CC -!- MISCELLANEOUS: This chain was derived from a monoclonal IgM
CC -!- cryoglobulin.
CC PIR; A02092; MHUUMC.
DR HSSP; P01820; 1A7N.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
FT Pyrolysine carboxylic acid.
FT DOMAIN 1 113 Ig-like.
FT MOD_RES 1 1 Pyrolysine carboxylic acid.
FT NON_TER 125 125
SQ SEQUENCE 125 AA; 13783 MW; 7A1ADF4C40F47BB5 CRC64;

Query Match 50.7%; Score 407; DB 1; Length 125;
Best Local Similarity 71.9%; Pred. No. 9.1e-33;
Matches 82; Conservative 9; Mismatches 17; Indels 6; Gaps 2;

Qy 2 PQTTLTCTSGSLITRGVGVWIRPPGKALQWLALIYWNDDKRYSPSLKSLRLTITK 61
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 14 PTETLTCTSGSLTSGVGVWIRQRPKALEWLAFINWDDNRYSPSLRSLRSLTGTK 73
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 62 DTSKNQVLTWNTMDPVDVTATYCAH---HFFDSSGYYPFDSWGQGLTVSVSS 111
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 74 DTSRNVLTITNMDPVDVDSGTYFCAHRPPWRFTGNL--GFDXWGQGLTVSVSS 125
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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RESULT 15
Q6IN78 PRELIMINARY; PRT; 466 AA.
ID Q6IN78
AC Q6IN78;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDE81076E CRC64;

Query Match 50.2%; Score 403; DB 2; Length 466;
Best Local Similarity 54.7%; Pred. No. 1.1e-31;
Matches 82; Conservative 21; Mismatches 37; Indels 10; Gaps 3;

Qy 2 PQTTLTCTSGSLITRGVGVWIRPPGKALQWLALIYWNDDKRYSPSLKSLRLTITK 61
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 33 PGSLTILSCAASGLTVSSN--YMHVVRQAPGKLEWVSVLIGATYVADSVKGRFTISR 90
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 62 DTSKNQVLTWNTMDPVDVTATYCAHHFFDSSGY--PFDSWGQGLTVSVSSASTKGPSV 119
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 91 DNSKNTLYLQMSLRARNTATYVYCAR-----GNVVPAPAPWGQGLTVTVSSASTKGPSV 144
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 120 FPLAPCSRSTSESTAALGCLVKDYFPEPTV 149
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

Db 145 FPLAPSSKSTGGTAALGCLVKDYFPEPVT 174

Search completed: March 8, 2005, 06:35:54  
Job time : 56.644 secs



GenCore version 5.1.6  
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## QM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 69.0805 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-35

Perfect score: 803

Sequence: 1 NPQTTTLTCTFGSLITR.....SESTALGCLVVDYFPEPVT 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

- 1: A\_Geneseq\_16Dec04:\*
- 2: Geneseqpl9808:\*
- 3: Geneseqpl9908:\*
- 4: Geneseqpl2000s:\*
- 5: Geneseqpl2001s:\*
- 6: Geneseqpl2002s:\*
- 7: Geneseqpl2003as:\*
- 8: Geneseqpl2003bs:\*
- 9: Geneseqpl2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	803	100.0	149	2 AAY34305	Aay34305 IGG antib
2	766	95.4	159	2 AAY34307	Aay34307 IGG antib
3	638.5	79.5	517	6 ABU08019	Abu08019 Monoclonal
4	638.5	79.5	518	7 ADF65782	Adf65782 Human ant
5	638.5	79.5	518	8 ADJ92518	Adj92518 Human SOJ
6	616.5	76.8	448	8 ADF71916	Adf71916 Hu3G8VH-2
7	608	75.7	453	6 ABP58287	Abp58287 Humanised
8	608	75.7	472	6 ABP58289	Abp58289 Humanised
9	602.5	75.0	448	8 ADF71908	Adf71908 Hu3G8VH-1
10	602.5	75.0	448	8 ADF71912	Adf71912 Hu3G8VH-5
11	602.5	75.0	228	7 ADJ32130	Adj32130 Human int
12	582.5	72.5	450	5 ABP66596	Abp66596 Human RSV
13	582.5	72.5	450	5 ABP66594	Abp66594 Human RSV
14	582.5	72.5	450	5 ABP66598	Abp66598 Human RSV
15	582.5	72.5	450	5 ABP66564	Abp66564 Human RSV
16	582.5	72.5	450	5 ABP66592	Abp66592 Human RSV
17	582.5	72.5	450	5 ABP66600	Abp66600 Human RSV
18	582.5	72.5	450	6 ABU69427	Abu69427 Respirato
19	582.5	72.5	450	6 ABU69455	Abu69455 Respirato
20	582.5	72.5	450	6 ABU69459	Abu69459 Respirato
21	582.5	72.5	450	6 ABU69457	Abu69457 Respirato
22	582.5	72.5	450	6 ABU69463	Abu69463 Respirato
23	582.5	72.5	450	6 ABU69461	Abu69461 Respirato
24	582.5	72.5	450	7 ADE35952	Ade35952 SYNAGIS a
25	582.5	72.5	450	7 ADE35956	Ade35956 SYNAGIS a

26	582.5	72.5	450	7 ADE35958	Ade35958 SYNAGIS a
27	582.5	72.5	450	7 ADE35954	Ade35954 SYNAGIS a
28	582.5	72.5	450	7 ADE35922	Ade35922 SYNAGIS a
29	582.5	72.5	450	7 ADE35950	Ade35950 SYNAGIS a
30	581.5	72.4	450	5 ABP66562	Abp66562 Human RSV
31	581.5	72.4	450	6 ABU69425	Abu69425 Respirato
32	581.5	72.4	450	7 ADE35920	Ade35920 SYNAGIS a
33	579.5	72.2	450	5 ABP66590	Abp66590 Human RSV
34	579.5	72.2	450	5 ABP66588	Abp66588 Human RSV
35	579.5	72.2	450	5 ABP66602	Abp66602 Human RSV
36	579.5	72.2	450	5 ABP66586	Abp66586 Human RSV
37	579.5	72.2	450	6 ABU69451	Abu69451 Respirato
38	579.5	72.2	450	6 ABU69453	Abu69453 Respirato
39	579.5	72.2	450	6 ABU69465	Abu69465 Respirato
40	579.5	72.2	450	6 ABU69449	Abu69449 Respirato
41	579.5	72.2	450	7 ADE35948	Ade35948 SYNAGIS a
42	579.5	72.2	450	7 ADE35946	Ade35946 SYNAGIS a
43	579.5	72.2	450	7 ADE35944	Ade35944 SYNAGIS a
44	578.5	72.0	450	4 AAE10517	Aae10517 Humanised
45	578.5	72.0	450	5 ABP66608	Abp66608 Human RSV

ALIGNMENTS

RESULT 1  
AAY34305  
ID AAY34305 standard; protein; 149 AA.

XX AC AAY34305;  
XX DT 19-NOV-1999 (first entry)  
XX DE IGG antibody 2.4.4 heavy chain sequence.  
XX KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX OS Homo sapiens.  
XX PN W09945031-A2.  
XX PD 10-SEP-1999.  
XX PF 03-MAR-1999; 99WO-US004583.  
XX PR 03-MAR-1998; 98US-00034607.  
XX PR 03-FEB-1999; 99US-00244253.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;  
XX DR WPI; 1999-540816/45.  
XX DR N-PSDB; AAZ20406.  
XX PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX PS Claim 60; Fig 30; 245pp; English.  
XX CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IGM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
SQ Sequence 149 AA;  
Query Match 100.0%; Score 803; DB 2; Length 149;  
Best Local Similarity 100.0%; Pred. No. 2.7e-65;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NPQTTLTCTFSGFSLITRGVGVDMIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLTIIT 60  
DB 1 NPQTTLTCTFSGFSLITRGVGVDMIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLTIIT 60  
QY 61 KDTSKNQVLTMTNMDPVDATYTCAHHFFDSSGYPPFDSWGQGLTVSVSSASTKGPSVF 120  
DB 61 KDTSKNQVLTMTNMDPVDATYTCAHHFFDSSGYPPFDSWGQGLTVSVSSASTKGPSVF 120  
QY 121 PLAPCSRSTSESTAALGCLVKDYFPEPVT 149  
DB 121 PLAPCSRSTSESTAALGCLVKDYFPEPVT 149  
RESULT 2  
ID AAY34307  
AC AAY34307  
DT 19-NOV-1999 (first entry)  
DE IgG antibody 2.3.2 heavy chain sequence.  
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
OS Homo sapiens.  
XX WO9945031-A2.  
XX 10-SEP-1999.  
XX 03-MAR-1999; 99WO-US004583.  
XX 03-MAR-1998; 98US-00034607.  
XX 03-FEB-1999; 99US-00244253.  
XX (ABGE-) ABGENIX INC.  
XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
XX Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX WPI; 1999-540816/45.  
XX N-PSDB; AAZ20408.  
XX New monoclonal antibody, used for treating e.g. graft versus host  
XX disease, cancers, autoimmune diseases and inflammatory diseases.  
XX Claim 60; Fig 32; 245pp; English.  
XX This sequence represents the heavy chain of an antibody of the invention.  
XX The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
XX complement and a variable region that binds to the epitope on CD147 bound  
XX by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
XX can selectively kill activated T-cells, activated B-cells or resting or  
XX activated monocytes. The products and methods can be used for treating  
XX diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
XX versus host disease (GVHD), organ transplant rejection diseases (e.g.  
XX renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
XX (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
XX (e.g. lupus), and inflammatory diseases (e.g. arthritis)

SQ Sequence 159 AA;  
Query Match 95.4%; Score 766; DB 2; Length 159;  
Best Local Similarity 100.0%; Pred. No. 6.8e-62;  
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 LTCFTSGFSLITRGVGVDMIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLTIITKDTSKNQ 67  
DB 1 LTCFTSGFSLITRGVGVDMIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLTIITKDTSKNQ 60  
QY 68 VLTTNMDPVDATYTCAHHFFDSSGYPPFDSWGQGLTVSVSSASTKGPSVPLAPCSR 127  
DB 61 VLTTNMDPVDATYTCAHHFFDSSGYPPFDSWGQGLTVSVSSASTKGPSVPLAPCSR 120  
QY 128 STSESTAALGCLVKDYFPEPVT 149  
DB 121 STSESTAALGCLVKDYFPEPVT 142  
RESULT 3  
ID ABU08019  
AC ABU08019  
DT 10-MAY-2003 (first entry)  
DE Monoclonal rabies virus antibody heavy chain, clone JB.1.  
XX Human; antibody; constant region; monoclonal antibody 57; Mab 57;  
XX variable region; Rabies; neurological disease; infection;  
XX central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;  
XX pathogen; vaccine; virucide; heavy chain.  
XX Homo sapiens.  
XX WO2003016501-A2.  
XX 27-FEB-2003.  
XX 21-AUG-2002; 2002WO-US026584.  
XX 21-AUG-2001; 2001US-0314023P.  
XX (UYJB-) UNIV JEFFERSON THOMAS.  
XX Hooper DC, Dietzschold B;  
XX WPI; 2003-278566/27.  
XX N-PSDB; ABX12861.  
XX New recombinant antibody comprising a constant region of Mab 57 linked to  
XX a non-Mab 57 variable region, useful for treating an individual exposed  
XX to a pathogen, e.g. rabies infection.  
XX Claim 1; Page 35; 38pp; English.  
XX The invention discloses a recombinant antibody comprising a constant  
XX region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable  
XX region. Rabies is an acute, neurological disease caused by infection of  
XX the central nervous system with the rabies virus, a member of the  
XX Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods  
XX for producing an isolated recombinant antibody by culturing a host cell,  
XX containing a recombinant expression vector comprising the nucleic acid  
XX molecule encoding the antibody, and isolating the recombinant antibody  
XX expressed and treating an individual exposed to a pathogen by  
XX administering to the individual the recombinant antibody. The recombinant  
XX antibodies are useful for preventing (vaccine) and treating an individual  
XX exposed to a pathogen, e.g. rabies infection. They are also useful for  
XX the qualitative and quantitative determination of the rabies virus. The  
XX sequences presented are the antibody protein fragments, the nucleic acids  
XX encoding them or the PCR primers used to construct the recombinant  
XX expression vector

XX SQ Sequence 517 AA;  
Query Match 79.5%; Score 638.5; DB 6; Length 517;  
Best Local Similarity 81.9%; Pred. No. 1e-49;  
Matches 122; Conservative 9; Mismatches 15; Indels 3; Gaps 2;  
QY 2 PQTTLTCTCFSGSLITRGVGVWIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLITTK 61  
Db 33 PTQTLTCTCFSGSLTSGVGVWIRQPPGKALEWTLIYWDKRYSPSLNRVTRK 92  
QY 62 DTSKNQVLTWNMDPVDATYYCAHFFDSSGYYP-FDSMGQGLTVSVSSASTKGPSVF 120  
Db 93 DTSKNQVLTWNMDPDLTGTYCAHROHIS--FPWFDSMGQGLTVSVSSASTKGPSVF 150  
QY 121 PLAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 151 PLAPCSRSTSGTAAALGCLVKDYFPEPVT 179  
RESULT 4  
ADF65782  
ID ADF65782 standard; protein; 518 AA.  
XX AC ADF65782;  
XX DT 12-FEB-2004 (first entry)  
XX DE Human anti-rabies MAb JB.1 antibody heavy chain.  
XX KW Immunoglobulin; Ig; heavy chain; light chain; human;  
KW monoclonal rabies virus neutralising antibody; rabies virus protein;  
KW neuronal tissue; antirabies; MAB JB.1.  
XX OS Homo sapiens.  
XX PN US2003157112-A1.  
XX PD 21-AUG-2003.  
XX PF 21-AUG-2002; 2002US-00225108.  
XX PR 16-MAY-2000; 2000US-0204518P.  
PR 04-MAY-2001; 2001US-00848832.  
PR 21-AUG-2001; 2001US-0314023P.  
XX PA (HOOP/) HOOPER D C.  
PA (DIET/) DIETZSCHOLD B.  
XX PI Hooper DC, Dietzschold B;  
XX WPI; 2003-777974/73.  
DR N-PSDB; ADF65781.  
XX PT New isolated nucleic acid molecule encoding a sequence that neutralizes  
PT an antibody that binds to rabies virus protein, useful for diagnosing,  
PT preventing or treating infection of pathogens that target neuronal  
PT tissues, e.g. rabies.  
XX PS Claim 2; SEQ ID NO 10; 22pp; English.  
XX CC The present invention relates to the isolation of immunoglobulin (Ig)  
CC heavy and light chains of human monoclonal rabies virus neutralising  
CC antibody, and the polynucleotide sequences encoding them. The antibody  
CC specifically binds to a rabies virus protein. Also disclosed is a fused  
CC gene encoding a chimeric immunoglobulin light or heavy chain comprising a  
CC first DNA sequence encoding an immunoglobulin light or heavy chain  
CC variable region of a monoclonal rabies virus neutralising antibody  
CC produced by a heterohybridoma cell line and a second DNA sequence  
CC encoding a human light or heavy chain constant region, and methods of  
CC producing a recombinant antibody. The polynucleotide sequences, and  
CC antibodies and methods are useful for diagnosing, preventing or treating  
CC an infection of pathogens that target neuronal tissues, particularly

CC rabies. The present sequence represents human anti-rabies MAB JB.1  
CC antibody heavy chain.  
XX SQ Sequence 518 AA;  
Query Match 79.5%; Score 638.5; DB 7; Length 518;  
Best Local Similarity 81.9%; Pred. No. 1.1e-49;  
Matches 122; Conservative 9; Mismatches 15; Indels 3; Gaps 2;  
QY 2 PQTTLTCTCFSGSLITRGVGVWIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLITTK 61  
Db 33 PTQTLTCTCFSGSLTSGVGVWIRQPPGKALEWTLIYWDKRYSPSLNRVTRK 92  
QY 62 DTSKNQVLTWNMDPVDATYYCAHFFDSSGYYP-FDSMGQGLTVSVSSASTKGPSVF 120  
Db 93 DTSKNQVLTWNMDPDLTGTYCAHROHIS--FPWFDSMGQGLTVSVSSASTKGPSVF 150  
QY 121 PLAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 151 PLAPCSRSTSGTAAALGCLVKDYFPEPVT 179  
RESULT 5  
ADJ92518  
ID ADJ92518 standard; protein; 518 AA.  
XX AC ADJ92518;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human SOJB monoclonal antibody heavy chain protein.  
XX KW Rabies virus infection; pharmaceutical; vaccine; gene therapy; virucide;  
KW human; SOJB monoclonal antibody.  
XX OS Homo sapiens.  
XX PN US2004013672-A1.  
XX PD 22-JAN-2004.  
XX PF 13-JUN-2003; 2003US-00461148.  
XX PR 16-MAY-2000; 2000US-0204518P.  
PR 04-MAY-2001; 2001US-00848832.  
PR 21-AUG-2001; 2001US-0314023P.  
PR 21-AUG-2002; 2002US-00225108.  
XX PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX PI Hooper DC, Dietzschold B;  
XX WPI; 2004-108190/11.  
DR N-PSDB; ADJ92517.  
XX PT New pharmaceutical composition comprising at least two recombinant rabies  
PT virus-neutralizing human antibodies, useful for treating or preventing  
PT rabies virus infection.  
XX PS Claim 1; SEQ ID NO 4; 28pp; English.  
XX CC The present invention relates to a method of treating or preventing a  
CC rabies virus infection in a subject. The invention also relates to novel  
CC pharmaceutical composition comprising a carrier and at least two  
CC recombinant rabies virus-neutralising human antibodies, where the  
CC antibody comprises an antibody comprising an antibody light chain or its  
CC homologue and an antibody heavy chain or its homologue. The  
CC pharmaceutical composition is useful for treating or preventing rabies  
CC virus infection. The invention is also useful as vaccine and in gene  
CC therapy. The pharmaceutical composition is useful for treating or  
CC preventing rabies virus infection. The present sequence is rabies virus-  
CC neutralising human SOJB monoclonal antibody heavy chain protein used in  
CC the invention.

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XX SQ Sequence 518 AA;
Query Match 79.5%; Score 638.5; DB 8; Length 518;
Best Local Similarity 81.9%; Pred. No. 1.1e-49;
Matches 122; Conservative 9; Mismatches 15; Indels 3; Gaps 2;

QY 2 PQTTLTCTFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 33 PTQTLLTCTFSGSLSTSGVGWIRQPPGKALEWTLIYWNDDKRYSPSLNRTVIRK 92

QY 62 DTSKNQVLTWMTNMDPVDATYTCYCAHHFFDSSGGYYP-FDSWGQGLTVSVSSASTKGPSVF 120
Db 93 DTSKNQVLTWMTNMDPLDTGYTCYCAHRRHSS--FPWFDSWGQGLTVSVSSASTKGPSVF 150

QY 121 PLAPCSRSTSESTAALGCLVKDYPPEPVT 149
Db 151 PLAPCSRSTSGGTAALGCLVKDYPPEPVT 179

RESULT 6
ID ADF71916 standard; protein; 448 AA.
XX
AC ADF71916;
XX
DT 26-FEB-2004 (first entry)
XX
DE HU3G8VH-22G1Ag amino acid sequence SEQ ID NO:115.
XX
anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW opthalmological; antiasthmatic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
XX WO2003101485-A1.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US017111.
XX
XX 30-MAY-2002; 2002US-0384689P.
XX
XX 10-JAN-2003; 2003US-0439320P.
XX
XX (MACR-) MACROGENICS INC.
XX
XX Johnson LS, Huang L, Li H, Tuailon N;
XX
XX WPI; 2004-042985/04.
XX
PT Novel anti-CD16A antibody comprising complementarity determining regions
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
PT lacks effector function, useful for treating deleterious immune response.
XX
XX Disclosure; SEQ ID NO 115; 103pp; English.
XX
XX The present invention describes an anti-CD16A antibody (I) comprising a
XX VH domain comprising complementarity determining regions (CDRs) derived
XX from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
XX derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A

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CC antibody (II) that lacks effector function and comprises all six CDRs of
CC mouse antibody 3G8. Also described is a method (M1) for reducing a
CC deleterious immune response in a mammal in need of such reduction, which
CC involves administering to the mammal a CD16A binding protein comprising
CC an Fc region derived from a human IgG heavy chain, where the Fc region
CC lacks effector function or is modified to reduce binding to an Fc
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
CC uropathic, opthalmological and antiasthmatic activities. (I) or (II) is
CC useful for reducing a deleterious immune response in a mammal which
CC involves administering to the mammal (I) or (II). The deleterious immune
CC response is an inflammatory response caused by autoimmune disease such as
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
CC and also for treating diseases susceptible to treatment with intravenous
CC immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence
CC is used in the exemplification of the present invention.
XX
SQ Sequence 448 AA;

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```

Query Match 76.8%; Score 616.5; DB 8; Length 448;
Best Local Similarity 81.1%; Pred. No. 9.1e-48;
Matches 120; Conservative 9; Mismatches 14; Indels 5; Gaps 2;

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QY 2 PQTTLTCTFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 14 PTQTLLTCTFSGSLSTSGVGWIRQPPGKALEWTLIYWNDDKRYSPSLKSLRLTISK 73

QY 62 DTSKNQVLTWMTNMDPVDATYTCYCAHHFFDSSGGYYPFDSWGQGLTVSVSSASTKGPSVFP 121
Db 74 DTSKNQVLTWMTNMDPVDATYTCYCAR---INPAYFAY--WGQGLTVTVSSASTKGPSVFP 128

QY 122 LAPCSRSTSESTAALGCLVKDYPPEPVT 149
Db 129 LAPCSRSTSGGTAALGCLVKDYPPEPVT 156

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RESULT 7
ABP58287
ID ABP58287 standard; protein; 453 AA.
XX
AC ABP58287;
XX
DT 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX
DE Humanised 10D5 antibody heavy chain.
XX
KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
XX Key Location/Qualifiers
XX Region 1..123
XX /note= "light chain variable region"
XX Region 31..35
XX /note= "CDR1"
XX Region 52..67
XX /note= "CDR2"
XX Region 100..112
XX /note= "CDR3"
XX
XX WO200288307-A2.
XX

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PD 07-NOV-2002.  
XX  
PF 26-APR-2002; 2002WO-US011854.  
XX  
PR 30-APR-2001; 2001US-0287653P.  
XX  
PA (ELIL ) LILLY & CO ELI.  
XX  
XX Hinton PR, Vasquez M;  
XX  
DR WPI; 2003-183836/18.  
XX  
XX New humanized 10D5 antibody, useful for the manufacture of a medicament  
PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's  
PT disease or cerebral amyloid angiopathy.  
XX  
PS Claim 5; Page 10-12; 52pp; English.  
XX  
XX The present sequence is the protein sequence of the heavy chain of a  
CC humanised antibody of the present invention. In the variable portion, the  
CC complementarity determining regions (CDRs) originate from murine  
CC monoclonal antibody 10D5 and the framework region originates from human  
CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies  
CC of the invention have CDRs from 10D5 and human framework sequences. These  
CC humanised antibodies have binding affinities (affinity and epitope  
CC location) approximately the same as those of the mouse 10D5 antibody. The  
CC invention includes antibodies, single chain antibodies, and their  
CC fragments, as well as nucleotide sequences, vectors, transformed host  
CC cells, and methods of using the humanised antibody to treat, prevent,  
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology  
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or  
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or  
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise  
CC OS field)  
XX  
SQ Sequence 453 AA;  
  
Query Match 75.7%; Score 608; DB 6; Length 453;  
Best Local Similarity 79.1%; Pred. No. 5.5e-47;  
Matches 117; Conservative 8; Mismatches 23; Indels 0; Gaps 0;  
  
Qy 2 PQTTLTCTCFSGSLITRGVGVDMIRPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61  
Db 14 PTEFLTCTCFSGSLTSGMGVSWIRPPGKALEWLAHIYWDKDKRYNPSLKSRLITSK 73  
  
Qy 62 DTSKNQVVLTMNDPVDVTATYYCAHHFFDSSGGYYPFDSWGQGLTVSVSSASTKGPSVFP 121  
Db 74 DTSKSQVVLTMNDPVDVTATYYCVRRTPTPVLVDAMDYWGQGLTVTVSSASTKGPSVFP 133  
  
Qy 122 LAPCSRSTSESTALGCLVKDYFPEPVT 149  
Db 134 LAPSSKSTSGTAAALGCLVKDYFPEPVT 161  
  
RESULT 8  
ABP58289  
ID ABP58289 standard; protein; 472 AA.  
XX  
AC ABP58289;  
XX  
DT 23-OCT-2003 (revised)  
DT 31-MAR-2003 (first entry)  
XX  
DE Humanised 10D5 antibody heavy chain.  
XX  
KW Monoclonal antibody; 10D5; complementarity determining region; CDR;  
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;  
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.  
XX  
OS Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX

EH Key Location/Qualifiers  
FT Peptide 1..19  
FT Peptide /label= Signal\_peptide  
FT Peptide 20..472  
FT /label= Mature protein  
FT /note= "the mature light chain is claimed in Claim 5"  
FT Region 20..142  
FT /note= "light chain variable region, claimed in Claim 4"  
FT Region 50..56  
FT /note= "CDR1"  
FT Region 71..86  
FT /note= "CDR2"  
FT Region 119..131  
FT /note= "CDR3"  
XX  
PN WO200288307-A2.  
XX  
XX 07-NOV-2002.  
PD  
XX  
DF 26-APR-2002; 2002WO-US011854.  
XX  
PR 30-APR-2001; 2001US-0287653P.  
XX  
PA (ELIL ) LILLY & CO ELI.  
XX  
PI Hinton PR, Vasquez M;  
XX  
XX WPI; 2003-183836/18.  
DR N-PSDB; ABZ24639, ABZ24641.  
XX  
XX New humanized 10D5 antibody, useful for the manufacture of a medicament  
PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's  
PT disease or cerebral amyloid angiopathy.  
XX  
PS Disclosure; Page 13-15; 52pp; English.  
XX  
XX The present sequence is the protein sequence of the heavy chain of a  
CC humanised antibody of the present invention. In the variable portion, the  
CC complementarity determining regions (CDRs) originate from murine  
CC monoclonal antibody 10D5 and the framework region originates from human  
CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies  
CC of the invention have CDRs from 10D5 and human framework sequences. These  
CC humanised antibodies have binding affinities (affinity and epitope  
CC location) approximately the same as those of the mouse 10D5 antibody. The  
CC invention includes antibodies, single chain antibodies, and their  
CC fragments, as well as nucleotide sequences, vectors, transformed host  
CC cells, and methods of using the humanised antibody to treat, prevent,  
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology  
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or  
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or  
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise  
CC OS field)  
XX  
SQ Sequence 472 AA;  
  
Query Match 75.7%; Score 608; DB 6; Length 472;  
Best Local Similarity 79.1%; Pred. No. 5.7e-47;  
Matches 117; Conservative 8; Mismatches 23; Indels 0; Gaps 0;  
  
Qy 2 PQTTLTCTCFSGSLITRGVGVDMIRPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61  
Db 33 PTEFLTCTCFSGSLTSGMGVSWIRPPGKALEWLAHIYWDKDKRYNPSLKSRLITSK 92  
  
Qy 62 DTSKNQVVLTMNDPVDVTATYYCAHHFFDSSGGYYPFDSWGQGLTVSVSSASTKGPSVFP 121  
Db 93 DTSKSQVVLTMNDPVDVTATYYCVRRTPTPVLVDAMDYWGQGLTVTVSSASTKGPSVFP 152  
  
Qy 122 LAPCSRSTSESTALGCLVKDYFPEPVT 149  
Db 153 LAPSSKSTSGTAAALGCLVKDYFPEPVT 180  
  
RESULT 9

AD71908  
ID ADF71908 standard; protein; 448 AA.  
AC ADF71908;  
XX  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Hu3G8VH-1G1 amino acid sequence SEQ ID NO:107.  
XX  
XX anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;  
KW immune response; haemostatic; antirheumatic; antiarthritic;  
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;  
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;  
KW ophthalmological; antiasthmatic; inflammatory response;  
KW autoimmune disease; idiopathic thrombocytopenic purpura;  
KW rheumatoid arthritis; systemic lupus erythematosus;  
KW autoimmune haemolytic anaemia; scleroderma;  
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;  
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;  
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;  
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;  
allergic asthma.  
XX  
OS Synthetic.  
OS Mus sp.  
OS Homo sapiens.  
XX  
XX WO2003101485-A1.  
XX  
XX 11-DEC-2003.  
XX  
XX 29-MAY-2003; 2003WO-US017111.  
XX  
XX 30-MAY-2002; 2002US-0384689P.  
XX  
XX 10-JAN-2003; 2003US-0439320P.  
XX  
XX (MACR-) MACROGENICS INC.  
XX  
XX Johnson LS, Huang L, Li H, Tuailon N;  
XX WPI; 2004-042985/04.  
XX  
XX Novel anti-CD16A antibody comprising complementarity determining regions  
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that  
PT lacks effector function, useful for treating deleterious immune response.  
XX  
XX Disclosure; SEQ ID NO 107; 103pp; English.  
XX  
XX The present invention describes an anti-CD16A antibody (I) comprising a  
CC VH domain comprising complementarity determining regions (CDRs) derived  
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs  
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A  
CC antibody (II) that lacks effector function and comprises all six CDRs of  
CC mouse antibody 3G8. Also described is a method (M1) for reducing a  
CC deleterious immune response in a mammal in need of such reduction, which  
CC involves administering to the mammal a CD16A binding protein comprising  
CC an FC region derived from a human IgG heavy chain, where the FC region  
CC lacks effector function or is modified to reduce binding to an FC  
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,  
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,  
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,  
CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is  
CC useful for reducing a deleterious immune response in a mammal which  
CC involves administering to the mammal (I) or (II). The deleterious immune  
CC response is an inflammatory response caused by autoimmune disease such as  
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),  
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),  
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis  
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis  
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,  
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis  
CC and also for treating diseases susceptible to treatment with intravenous  
CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence

CC is used in the exemplification of the present invention.  
XX  
SQ Sequence 448 AA;  
XX  
XX Query Match 75.0%; Score 602.5; DB 8; Length 448;  
XX Best Local Similarity 78.7%; Pred. No. 1.7e-46;  
XX Matches 118; Conservative 9; Mismatches 14; Indels 9; Gaps 2;  
XX  
QY 2 PQTTLTCTCFSGSLITRGVGVDRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61  
DB 14 PTQTLTCTCFSGSLTSGMGVGRQPPGKALEWLHLHWDDDKRYNPAKSLRLTISK 73  
QY 62 DTSKNQVLLTMTNMDPVDATYTCYCAHHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSV 119  
DB 74 DTSKNQVLLTMTNMDPVDATYTCAR-----INPAWFAYMGQGLTVTVSSASTKGPSV 126  
QY 120 FPLAPCSRSTSESTAALGCLVKDYFPEPVT 149  
DB 127 FPLAPSKSTSGTAALGCLVKDYFPEPVT 156  
XX  
XX RESULT 10  
XX ADF71912  
XX ID ADF71912 standard; protein; 448 AA.  
XX  
XX ADF71912;  
XX  
XX 26-FEB-2004 (first entry)  
XX  
XX Hu3G8VH-5G1ag amino acid sequence SEQ ID NO:111.  
XX  
XX anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;  
KW immune response; haemostatic; antirheumatic; antiarthritic;  
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;  
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;  
KW ophthalmological; antiasthmatic; inflammatory response;  
KW autoimmune disease; idiopathic thrombocytopenic purpura;  
KW rheumatoid arthritis; systemic lupus erythematosus;  
KW autoimmune haemolytic anaemia; scleroderma;  
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;  
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;  
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;  
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;  
allergic asthma.  
XX  
XX Synthetic.  
XX Mus sp.  
XX Homo sapiens.  
XX  
XX WO2003101485-A1.  
XX  
XX 11-DEC-2003.  
XX  
XX 29-MAY-2003; 2003WO-US017111.  
XX  
XX 30-MAY-2002; 2002US-0384689P.  
XX  
XX 10-JAN-2003; 2003US-0439320P.  
XX  
XX (MACR-) MACROGENICS INC.  
XX  
XX Johnson LS, Huang L, Li H, Tuailon N;  
XX WPI; 2004-042985/04.  
XX  
XX Novel anti-CD16A antibody comprising complementarity determining regions  
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that  
PT lacks effector function, useful for treating deleterious immune response.  
XX  
XX Disclosure; SEQ ID NO 111; 103pp; English.  
XX  
XX The present invention describes an anti-CD16A antibody (I) comprising a  
CC VH domain comprising complementarity determining regions (CDRs) derived  
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs  
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A  
CC antibody (II) that lacks effector function and comprises all six CDRs of  
CC mouse antibody 3G8. Also described is a method (M1) for reducing a  
CC deleterious immune response in a mammal in need of such reduction, which  
CC involves administering to the mammal a CD16A binding protein comprising  
CC an FC region derived from a human IgG heavy chain, where the FC region  
CC lacks effector function or is modified to reduce binding to an FC  
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,  
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,  
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,  
CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is  
CC useful for reducing a deleterious immune response in a mammal which  
CC involves administering to the mammal (I) or (II). The deleterious immune  
CC response is an inflammatory response caused by autoimmune disease such as  
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),  
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),  
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis  
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis  
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,  
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis  
CC and also for treating diseases susceptible to treatment with intravenous  
CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence

CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A  
 CC antibody (II) that lacks effector function and comprises all six CDRs of  
 CC mouse antibody 3G8. Also described is a method (M1) for reducing a  
 CC deleterious immune response in a mammal in need of such reduction, which  
 CC involves administering to the mammal a CD16A binding protein comprising  
 CC an Fc region derived from a human Igg heavy chain, where the Fc region  
 CC lacks effector function or is modified to reduce binding to an Fc  
 CC effector ligand. (I) and (II) have haemostatic, antirheumatic,  
 CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,  
 CC antianemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,  
 CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is  
 CC useful for reducing a deleterious immune response in a mammal which  
 CC involves administering to the mammal (I) or (II). The deleterious immune  
 CC response is an inflammatory response caused by autoimmune disease such as  
 CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),  
 CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),  
 CC scleroderma, autoantibody triggered arthritis, pemphigus, vasculitis  
 CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis  
 CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,  
 CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis  
 CC and also for treating diseases susceptible to treatment with intravenous  
 CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence  
 CC is used in the exemplification of the present invention.

XX Sequence 448 AA;

Query Match 75.0%; Score 602.5; DB 8; Length 448;  
 Best Local Similarity 78.7%; Pred. No. 1.7e-46;  
 Matches 118; Conservative 9; Mismatches 14; Indels 9; Gaps 2;

Qy 2 PQTTLTCTFSGLITRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61  
 Db 14 PTQTLTCTFSGLITRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITK 73  
 Qy 62 DTSKNQVLLTNTNDPVDVATYYCAHHFFDSSGYVP--FDSWGQGLTVSVSSASTKGPSV 119  
 Db 74 DTSKNQVLLTNTNDPVDVATYYCAQ-----INPAWFAYWGQGLTVSVSSASTKGPSV 126

Qy 120 FPLAPCSRSTSESTAALGCLVKDYFPEPT 149

Db 127 FPLAPSSKSTSGGTAALGCLVKDYFPEPT 156

RESULT 11

ID ADJ32130  
 AC ADJ32130 standard; protein; 228 AA.

XX ADJ32130;

XX 22-APR-2004 (first entry)

XX Human interferon-gamma antibody heavy chain amino acid sequence SeqID84.  
 XX antibody; antigen binding domain; interferon-gamma; INF-gamma;  
 KW antagonist antibody; antiinflammatory; immunosuppressive;  
 KW autoimmune disease; inflammatory condition; human; heavy chain.

XX Homo sapiens.

XX US2003099647-A1.

XX 29-MAY-2003.

XX 05-OCT-2001; 2001US-00972656.

XX 05-OCT-2001; 2001US-00972656.

XX (DESH/) DESHPANDE R V.  
 XX (TSAI/) TSAI M.

XX Deshpande RV, Tsai M;

XX WPI; 2003-696068/66.

DR N-PSDB; ADJ32129.

XX New antibody or antigen binding domain, or its fragment, variant or  
 PT derivative, which binds to an interferon-gamma protein, useful for  
 PT preparing a composition for preventing or treating inflammatory or  
 PT autoimmune disorders.

XX Claim 10; SEQ ID NO 84; 113pp; English.

XX This invention relates to a novel antibody or antigen binding domain, or  
 CC its fragment, variant or derivative, which binds to an interferon-gamma  
 CC (INF-gamma) protein, and is an antagonist antibody. The invention may be  
 CC useful for the development of compounds with an antiinflammatory or  
 CC immunosuppressive activity through action as interferon-gamma agonists. A  
 CC composition containing the antibody is useful for preventing or treating  
 CC an autoimmune disease and an inflammatory condition. The present sequence  
 CC is that of an antibody heavy chain of a human IFN-gamma antibody which  
 CC may be part of the invention.

XX Sequence 228 AA;

Query Match 75.0%; Score 602; DB 7; Length 228;  
 Best Local Similarity 76.0%; Pred. No. 9e-47;  
 Matches 114; Conservative 11; Mismatches 23; Indels 2; Gaps 1;

Qy 2 PQTTLTCTFSGLITRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61  
 Db 14 PTQTLTCTFSGLITRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITK 73  
 Qy 62 DTSKNQVLLTNTNDPVDVATYYCAHHFFDSSGYVP--FDSWGQGLTVSVSSASTKGPSV 119  
 Db 74 DTSKNQVLLTNTNDPVDVATYYCAHRLVRYGSGTGGFDVWGQGLTVTVSSASTKGPSV 133  
 Qy 120 FPLAPCSRSTSESTAALGCLVKDYFPEPT 149  
 Db 134 FPLAPSSKSTSGGTAALGCLVKDYFPEPT 163

RESULT 12

ID ABP66596

XX ABP66596 standard; protein; 450 AA.

XX AC ABP66596;

XX 04-DEC-2002 (first entry)

XX Human RSV antibody variable heavy chain.

XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;  
 KW complementarity determining region; respiratory syncytial virus;  
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;  
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;  
 KW bronchopulmonary dysplasia; congenital heart disease;  
 KW congenital immunodeficiency; acquired immunodeficiency.

XX Homo sapiens.

XX WO200243660-A2.

XX 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044807.

XX 28-NOV-2000; 2000US-00724396.

XX 28-NOV-2000; 2000US-00724531.

XX (MEDI-) MEDIUMUNE INC.

XX Young JF, Koenig S, Johnson LS;

XX WPI; 2002-706803/76.

XX Antibody for treating respiratory syncytial virus (RSV) infection,

PT comprises a variable heavy/light domain or complementarity determining  
PT regions 1 - 3 of variable light/heavy chains, that immunospecifically  
XX binds to RSV antigen.  
PS Disclosure; Page 279-281; 298pp; English.  
XX  
XX The invention relates to a novel antibody comprising a variable heavy  
CC (VH) domain, variable light (VL) domain, VH complementarity determining  
CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the  
CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)  
CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the  
CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,  
CC and immunostimulant activity. The polynucleotides of the invention may  
CC have a use in a vaccine, and in gene therapy. The antibody is useful for  
CC treating or ameliorating a RSV infection in a human. The antibody is also  
CC useful for preventing, treating or ameliorating one or more symptoms  
CC associated with RSV infection in a mammal, e.g. cystic fibrosis,  
CC bronchopulmonary dysplasia, congenital heart disease, congenital  
CC immunodeficiency or acquired immunodeficiency, or after a bone marrow  
CC transplant. The sequence represents a variable domain of a human RSV  
XX antibody of the invention  
XX  
SQ Sequence 450 AA;

Query Match 72.5%; Score 582.5; DB 5; Length 450;  
Best Local Similarity 76.4%; Pred. No. 1.1e-44;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;  
QY 2 PQTLLTCTFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61  
Db 14 PTQTLTCTFSGSLTAGSVGWIRQPPGKALEWLADIWDDKKDYNFSLKSLRLITK 73  
QY 62 DTSKNQVVLVTNNMDPVDATYTCYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVVLVTNNMDPADTATYTCYCAHMI--TNFY-FDVMGQGTIVTVSSASTKGPSVFP 130  
QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158  
RESULT 13  
ID ABP66594 standard; protein; 450 AA.  
XX  
AC ABP66594;  
XX  
DT 04-DEC-2002 (first entry)  
XX  
XX Human RSV antibody variable heavy chain.  
XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;  
KW complementarity determining region; respiratory syncytial virus;  
KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;  
KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;  
KW bronchopulmonary dysplasia; congenital heart disease;  
KW congenital immunodeficiency; acquired immunodeficiency.  
XX  
OS Homo sapiens.  
XX  
XX WO200243660-A2.  
XX  
XX 06-JUN-2002.  
XX  
XX 28-NOV-2001; 2001WO-US044807.  
XX  
XX 28-NOV-2000; 2000US-00724396.  
XX  
XX 28-NOV-2000; 2000US-00724531.  
XX  
XX (MEDI-) MEDIUMMUNE INC.  
XX  
XX Young JF, Koenig S, Johnson LS;  
XX

DR WPI; 2002-706803/76.  
XX  
XX Antibody for treating respiratory syncytial virus (RSV) infection,  
PT comprises a variable heavy/light domain or complementarity determining  
PT regions 1 - 3 of variable light/heavy chains, that immunospecifically  
PT binds to RSV antigen.  
XX  
XX Disclosure; Page 277-278; 298pp; English.  
PS  
XX  
XX The invention relates to a novel antibody comprising a variable heavy  
CC (VH) domain, variable light (VL) domain, VH complementarity determining  
CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the  
CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)  
CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the  
CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,  
CC and immunostimulant activity. The polynucleotides of the invention may  
CC have a use in a vaccine, and in gene therapy. The antibody is useful for  
CC treating or ameliorating a RSV infection in a human. The antibody is also  
CC useful for preventing, treating or ameliorating one or more symptoms  
CC associated with RSV infection in a mammal, e.g. cystic fibrosis,  
CC bronchopulmonary dysplasia, congenital heart disease, congenital  
CC immunodeficiency or acquired immunodeficiency, or after a bone marrow  
CC transplant. The sequence represents a variable domain of a human RSV  
XX antibody of the invention  
XX  
SQ Sequence 450 AA;  
Query Match 72.5%; Score 582.5; DB 5; Length 450;  
Best Local Similarity 76.4%; Pred. No. 1.1e-44;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;  
QY 2 PQTLLTCTFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61  
Db 14 PTQTLTCTFSGSLTAGSVGWIRQPPGKALEWLADIWDDKKDYNFSLKSLRLITK 73  
QY 62 DTSKNQVVLVTNNMDPVDATYTCYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVVLVTNNMDPADTATYTCYCARSMI--TNFY-FDVMGQGTIVTVSSASTKGPSVFP 130  
QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158  
RESULT 14  
ID ABP66598 standard; protein; 450 AA.  
XX  
AC ABP66598;  
XX  
DT 04-DEC-2002 (first entry)  
XX  
XX Human RSV antibody variable heavy chain.  
XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;  
KW complementarity determining region; respiratory syncytial virus;  
KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;  
KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;  
KW bronchopulmonary dysplasia; congenital heart disease;  
KW congenital immunodeficiency; acquired immunodeficiency.  
XX  
OS Homo sapiens.  
XX  
XX WO200243660-A2.  
XX  
XX 06-JUN-2002.  
XX  
XX 28-NOV-2001; 2001WO-US044807.  
XX  
XX 28-NOV-2000; 2000US-00724396.  
XX  
XX 28-NOV-2000; 2000US-00724531.  
XX  
XX (MEDI-) MEDIUMMUNE INC.  
XX



XX Young JF, Koenig S, Johnson LS;  
XX WPI; 2002-706803/76.  
XX Antibody for treating respiratory syncytial virus (RSV) infection,  
XX comprises a variable heavy/light domain or complementarity determining  
XX regions 1 - 3 of variable light/heavy chains, that immunospecifically  
XX binds to RSV antigen.  
XX Disclosure; Page 282-283; 298pp; English.  
XX The invention relates to a novel antibody comprising a variable heavy  
XX (VH) domain, variable light (VL) domain, VH complementarity determining  
XX region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the  
XX antibody immunospecifically binds to a respiratory syncytial virus (RSV)  
XX antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the  
XX invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,  
XX and immunostimulant activity. The polynucleotides of the invention may  
XX have a use in a vaccine, and in gene therapy. The antibody is useful for  
XX treating or ameliorating a RSV infection in a human. The antibody is also  
XX useful for preventing, treating or ameliorating one or more symptoms  
XX associated with RSV infection in a mammal, e.g. cystic fibrosis,  
XX bronchopulmonary dysplasia, congenital heart disease, congenital  
XX immunodeficiency or acquired immunodeficiency, or after a bone marrow  
XX transplant. The sequence represents a variable domain of a human RSV  
XX antibody of the invention  
XX Sequence 450 AA;  
Query Match 72.5%; Score 582.5; DB 5; Length 450;  
Best Local Similarity 76.4%; Pred. No. 1.1e-44;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;  
Qy 2 PQTTLTCTSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61  
Db 14 PTQTLTCTSGSLITRGVGVWIRQPPGKALEWLADIWDDKDYNPSPSLKSLRLITSK 73  
Qy 62 DTSKNQVVLVTNMDPVDATYTCYCAHHFFDSSGGYYPFDSWGQGLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVVLVTNMDPADATYTCYCARDMI--TNFY-FDVMGQGTVTVTSSASTKGPSVFP 130  
Qy 122 LAPCSRSTSESTALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158  
RESULT 15  
ABP66564  
ID ABP66564 standard; protein; 450 AA.  
XX AC ABP66564;  
XX DT 04-DEC-2002 (first entry)  
XX DE Human RSV antibody variable heavy chain.  
XX KW Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;  
XX complementarity determining region; respiratory syncytial virus;  
XX virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;  
XX immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;  
XX bronchopulmonary dysplasia; congenital heart disease;  
XX congenital immunodeficiency; acquired immunodeficiency.  
XX Homo sapiens.  
XX WO200243660-A2.  
XX 06-JUN-2002.  
XX 28-NOV-2001; 2001WO-US044807.  
XX 28-NOV-2000; 2000US-00724396.

PR 28-NOV-2000; 2000US-00724531.  
XX (MEDI-) MEDIUMMUNE INC.  
XX Young JF, Koenig S, Johnson LS;  
XX WPI; 2002-706803/76.  
XX Antibody for treating respiratory syncytial virus (RSV) infection,  
XX comprises a variable heavy/light domain or complementarity determining  
XX regions 1 - 3 of variable light/heavy chains, that immunospecifically  
XX binds to RSV antigen.  
XX Disclosure; Page 243-245; 298pp; English.  
XX The invention relates to a novel antibody comprising a variable heavy  
XX (VH) domain, variable light (VL) domain, VH complementarity determining  
XX region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the  
XX antibody immunospecifically binds to a respiratory syncytial virus (RSV)  
XX antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the  
XX invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,  
XX and immunostimulant activity. The polynucleotides of the invention may  
XX have a use in a vaccine, and in gene therapy. The antibody is useful for  
XX treating or ameliorating a RSV infection in a human. The antibody is also  
XX useful for preventing, treating or ameliorating one or more symptoms  
XX associated with RSV infection in a mammal, e.g. cystic fibrosis,  
XX bronchopulmonary dysplasia, congenital heart disease, congenital  
XX immunodeficiency or acquired immunodeficiency, or after a bone marrow  
XX transplant. The sequence represents a variable domain of a human RSV  
XX antibody of the invention  
XX Sequence 450 AA;  
Query Match 72.5%; Score 582.5; DB 5; Length 450;  
Best Local Similarity 76.4%; Pred. No. 1.1e-44;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;  
Qy 2 PQTTLTCTSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61  
Db 14 PTQTLTCTSGSLITRGVGVWIRQPPGKALEWLADIWDDKDYNPSPSLKSLRLITSK 73  
Qy 62 DTSKNQVVLVTNMDPVDATYTCYCAHHFFDSSGGYYPFDSWGQGLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVVLVTNMDPADATYTCYCARDMI--TNFY-FDVMGQGTVTVTSSASTKGPSVFP 130  
Qy 122 LAPCSRSTSESTALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158  
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Job time : 70.0805 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 79.0704 Seconds

(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-35

Perfect score: 803

Sequence: 1 NQPTLTTLCTFSGFSLITR.....SESTALGCLVKDYFPPVPT 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	638.5	79.5	518	14	US-10-225-108A-10
2	638.5	79.5	518	15	US-10-461-148-4
3	616.5	76.8	448	15	US-10-449-566-115
4	602.5	75.0	448	15	US-10-449-566-107
5	602.5	75.0	448	15	US-10-449-566-111
6	602	75.0	228	10	US-09-972-656-84
7	582.5	72.5	450	9	US-09-996-288-210
8	582.5	72.5	450	9	US-09-996-288-238
9	582.5	72.5	450	9	US-09-996-288-240
10	582.5	72.5	450	9	US-09-996-288-242
11	582.5	72.5	450	9	US-09-996-288-244
12	582.5	72.5	450	9	US-09-996-288-246
13	582.5	72.5	450	10	US-09-996-265-210

14	582.5	72.5	450	10	US-09-996-265-238	Sequence 238, App
15	582.5	72.5	450	10	US-09-996-265-240	Sequence 240, App
16	582.5	72.5	450	10	US-09-996-265-242	Sequence 242, App
17	582.5	72.5	450	10	US-09-996-265-244	Sequence 244, App
18	582.5	72.5	450	10	US-09-996-265-246	Sequence 246, App
19	582.5	72.5	450	16	US-10-900-230-210	Sequence 210, App
20	582.5	72.5	450	16	US-10-900-230-238	Sequence 238, App
21	582.5	72.5	450	16	US-10-900-230-240	Sequence 240, App
22	582.5	72.5	450	16	US-10-900-230-242	Sequence 242, App
23	582.5	72.5	450	16	US-10-900-230-244	Sequence 244, App
24	582.5	72.5	450	16	US-10-900-230-246	Sequence 246, App
25	581.5	72.4	450	9	US-09-996-288-208	Sequence 208, App
26	581.5	72.4	450	10	US-09-996-265-208	Sequence 208, App
27	581.5	72.4	450	16	US-10-900-230-208	Sequence 208, App
28	579.5	72.2	450	9	US-09-996-288-232	Sequence 232, App
29	579.5	72.2	450	9	US-09-996-288-234	Sequence 234, App
30	579.5	72.2	450	9	US-09-996-288-236	Sequence 236, App
31	579.5	72.2	450	9	US-09-996-288-248	Sequence 248, App
32	579.5	72.2	450	10	US-09-996-265-232	Sequence 232, App
33	579.5	72.2	450	10	US-09-996-265-234	Sequence 234, App
34	579.5	72.2	450	10	US-09-996-265-236	Sequence 236, App
35	579.5	72.2	450	10	US-09-996-265-248	Sequence 248, App
36	579.5	72.2	450	16	US-10-900-230-232	Sequence 232, App
37	579.5	72.2	450	16	US-10-900-230-234	Sequence 234, App
38	579.5	72.2	450	16	US-10-900-230-236	Sequence 236, App
39	579.5	72.2	450	16	US-10-900-230-248	Sequence 248, App
40	578.5	72.0	450	9	US-09-996-288-45	Sequence 45, Appl
41	578.5	72.0	450	9	US-09-996-288-226	Sequence 226, App
42	578.5	72.0	450	9	US-09-996-288-252	Sequence 252, App
43	578.5	72.0	450	9	US-09-996-288-254	Sequence 254, App
44	578.5	72.0	450	9	US-09-996-288-256	Sequence 256, App
45	578.5	72.0	450	10	US-09-996-265-226	Sequence 226, App

#### ALIGNMENTS

RESULT 1  
US-10-225-108A-10  
; Sequence 10, Application US/10225108A  
; Publication No. US20030157112A1  
; GENERAL INFORMATION:  
; APPLICANT: HOOPER, Craig  
; APPLICANT: DIETZSCHOLD, Bernhard  
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions  
; TITLE OF INVENTION: and Methods for Making Them  
; FILE REFERENCE: 8321-110  
; CURRENT APPLICATION NUMBER: US/10/225.108A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-108A-10

Query Match 79.5%; Score 638.5; DB 14; Length 518;

Best Local Similarity 81.9%; Pred. No. 7.6e-46;

Matches 122; Conservative 9; Mismatches 15; Indels 3; Gaps 2;

Qy 2 PQTTLTCTFSGFSLITRGGVDWIRQPPGKALQWLALYWNDDKRYSPSLKRLITTK 61

Db 33 PQTTLTCTFSGFSLITRGGVDWIRQPPGKALEWTLIYWDKRYSPSLKRLITRK 92

Qy 62 DTSKNQVLTWNPDVTATYCAHHFFDFSSGGYYP-FDSWGQCTLYSVSSASTKGRSVF 120

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Db 93 DTSKNQVLTWNTNDPLDTGTYCAHRQHISS--FPWFDSWGQGLTVTVSSASTKGPSVF 150
QY 121 PLAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 151 PLAPCSRSTSGGTAALGCLVKDYFPEPVT 179

RESULT 2
US-10-461-148-4
; Sequence 4, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 8321-110C11-185685
; CURRENT APPLICATION NUMBER: US/10/461,148
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 10/225,108
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human
US-10-461-148-4

Query Match 79.5%; Score 638.5; DB 15; Length 518;
Best Local Similarity 81.9%; Pred. No. 7.6e-46;
Matches 122; Conservative 9; Mismatches 15; Indels 3; Gaps 2;

QY 2 PQTTLTCTCFSGFSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db 33 PTQTLTCTCFSGFSLSTSGVGWIRQPPGKALEWTLIYWNDDKRYSPSLKSLRNVIRK 92
QY 62 DTSKNQVLTWNTNDPVDYATYYCAHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSVF 120
Db 93 DTSKNQVLTWNTNDPLDTGTYCAHRQHISS--FPWFDSWGQGLTVTVSSASTKGPSVF 150
QY 121 PLAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 151 PLAPCSRSTSGGTAALGCLVKDYFPEPVT 179

RESULT 3
US-10-449-566-115
; Sequence 115, Application US/10449566
; Publication No. US20040010124A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Leslie S.
; APPLICANT: LI, Hua
; APPLICANT: HUANG, Ling
; APPLICANT: TUAILLON, Nadine
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 529392000100
; CURRENT APPLICATION NUMBER: US/10/449,566
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,689
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/439,320
; PRIOR FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
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; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-449-566-115

Query Match 76.8%; Score 616.5; DB 15; Length 448;
Best Local Similarity 81.1%; Pred. No. 4.8e-44;
Matches 120; Conservative 9; Mismatches 14; Indels 5; Gaps 2;

QY 2 PQTTLTCTCFSGFSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db 14 PTQTLTCTCFSGFSLSTSGVGWIRQPPGKALEWTLIYWNDDKRYSPSLKSLRLITK 73
QY 62 DTSKNQVLTWNTNDPVDYATYYCAHFFDSSGYYPFDSWGQGLTVSVSSASTKGPSVF 121
Db 74 DTSKNQVLTWNTNDPVDYATYYCAR---INPAYFAY--WGQGLTVTVSSASTKGPSVF 128
QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 129 LAPSSKSTSGGTAALGCLVKDYFPEPVT 156

RESULT 4
US-10-449-566-107
; Sequence 107, Application US/10449566
; Publication No. US20040010124A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Leslie S.
; APPLICANT: HUANG, Ling
; APPLICANT: LI, Hua
; APPLICANT: TUAILLON, Nadine
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 529392000100
; CURRENT APPLICATION NUMBER: US/10/449,566
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,689
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/439,320
; PRIOR FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-449-566-107

Query Match 75.0%; Score 602.5; DB 15; Length 448;
Best Local Similarity 78.7%; Pred. No. 7.3e-43;
Matches 118; Conservative 9; Mismatches 14; Indels 9; Gaps 2;

QY 2 PQTTLTCTCFSGFSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db 14 PTQTLTCTCFSGFSLSTSGVGWIRQPPGKALEWTLIYWNDDKRYSPSLKSLRLITK 73
QY 62 DTSKNQVLTWNTNDPVDYATYYCAHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSV 119
Db 74 DTSKNQVLTWNTNDPVDYATYYCAR-----INPAWFAWVGQGLTVTVSSASTKGPSV 126
QY 120 FPLAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 127 FPLAPSKSTSGGTAALGCLVKDYFPEPVT 156

RESULT 5
US-10-449-566-111
; Sequence 111, Application US/10449566
; Publication No. US20040010124A1
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## ; GENERAL INFORMATION:

; APPLICANT: JOHNSON, Leslie S.  
; APPLICANT: HUANG, Ling  
; APPLICANT: Li, Hua  
; APPLICANT: TUAILON, Nadine  
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE  
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS  
; FILE REFERENCE: 529392000100  
; CURRENT APPLICATION NUMBER: US/10/449,566  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: 60/384,689  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: 60/439,320  
; PRIOR FILING DATE: 2003-01-10  
; NUMBER OF SEQ ID NOS: 119  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 111  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-449-566-111

Query Match 75.0%; Score 602.5; DB 15; Length 448;  
Best Local Similarity 78.7%; Pred. No. 7.3e-43;  
Matches 118; Conservative 9; Mismatches 14; Indels 9; Gaps 2;  
  
QY 2 PQTTLTCTCFSGSLITRGVGVWIRQPPGKALQWLALYVNDKRYSPSLKSLRLTITK 61  
Db 14 PTQTLTCTCFSGSLITRGVGVWIRQPPGKALEWLAH1WDDDKRYNPA1KSLRLTISK 73  
  
QY 62 DTSKNQVLTMTNMDPVDATYTCYCAHFFDSSGYYP--FDSWGQGTLLVSVSSASTKGPSV 119  
Db 74 DTSKNQVLTMTNMDPVDATYTCYCAQ-----INPAWFAWYGQTLTVTVSSASTKGPSV 126  
  
QY 120 FPLAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 127 FPLAPSKSTSGGTAALGCLVKDYFPEPVT 156

## RESULT 6

US-09-972-656-84  
; Sequence 84, Application US/09972656  
; Publication No. US20030099647A1  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Tsai, Mei-Mei  
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
; TITLE OF INVENTION: Neutralizing Activity  
; FILE REFERENCE: A-799  
; CURRENT APPLICATION NUMBER: US/09/972,656  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 84  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-656-84

Query Match 75.0%; Score 602; DB 10; Length 228;  
Best Local Similarity 76.0%; Pred. No. 4e-43;  
Matches 114; Conservative 11; Mismatches 23; Indels 2; Gaps 1;  
  
QY 2 PQTTLTCTCFSGSLITRGVGVWIRQPPGKALQWLALYVNDKRYSPSLKSLRLTITK 61  
Db 14 PTQTLTCTCFSGSLITRGVGVWIRQPPGKALEWLAH1WDDDKRYNPA1KSLRLTISK 73  
  
QY 62 DTSKNQVLTMTNMDPVDATYTCYCAHFFDSSGYYP--FDSWGQGTLLVSVSSASTKGPSV 119  
Db 74 DTSKNQVLTMTNMDPVDATYTCYCAHRLVRYGGYSTGDFVWGGQTTTVTVSSASTKGPSV 133

QY 120 FPLAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 134 FPLAPSKSTSGGTAALGCLVKDYFPEPVT 163

## RESULT 7

US-09-996-288-210  
; Sequence 210, Application US/09996288  
; Patent No. US20020177126A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 210  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-210

Query Match 72.5%; Score 582.5; DB 9; Length 450;  
Best Local Similarity 76.4%; Pred. No. 3.6e-41;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;  
  
QY 2 PQTTLTCTCFSGSLITRGVGVWIRQPPGKALQWLALYVNDKRYSPSLKSLRLTITK 61  
Db 14 PTQTLTCTCFSGSLITRGVGVWIRQPPGKALEWLAH1WDDDKRYNPA1KSLRLTISK 73  
  
QY 62 DTSKNQVLTMTNMDPVDATYTCYCAHFFDSSGYYPFDSWGQGTLLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVLTMTNMDPVDATYTCYCAQSMI--TNFY-FDVGQGTTVTVSVSSASTKGPSVFP 130  
  
QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 131 LAPSKSTSGGTAALGCLVKDYFPEPVT 158

## RESULT 8

US-09-996-288-238  
; Sequence 238, Application US/09996288  
; Patent No. US20020177126A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 238  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-238

Query Match 72.5%; Score 582.5; DB 9; Length 450;  
Best Local Similarity 76.4%; Pred. No. 3.6e-41;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;  
  
QY 2 PQTTLTCTCFSGSLITRGVGVWIRQPPGKALQWLALYVNDKRYSPSLKSLRLTITK 61  
Db 14 PTQTLTCTCFSGSLITRGVGVWIRQPPGKALEWLAH1WDDDKRYNPA1KSLRLTISK 73  
  
QY 62 DTSKNQVLTMTNMDPVDATYTCYCAHFFDSSGYYPFDSWGQGTLLVSVSSASTKGPSVFP 121

Db 74 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130  
QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

## RESULT 9

US-09-996-288-240  
; Sequence 240, Application US/09996288  
; Patent No. US20020177126A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 240  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-240

Query Match 72.5%; Score 582.5; DB 9; Length 450;  
Best Local Similarity 76.4%; Pred. No. 3.6e-41;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 2 PQTTLTCTCFSGSLITRGVGVWDIROPKALQWLALYWNDDKRYSPSLKSLRTITK 61  
Db 14 PTQTLTCTCFSGSLITRGVGVWDIROPKALQWLALYWNDDKRYSPSLKSLRTITK 73  
QY 62 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 121  
Db 74 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130  
QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

## RESULT 10

US-09-996-288-242  
; Sequence 242, Application US/09996288  
; Patent No. US20020177126A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 242  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-242

Query Match 72.5%; Score 582.5; DB 9; Length 450;  
Best Local Similarity 76.4%; Pred. No. 3.6e-41;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 2 PQTTLTCTCFSGSLITRGVGVWDIROPKALQWLALYWNDDKRYSPSLKSLRTITK 61

Db 14 PTQTLTCTCFSGSLITRGVGVWDIROPKALQWLALYWNDDKRYSPSLKSLRTITK 73  
QY 62 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 121  
Db 74 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130  
QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

## RESULT 11

US-09-996-288-244  
; Sequence 244, Application US/09996288  
; Patent No. US20020177126A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 244  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-244

Query Match 72.5%; Score 582.5; DB 9; Length 450;  
Best Local Similarity 76.4%; Pred. No. 3.6e-41;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 2 PQTTLTCTCFSGSLITRGVGVWDIROPKALQWLALYWNDDKRYSPSLKSLRTITK 61  
Db 14 PTQTLTCTCFSGSLITRGVGVWDIROPKALQWLALYWNDDKRYSPSLKSLRTITK 73  
QY 62 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 121  
Db 74 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130  
QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

## RESULT 12

US-09-996-288-246  
; Sequence 246, Application US/09996288  
; Patent No. US20020177126A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 246  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-246

Query Match 72.5%; Score 582.5; DB 9; Length 450;  
Best Local Similarity 76.4%; Pred. No. 3.6e-41;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy	2	PQTLLTCTCFSGSLITRGVGVWIRPPGKALOWLALIYWNDDKRYSPSLKSRLTI	T	K	61
		:	:	:	
Db	14	PTQILLTCTCFSGSLTAGSVGVIRPPGKALEWLADIWNDDKYNP	S	L	73
		:	:	:	
Qy	62	DTSKNQVLTWNMDPVDTATYCAHHPDSSGYVPFDSGGTILVSYSSASTKGPSVFP			121
		:	:	:	
Db	74	DTSKNQVLTWNMDPADTATYCARDMI--TNFY-FDVWGQGTIVTVSSASTKGPSVFP			130

RESULT 13  
 US-09-996-265-210  
 ; Sequence 210, Application US/09996265  
 ; Publication No. US20030091584A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, James  
 ; APPLICANT: Scott, Koenig  
 ; APPLICANT: Leslie, Johnson  
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
 ; TITLE OF INVENTION: and Treatment  
 ; FILE REFERENCE: 10271-048-999  
 ; CURRENT APPLICATION NUMBER: US/09/996, 265  
 ; CURRENT FILING DATE: 2001-11-28  
 ; NUMBER OF SEQ ID NOS: 259  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 210  
 ; LENGTH: 450  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-996-265-210

	Query Match	72.5%	Score 582.5;	DB 10;	Length 450;
	Best Local Similarity	76.4%;	Pred. No. 3.6e-41;		
	Matches 113; Conservative	11;	Mismatches 21;	Indels 3;	Gaps 2;
QY	2	PQTLLTCTCFSGFSLITRGVGVDMIRQPCKALQLWALIYNDDKYSPELSKSRLTIWK	61		
Dd	14	PQTLLTCTCFSGFSLTAGMSGVIHQPPGKALEWLADIWMDDKYDNPGLSKSRLTRISK	73		
QY	62	DTSNQVVTLWTNMDPVDTATYYCAHHFFSDSSWGQGFTLVSVSSASTKGPSVF	121		
Dd	74	DTSNQVVVLVTNMNDPDTATYYCARSMI--TNFY-FDVWGQGTIVTVSSASTKGPSVF	130		
QY	122	LAPCSRSTSESTAALGCILVKDPFPVPVT	149		
Dd	131	LAPSRSSTGGTAALGCILVKDYFPFPTV	158		

RESULT 14  
 US-09-996-265-238  
 ; Sequence 238, Application US/09996265  
 ; Publication No. US20030091584A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, James  
 ; APPLICANT: Scott, Koenig  
 ; APPLICANT: Leslie, Johnson  
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
 ; TITLE OF INVENTION: and Treatment  
 ; FILE REFERENCE: 10271-048-999  
 ; CURRENT APPLICATION NUMBER: US/09/996,265  
 ; CURRENT FILING DATE: 2001-11-28  
 ; NUMBER OF SEQ ID NOS: 259  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 238  
 ; LENGTH: 450  
 ; TYPE: prt  
 ; ORGANISM: Homo sapiens  
 US-09-996-265-238

	Query Match	72.5%;	Score 582.5;	DB 10;	Length 450;
	Best Local Similarity	76.4%;	Pred. No. 3.6e-41;		
	Matches 113;	Conservative 11;	Mismatches 21;	Indels 3;	Gaps 2
Qy	2	PQTTLTCTCFSGSLITRGGVDWIROPCKALQWLALIVWDDKRYSPISKSRLTITK	61		
Db	14	PTOTLTCTCFSGSLTAGMSGVGIROPCKALEWLADIWDDKKOYNPISKSRLTITK	73		
Qy	62	DTSKNQVVLWTWNMDPVDATYTYCAHHFFPDSSGQGTIVSVSSASTKGPSVFP	121		
Db	74	DTSKNQVVLKVTWNMDPADTATYTCARDMI--TNYF-EDVWGQGTIVTVSSASTKGPSVFP	130		
Qy	122	LAPCSRSTSESTAALGCLVKDYFPEPVY	149		
Db	131	LAPSSKSTSGCTAALGCLVKDYFPEPVY	158		

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RESULT 15
US-09-996-265-240
; Sequence 240, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administeri
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-240

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Query Match	72.5%	Score 582.5	DB 10	Length 450
Best Local Similarity	76.4%	Pred. No. 3.6e-41		
Matches 113	Conservative 11	Mismatches 21	Indels 3	Gaps 2
Qy	2	PQTTLTCTCFSGSLITRGVGVWDITROPGKALQWLALVWDDKYSPSLKSRLTITK	61	
Db	14	PTQTTLTCTCFSGSLTAGMSYGVINQPPGKALEWLADVWDDKDYINPSLKSRLTISK	73	
Qy	62	DTSKNOVLWLTWNMDPVDATTATYCAHHFFDSGGYYPFDSWGQGTLVSVSSASTKGPSVFP	121	
Db	74	DTSENQVVLKVTWNMDPADTATTYCARSMI--TNPY-FDVWGQGTITVTVSSASTKGPSVFP	130	
Qy	122	LAPCSRSTSESTAALGCLVKDYFPEPVV	149	
Db	131	LAPSSKSTSGTAAALGCLVKDYFPEPVV	158	

Search completed: March 8, 2005, 07:05:56  
Job time : 80.0704 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.3835 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-35

Perfect score: 803

Sequence: 1 NPQTLTLTCTFSGFSLITR.....SESTAALGCLVKDYFPEPVT 149

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap:\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582.5	72.5	450	4	US-09-996-288-210, App
2	582.5	72.5	450	4	US-09-996-288-238
3	582.5	72.5	450	4	US-09-996-288-240
4	582.5	72.5	450	4	US-09-996-288-242
5	582.5	72.5	450	4	US-09-996-288-244
6	582.5	72.5	450	4	US-09-996-288-246
7	581.5	72.4	450	4	US-09-996-288-208
8	579.5	72.2	450	4	US-09-996-288-232
9	579.5	72.2	450	4	US-09-996-288-234
10	579.5	72.2	450	4	US-09-996-288-236
11	579.5	72.2	450	4	US-09-996-288-248
12	578.5	72.0	450	4	US-09-996-288-226
13	578.5	72.0	450	4	US-09-996-288-252
14	578.5	72.0	450	4	US-09-996-288-354
15	578.5	72.0	450	4	US-09-996-288-256
16	578.5	72.0	475	4	US-09-740-002-27
17	577.5	71.9	450	4	US-09-996-288-212
18	577.5	71.9	450	4	US-09-996-288-214
19	576.5	71.8	450	4	US-09-996-288-238
20	571	71.1	451	4	US-09-996-288-230
21	570.5	71.0	450	4	US-09-996-288-218
22	570.5	71.0	450	4	US-09-996-288-222
23	570.5	71.0	450	4	US-09-996-288-224
24	570.5	71.0	450	4	US-09-996-288-250
25	569.5	70.9	450	4	US-09-996-288-216
26	569.5	70.9	450	4	US-09-996-288-220
27	561.5	69.9	462	4	US-09-288-942A-7

28	549.5	68.4	475	4	US-09-740-002-25	Sequence 25, Appl
29	534	66.5	499	3	US-09-049-672A-1	Sequence 1, Appl
30	488.5	60.8	172	4	US-09-472-087-7	Sequence 7, Appl
31	488.5	60.8	172	4	US-09-472-087-86	Sequence 86, Appl
32	467.5	58.2	473	3	US-09-049-672A-4	Sequence 4, Appl
33	465.5	58.0	832	3	US-08-630-820-7	Sequence 7, Appl
34	465.5	58.0	832	4	US-09-273-453-7	Sequence 7, Appl
35	461.5	57.5	241	4	US-09-726-219A-187	Sequence 187, App
36	461.5	57.5	255	3	US-09-171-945-57	Sequence 57, Appl
37	456.5	56.8	167	4	US-09-472-087-74	Sequence 74, Appl
38	456.5	56.8	463	4	US-09-472-087-1	Sequence 1, Appl
39	456.5	56.8	463	4	US-09-472-087-63	Sequence 63, Appl
40	456.5	56.8	463	4	US-09-472-087-64	Sequence 64, Appl
41	452	56.3	166	4	US-09-472-087-75	Sequence 75, Appl
42	452	56.3	464	4	US-09-472-087-2	Sequence 2, Appl
43	452	56.3	464	4	US-09-472-087-66	Sequence 66, Appl
44	451.5	56.2	273	3	US-08-397-411-6	Sequence 6, Appl
45	451.5	56.2	446	3	US-08-397-411-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-996-288-210  
; Sequence 210, Application US/09996288  
; Patent No. 6818216  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 210  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-210

Query Match 72.5%; Score 582.5; DB 4; Length 450;

Best Local Similarity 76.4%; Pred. No. 2.5e-49;

Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy	2	PQTTLTCTFSGFSLITRGVGVWIRQPPGKALQWLALIYWNDDKRYSPSLKSLRTITK	61
Db	14	PTQTLTLTCTFSGFSLSLSTAGMSVGVIRQPPGKALEWLADIWDDKDYNPSLKSLRTITK	73
Qy	62	DTSKNQVVLWNNMDPVDATYTCARHFFDSSGGYYPFDSWGQGLVSVSSASTGKPSVFP	121
Db	74	DTSKNQVVLWNNMDPADATYTCARSMI--TNFY-FDVGQGTVTTVSSASTGKPSVFP	130
Qy	122	LAPCSRSTSESTAALGCLVKDYFPEPVT	149
Db	131	LAPSKSTSGTAAALGCLVKDYFPEPVT	158

RESULT 2

US-09-996-288-238  
; Sequence 238, Application US/09996288  
; Patent No. 6818216  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288

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; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-238

Query Match          72.5%; Score 582.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 2.5e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy  2 PQTTLTCTFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db  14 PTQTLTCTFSGFSLITRGVGDWIRQPPGKALEWLADIWDDKKDYNFSLKSLRLISK 73

Qy  62 DTSKNQVLTMTNMDPVDATYYCAHHFFDSSGGYPPDSMGQGTLSVSSASTKGPSVFP 121
Db  74 DTSKNQVLTMTNMDPVDATYYCARDMI--TNFY-FDVWGQGTITVTSSASTKGPSVFP 130

Qy  122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db  131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 3
US-09-996-288-240
; Sequence 240, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-240

Query Match          72.5%; Score 582.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 2.5e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy  2 PQTTLTCTFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db  14 PTQTLTCTFSGFSLITRGVGDWIRQPPGKALEWLADIWDDKKDYNFSLKSLRLISK 73

Qy  62 DTSKNQVLTMTNMDPVDATYYCAHHFFDSSGGYPPDSMGQGTLSVSSASTKGPSVFP 121
Db  74 DTSKNQVLTMTNMDPVDATYYCARDMI--TNFY-FDVWGQGTITVTSSASTKGPSVFP 130

Qy  122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db  131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 4
US-09-996-288-242
; Sequence 242, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
```

```
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 242
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-242

Query Match          72.5%; Score 582.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 2.5e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy  2 PQTTLTCTFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db  14 PTQTLTCTFSGFSLITRGVGDWIRQPPGKALEWLADIWDDKKDYNFSLKSLRLISK 73

Qy  62 DTSKNQVLTMTNMDPVDATYYCAHHFFDSSGGYPPDSMGQGTLSVSSASTKGPSVFP 121
Db  74 DTSKNQVLTMTNMDPVDATYYCARDMI--TNFY-FDVWGQGTITVTSSASTKGPSVFP 130

Qy  122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db  131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 5
US-09-996-288-244
; Sequence 244, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 244
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-244

Query Match          72.5%; Score 582.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 2.5e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy  2 PQTTLTCTFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db  14 PTQTLTCTFSGFSLITRGVGDWIRQPPGKALEWLADIWDDKKDYNFSLKSLRLISK 73

Qy  62 DTSKNQVLTMTNMDPVDATYYCAHHFFDSSGGYPPDSMGQGTLSVSSASTKGPSVFP 121
Db  74 DTSKNQVLTMTNMDPVDATYYCARDMI--TNFY-FDVWGQGTITVTSSASTKGPSVFP 130

Qy  122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db  131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 6
US-09-996-288-246
; Sequence 246, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
```

; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 246  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-246

Query Match 72.5%; Score 582.5; DB 4; Length 450;  
Best Local Similarity 76.4%; Pred. No. 2.5e-49;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy 2 PQTTLTCTGSLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61  
Db 14 PTQTLTCTGSLTSGVSGWIRQPPGKALEWLADIWDDKDYNPSPSLKSLRLITSK 73  
Qy 62 DTSKNQVVLWTNMDPVDATATYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVVLKVTNMDPADATATYCARMI--TNYF-FDVMGQGTVTVTSSASTKGPSVFP 130  
Qy 122 LAPCSRSTSESTAALGCLVKDYFPPEPVT 149  
Db 131 LAPSSKSTSGGTAALGCLVKDYFPPEPVT 158

## RESULT 7

US-09-996-288-208  
; Sequence 208, Application US/09996288  
; Patent No. 6818216  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 208  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-208

Query Match 72.4%; Score 581.5; DB 4; Length 450;  
Best Local Similarity 76.4%; Pred. No. 3.1e-49;  
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy 2 PQTTLTCTGSLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61  
Db 14 PTQTLTCTGSLTSGVSGWIRQPPGKALEWLADIWDDKDYNPSPSLKSLRLITSK 73  
Qy 62 DTSKNQVVLWTNMDPVDATATYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVVLKVTNMDPADATATYCARSMI--TNYF-FDVMGQGTVTVTSSASTKGPSVFP 130  
Qy 122 LAPCSRSTSESTAALGCLVKDYFPPEPVT 149  
Db 131 LAPSSKSTSGGTAALGCLVKDYFPPEPVT 158

## RESULT 8

US-09-996-288-232  
; Sequence 232, Application US/09996288

; Patent No. 6818216  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 232  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-232

Query Match 72.2%; Score 579.5; DB 4; Length 450;  
Best Local Similarity 76.4%; Pred. No. 5e-49;  
Matches 113; Conservative 10; Mismatches 22; Indels 3; Gaps 1;

Qy 2 PQTTLTCTGSLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61  
Db 14 PTQTLTCTGSLTSGVSGWIRQPPGKALEWLADIWDDKDYNPSPSLKSLRLITSK 73  
Qy 62 DTSKNQVVLWTNMDPVDATATYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVVLKVTNMDPADATATYCAR--DMIFNWYFDVMGQGTVTVTSSASTKGPSVFP 130  
Qy 122 LAPCSRSTSESTAALGCLVKDYFPPEPVT 149  
Db 131 LAPSSKSTSGGTAALGCLVKDYFPPEPVT 158

## RESULT 9

US-09-996-288-234  
; Sequence 234, Application US/09996288  
; Patent No. 6818216  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 234  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-234

Query Match 72.2%; Score 579.5; DB 4; Length 450;  
Best Local Similarity 76.4%; Pred. No. 5e-49;  
Matches 113; Conservative 10; Mismatches 22; Indels 3; Gaps 1;

Qy 2 PQTTLTCTGSLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61  
Db 14 PTQTLTCTGSLTSGVSGWIRQPPGKALEWLADIWDDKDYNPSPSLKSLRLITSK 73  
Qy 62 DTSKNQVVLWTNMDPVDATATYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVVLKVTNMDPADATATYCAR--DMIFNWYFDVMGQGTVTVTSSASTKGPSVFP 130  
Qy 122 LAPCSRSTSESTAALGCLVKDYFPPEPVT 149  
Db 131 LAPSSKSTSGGTAALGCLVKDYFPPEPVT 158



Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158

## RESULT 14

US-09-996-288-254  
; Sequence 254, Application US/09996288  
; Patent No. 6818216  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 254  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-254

Query Match 72.0%; Score 578.5; DB 4; Length 450;  
Best Local Similarity 75.7%; Pred. No. 6.2e-49;  
Matches 112; Conservative 10; Mismatches 23; Indels 3; Gaps 1;  
Qy 2 PQTTLTCTSGFSLSITRGVGVWIRPPGKALQWLAIYWNDDKRYSPSLKRLTITK 61  
Db 14 PTQTLTCTSGFSLSITRGVGVWIRPPGKALEWLADIWNDDKRYNPSLKDRLTISK 73  
Qy 62 DTSKNQVVLWTNMDPVDATYICAHFFDSSGGYYPDSWOGTLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVVLKVTNMDPADATYICAR---DMIFNFYFDVMGOGTTVTVSSASTKGPSVFP 130  
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158

## RESULT 15

US-09-996-288-256  
; Sequence 256, Application US/09996288  
; Patent No. 6818216  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 256  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-256

Query Match 72.0%; Score 578.5; DB 4; Length 450;  
Best Local Similarity 75.7%; Pred. No. 6.2e-49;  
Matches 112; Conservative 10; Mismatches 23; Indels 3; Gaps 1;  
Qy 2 PQTTLTCTSGFSLSITRGVGVWIRPPGKALQWLAIYWNDDKRYSPSLKRLTITK 61  
Db 14 PTQTLTCTSGFSLSITRGVGVWIRPPGKALEWLADIWNDDKRYNPSLKDRLTISK 73

Qy 62 DTSKNQVVLWTNMDPVDATYICAHFFDSSGGYYPDSWOGTLVSVSSASTKGPSVFP 121  
Db 74 DTSKNQVVLKVTNMDPADATYICAR---DMIFNFYFDVMGOGTTVTVSSASTKGPSVFP 130  
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149  
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158

Search completed: March 8, 2005, 05:54:11  
Job time : 16.3835 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.5183 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-36

Perfect score: 772

Sequence: 1 VTQSPLSVTPGPASISCSQSLSVHSGNTLYWYLOKPGQPKPLIYRVSNRFSGV 148

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.\*
- 2: pir2.\*
- 3: pir3.\*
- 4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	74.2	219	2 S16112	Ig kappa chain V r
2	568	73.6	219	2 S38865	Ig kappa chain - m
3	567	73.4	219	2 S52028	Ig kappa chain - m
4	567	73.4	219	2 PC4203	Ig kappa chain (mo
5	564	73.1	197	2 S29593	Ig kappa chain (WM
6	564	73.1	217	2 S42772	Ig kappa chain - m
7	548	71.0	225	2 J10029	Ig kappa chain pre
8	522	67.6	215	2 J20242	Ig kappa chain NIG
9	515	66.7	215	2 J20244	Ig kappa chain NIG
10	506	65.5	215	2 A23746	Ig kappa chain V-I
11	501	64.9	121	2 S40371	Ig kappa chain - h
12	498.5	64.6	240	2 S06084	Ig kappa chain pre
13	495	64.1	135	2 S40342	Ig kappa chain - h
14	490.5	63.5	214	2 S68212	Ig kappa chain (Ma
15	490.5	63.5	220	2 A31790	Ig kappa chain V r
16	489.5	63.4	210	2 A56169	Ig kappa chain V r
17	489	63.3	124	2 S03876	Ig kappa chain V-I
18	488	63.2	125	2 S40356	Ig kappa chain - h
19	488	63.2	215	2 J20243	Ig kappa chain NIG
20	485	62.8	120	2 S42266	Ig kappa chain V-J
21	484	62.7	136	2 S40357	Ig kappa chain V-J
22	478.5	62.0	216	2 J20241	Ig kappa chain Am3
23	475.5	61.6	218	2 S68241	Ig kappa chain V r
24	475.5	61.6	218	2 J25810	Ig kappa chain V r
25	469	60.8	112	2 S58206	Ig kappa chain V r
26	466	60.4	112	2 S58207	Ig kappa chain V r
27	465	60.2	113	1 K2HUTW	Ig kappa chain V-I
28	462	59.8	132	2 S26882	Ig kappa chain V r
29	458.5	59.4	140	2 S22658	Ig kappa chain pre

30	458	59.3	117	1 K2HUCM	Ig kappa chain pre
31	457	59.2	126	2 S40312	Ig kappa chain - h
32	457	59.2	128	2 S40373	Ig kappa chain - h
33	456.5	59.1	130	2 S40321	Ig kappa chain - h
34	455	58.9	115	2 S38715	Ig kappa chain V r
35	453	58.7	118	2 PT0359	Ig kappa chain V r
36	451	58.4	115	2 S60066	Ig kappa chain V r
37	450	58.3	112	2 E27887	Ig kappa chain V r
38	449.5	58.2	131	2 S40355	Ig kappa chain - h
39	448	58.0	131	2 B34904	Ig kappa chain pre
40	447.5	58.0	126	2 S40339	Ig kappa chain - h
41	447	57.9	131	2 D29380	Ig kappa chain pre
42	445	57.6	112	2 E27887	Ig kappa chain V r
43	445	57.6	114	2 A32967	Ig kappa chain V-I
44	445	57.6	131	2 B30577	Ig kappa chain pre
45	444	57.5	112	2 S53750	antibody Fab Jcl 1

ALIGNMENTS

RESULT 1

S16112  
Ig kappa chain V region (G2a) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S16112  
R:Vaesen, M.; Froesch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.; f Biol. Chem. Hoppe-Seyler 372, 451-453, 1991  
A:Title: Primary structure of the murine monoclonal ICG2a antibody mAb735 against alpha(2; A:Reference number: S16112; MUID:92000313; PMID:1910583  
A:Accession: S16112  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-219 <BIT>  
A:Cross-references: UNIPROT:Q8VC16; UNIPROT:Q99M37  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match	74.2%	Score	573	DB	2	Length	219
Best Local Similarity	74.3%	Pred. No.	3.1e-41				
Matches	107	Conservative	16	Mismatches	21	Indels	0
Gaps	0						
Oy	1	VTQSPLSVTPGPASISCSQSLSVHSGNTLYWYLOKPGQPKPLIYRVSNRFSGV	60				
Db	4	MTQTPLSVSLGPDQASISCRSSQSLVHSGNTLYWYLOKPGQPKPLIYRVSNRFSGV	63				
Oy	61	PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIETLFTFGGCTKVKIKRTVAAPSVEIF	120				
Db	64	PDRFSGSGSGTDFTLKISRVEAEDLVGYFCQGHVPTFGGTRLEIKRADAAPTVSIF	123				
Oy	121	PPSDEQLKSGTASVVCVLLNNFYPR	144				
Db	124	PPSSEQLTSGGASVVCFLNNFYPK	147				

RESULT 2

S38865  
Ig kappa chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 15-Jun-2001  
C:Accession: S38865  
R:Kipp, B.; Becker, W.; Schlaak, M.  
submitted to the EMBL Data Library, November 1993  
A:Description: Combination of a defined specificity and desired isotype by cloning of an A:Reference number: S38864  
A:Accession: S38865  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-219 <KIP>  
A:Cross-references: EMBL:Z27396; NID:g416538; PIDN:CAA81787.1; PID:g416539  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 73.6%; Score 568; DB 2; Length 219;  
Best Local Similarity 75.0%; Pred. No. 8.1e-41;  
Matches 108; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIYEAFNRFSGV 60

Db 4 MTQSPSLSVSLGDAQSISCRSSQSLVHTNGNTLYLWYLOKPGSLKLLIYVSNRFSGV 63

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVIRKRTVAAPSVPFIF 120

Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVIRKRTVAAPSVPFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNFFYPR 144

Db 124 PPSSEQLTSGGASVVCFLNFFYPK 147

#### RESULT 3

S52028

Ig kappa chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000

C;Accession: S52028

R;van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;  
submitted to the EMBL Data Library, August 1994

A;Description: Coordinate expression of antibody subunit genes yields high levels of fur

A;Reference number: S52028

A;Accession: S52028

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-219 <KWA>

A;Cross-references: EMBL:L35138; NID:g522336; PIDN:AA67525.1; PID:g522337

A;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 73.4%; Score 567; DB 2; Length 219;

Best Local Similarity 75.0%; Pred. No. 9.8e-41;

Matches 108; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIYEAFNRFSGV 60

Db 4 MTQSPSLSVSLGDAQSISCRSSQSLVHTNGNTLYLWYLOKPGQSLKLLIYVSNRFSGV 63

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVIRKRTVAAPSVPFIF 120

Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVIRKRTVAAPSVPFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNFFYPR 144

Db 124 PPSSEQLTSGGASVVCFLNFFYPK 147

#### RESULT 4

PC4203

Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 11-Jan-2000

C;Accession: PC4203

R;Kwak, J.W.; Lee, 1996

A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m

A;Reference number: PC4202; MUID:97082978; PMID:8964510

A;Accession: PC4203

A;Molecule type: mRNA

A;Residues: 1-219 <KWA>

A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226

C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;1-112/Domain: V region #status predicted <VRG>

F;113-219/Domain: C region #status predicted <CRG>

#### Query Match

Best Local Similarity

Matches 106; Conservative

17; Mismatches 21; Indels 0; Gaps 0;

#### Query Match

Best Local Similarity

Matches 107; Conservative

16; Mismatches 21; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIYEAFNRFSGV 60

Db 4 MTQSPSLSVSLGDAQSISCRSSQSLVHTNGNTLYLWYLOKPGQSLKLLIYVSNRFSGV 63

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVIRKRTVAAPSVPFIF 120

Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVIRKRTVAAPSVPFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNFFYPR 144

Db 124 PPSSEQLTSGGASVVCFLNFFYPK 147

#### RESULT 5

S29593

Ig kappa chain (WM65) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 11-Jan-2000

C;Accession: S29593

R;Seymour, R.

submitted to the EMBL Data Library, February 1991

A;Reference number: S29593

A;Accession: S29593

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-197 <SEY>

A;Cross-references: EMBL:X57856; NID:g52588; PIDN:CAA40991.1; PID:g52589

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

#### Query Match

Best Local Similarity

Matches 106; Conservative

16; Mismatches 22; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIYEAFNRFSGV 60

Db 19 MTQAPSPVTPGESASISCRSSQSLHSDGTYLYWYLOKPGQPPOLLIYRMSNLASGV 78

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVIRKRTVAAPSVPFIF 120

Db 79 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVIRKRTVAAPSVPFIF 138

Qy 121 PPSDEQLKSGTASVVCLLNFFYPR 144

Db 139 PPSSEQLTSGGASVVCFLNFFYPK 162

#### RESULT 6

S42772

Ig kappa chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C;Accession: S42772

R;Schellekens, G.A.

submitted to the EMBL Data Library, November 1993

A;Reference number: S42771

A;Accession: S42772

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-217 <SCH>

A;Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;14-93/Domain: immunoglobulin homology <IMM>

#### Query Match

Best Local Similarity

Matches 106; Conservative

17; Mismatches 21; Indels 0; Gaps 0;



```
Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYEAENRFSGV 60
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 2 MTQSPSLPVLGDAQASISCRSSQSLVHTNGNTYLHWYLPKPGQSPKLLIYKVSRTFSGV 61
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQSIELPFTFGGKTKVEIKRTVAAPSVPF 120
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 62 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQSIELPFTFGGKTKVEIKRTVAAPSVPF 121
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Qy 121 PPSDEQLKSGTASVVCLLNNFYPR 144
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 122 PPSDEQLKSGTASVVCFLNNFYPK 145
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||

RESULT 7
JL0029
Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaynard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor
A:Reference number: JL0029; MUID:88171315; PMID:3127529
A:Accession: JL0029
A:Molecule type: mRNA
A:Residues: 1-225 <CHI>
A:Cross-references: UNIPROT:Q99M37
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A:Note: the authors translated the codon CGG for residue 106 as Pro. ACC for residue 132
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because
      ect except for four positions shown above
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:7-106/Domain: Ig kappa chain #status predicted <ILC>
F:7-106/Domain: V region #status predicted <VAR>
F:107-119/Domain: J region #status predicted <JIR>
F:120-225/Domain: C region #status predicted <COR>

Query Match 71.0%; Score 548; DB 2; Length 225;
Best Local Similarity 72.2%; Pred. No. 4e-39;
Matches 104; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYEAENRFSGV 60
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 10 MTQSPSLPVLGDAQASISCRSSQSLVHTNGNTYLHWYLPKPGQSPNLLIYKISNRFSGV 69
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQSIELPFTFGGKTKVEIKRTVAAPSVPF 120
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 70 PDRFSGSGSGTDFSLKISRVEAEDVGLYVCMQSIELPFTFGGKTKVEIKRTVAAPSVPF 129
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Qy 121 PPSDEQLKSGTASVVCLLNNFYPR 144
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 130 PPSDEQLKSGTASVVCFLNNFYPK 153
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||

RESULT 8
JL0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>
```

```
Query Match 67.6%; Score 522; DB 2; Length 215;
Best Local Similarity 68.2%; Pred. No. 5.9e-37;
Matches 101; Conservative 19; Mismatches 24; Indels 4; Gaps 1;

Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYEAENRFSGV 60
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 4 LTQSPGTLSPGERATLSCRASQSV---SNNYLANVQKPKGQAPSLIIYDASRATGI 59
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQSIELPFTFGGKTKVEIKRTVAAPSVPF 120
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 60 PDRFSGSGSGTDFTLTISGLEPEDFAVYVCOQYDRPPTFGQTKVEIKRTVAAPSVPF 119
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 120 PPSDEQLKSGTASVVCFLNNFYPREKV 147
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||

RESULT 9
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T.
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 515; DB 2; Length 215;
Best Local Similarity 69.1%; Pred. No. 2.3e-36;
Matches 103; Conservative 19; Mismatches 21; Indels 6; Gaps 3;

Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYEAENRFSGV 60
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 4 LTQSPATLSVSPGERATLSCRASQSV---VHSN---LAWYQKPKGQAPRLIIYRSTRATGI 58
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQSIELPFTFGGKTKVEIKRTVAAPSVPF 119
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 59 PARFSGSGSGTDFTLTISQSEDFALYVCOQYNTWPPLTFGGGKTKVEIKRTVAAPSVPF 118
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Qy 120 FPPSDEQLKSGTASVVCFLNNFYPRKERV 148
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 119 FPPSDEQLKSGTASVVCFLNNFYPREKV 147
      :|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||

RESULT 10
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 506; DB 2; Length 215;
Best Local Similarity 68.2%; Pred. No. 1.3e-35;
Matches 101; Conservative 18; Mismatches 25; Indels 4; Gaps 1;

Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYEAENRFSGV 60
```

Db 4 LTQSPATLSLSPGRATLSGASQSV-----SSNYLAWYQQKPGQAPRLIIYDASSRATGI 59  
 Qy 61 PDRESGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 120  
 Db 60 PDRESGSGGTDFTLTISRLEPEDAFVYVYQQYSGSLPTFGGGTKVEIKRTVAAPSVFIF 119

Qy 121 PPSDEQLKSGTASVVLNNFYPRKERV 148  
 Db 120 PPSDEQLKSGTASVVLNNFYPREAKV 147

RESULT 11  
 S40371  
 Ig kappa chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C/Accession: S40371  
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A/Reference number: S40312; MUID:94080891; PMID:8258341  
 A/Accession: S40371  
 A/Status: preliminary; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-121 <KLE>  
 A/Cross-references: EMBL:X72481; NID:g441430; PIDN:CAA51149.1; PID:g441431  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/13-92/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 501; DB 2; Length 121;  
 Best Local Similarity 80.2%; Pred. No. 1.9e-35;  
 Matches 97; Conservative 9; Mismatches 15; Indels 0; Gaps 0;  
 Qy 1 VTQSPLSVTPGQASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 60  
 Db 1 MTQSPLSLPVTGPGASISCRSSQSLSYSTGYNYLDWYLOKPGKSPQLLIYLGSKRASGV 60  
 Qy 61 PDRESGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 120  
 Db 61 PDRESGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 120

Qy 121 P 121  
 Db 121 P 121

RESULT 12  
 S06084  
 Ig kappa chain precursor - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
 C/Accession: S06084  
 R/Crowe, J.S.; Smith, M.A.; Cooper, H.J.  
 Nucleic Acids Res. 17, 7992, 1989  
 A/Title: Nucleotide sequence of Y3-Ag 1-2.3. rat myeloma immunoglobulin kappa chain cDNA  
 A/Reference number: S06084; MUID:90016888; PMID:2508067  
 A/Accession: S06084  
 A/Molecule type: mRNA  
 A/Residues: 1-240 <CRO>  
 A/Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/1-20/Domain: signal sequence #status predicted <SIG>  
 F/21-240/Product: Ig kappa chain #status predicted <MAT>  
 F/153-222/Domain: immunoglobulin homology <IMM>

Query Match 64.6%; Score 498.5; DB 2; Length 240;  
 Best Local Similarity 66.9%; Pred. No. 6.3e-35;  
 Matches 97; Conservative 19; Mismatches 28; Indels 1; Gaps 1;  
 Qy 1 VTQSPLSVTPGQASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 59

Db 24 MTQSPSSLAWSAGETVTINCKSSQSLFYSGNKNYLAWYQQKQSPKLLIYWASTRQSG 83  
 Qy 60 VPRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 119  
 Db 84 VPRFSGSGGTDFTLTISRLEDAIYYCLQYETFTFGAGTKLELRADAAPTFSI 143  
 Qy 120 FPPSDEQLKSGTASVVLNNFYPR 144  
 Db 144 FPPSDEQLKSGTASVVLNNFYPR 168

RESULT 13  
 S40342  
 Ig kappa chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
 C/Accession: S40342  
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A/Reference number: S40312; MUID:94080891; PMID:8258341  
 A/Accession: S40342  
 A/Status: preliminary; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-135 <KLE>  
 A/Cross-references: UNIPROT:Q8NEK0; EMBL:X72452; NID:g441372; PID:g441373  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/29-108/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 495; DB 2; Length 135;  
 Best Local Similarity 82.8%; Pred. No. 6.9e-35;  
 Matches 96; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
 Qy 1 VTQSPLSVTPGQASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 60  
 Db 17 MTQSPLSLPVTGPGASISCRSSQSLHSGYNYLDWYLOKPGQSPQLLIYLGSNRASGV 76  
 Qy 61 PDRESGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPS 116  
 Db 77 PDRESGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPS 132

RESULT 14  
 S68212

Ig kappa chain (Mab03-1) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 29-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 11-Jan-2000  
 C/Accession: S68212  
 R/Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
 FEBS Lett. 375, 273-276, 1995  
 A/Title: Thermolabile peroxidase activity with a recombinant antibody L chain-porphyrin  
 A/Reference number: S68211; MUID:96085223; PMID:7498516  
 A/Accession: S68212  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-214 <TAK>  
 A/Cross-references: EMBL:D29668  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 63.5%; Score 490.5; DB 2; Length 214;  
 Best Local Similarity 66.9%; Pred. No. 2.7e-34;  
 Matches 97; Conservative 17; Mismatches 30; Indels 1; Gaps 1;  
 Qy 1 VTQSPLSVTPGQASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 59  
 Db 4 MTQSPSSLAWSVQKVTMSCKSSQSLNSRNKNYLAWSQKQSPKLLIYFASTRSG 63  
 Qy 60 VPRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 119  
 Db 64 VPRFSGSGGTDFTLTISTVQAEDLADYFCQQHYSTFTFGGTKLEIKRADAAPTFSI 123

Qy 120 FPPSDEQLKSGTASVVCILNNFYPR 144  
Db 124 FPPSSEQLTSGGASVVCFLNNFYPK 148

RESULT 15

A31790  
Ig kappa chain V region (17/9) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
C:Accession: A31790  
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.  
J. Biol. Chem. 263, 17100-17105, 1988  
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an an  
A:Reference number: A92686; MUID:89034213; PMID:3182835  
A:Accession: A31790  
A:Molecule type: mRNA  
A:Residues: 1-220 <SCH>  
A:Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 490.5; DB 2; Length 220;  
Best Local Similarity 66.2%; Pred. No. 2.7e-34;  
Matches 96; Conservative 16; Mismatches 32; Indels 1; Gaps 1;  
Qy 1 VTQSPLSLSVTPGQPASISCKSSQSLHS-DGKTYLYWYLOKPGQPOLLIIYEAFNRFSG 59  
Db 4 MTQSPSSLTVTAGEKVTWSTCTSSQSLFNSGKQKNYLTWYQKPGQPPKVLIIYWASTRESG 63  
Qy 60 VPDPSGSGSGTDFTLKLSRVEADVGLYYCMQSIELPFTGGGTYKVEIKRTVAAPSVPI 119  
Db 64 VPDRTGSGSGTDFTLTISVQAEADLAVYYCQNDYSNPLTFGGGTYKLELRADAAPT VSI 123  
Qy 120 FPPSDEQLKSGTASVVCILNNFYPR 144  
Db 124 FPPSSEQLTSGGASVVCFLNNFYPK 148

Search completed: March 8, 2005, 06:39:29  
Job time : 11.5683 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 55.2705 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-36

Perfect score: 772

Sequence: 1 VTQSPLSLSTPGQPASISC.....SGTASVCLNNFPRKERV 148

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	651	84.3	239	2	Q8NEK0	Q8nek0 homo sapien
2	637.5	82.6	240	2	Q8PIH6	Q8pih6 homo sapien
3	621	80.4	239	2	Q8P491	Q8p491 homo sapien
4	607	78.6	239	2	Q8TCD0	Q8tcd0 homo sapien
5	570	73.8	219	2	Q65ZC0	Q65zc0 mus musculus
6	532	68.9	235	2	Q6GMV9	Q6gmv9 homo sapien
7	516.5	66.9	236	2	Q8PIL8	Q8pil8 homo sapien
8	507.5	65.7	236	2	Q8P5S8	Q8p5s8 homo sapien
9	504	65.3	235	2	Q8PJF2	Q8pjf2 homo sapien
10	496	64.2	235	2	Q6GMW0	Q6gmw0 homo sapien
11	495.5	64.2	236	2	Q6GMX0	Q6gmx0 homo sapien
12	493.5	63.9	234	2	Q72473	Q72473 homo sapien
13	493.5	63.9	236	2	Q6GMX8	Q6gmx8 homo sapien
14	492.5	63.8	236	2	Q6GMW1	Q6gmw1 homo sapien
15	485.5	62.9	236	2	Q6PIH7	Q6pih7 homo sapien
16	475.5	61.6	236	2	Q6GMX9	Q6gmx9 homo sapien
17	475.5	61.6	236	2	Q6PIT5	Q6pit5 homo sapien
18	473.5	61.3	238	2	Q66JS7	Q66js7 mus musculus
19	468.5	60.7	236	2	Q723Y4	Q723y4 homo sapien
20	465	60.2	113	1	KV2D_HUMAN	P01617 homo sapien
21	458	59.3	117	1	KV2E_HUMAN	P06309 homo sapien
22	458	59.3	243	2	Q6NTU5	Q6ntu5 xenopus lae
23	446.5	57.8	236	2	Q6PIH4	Q6pih4 homo sapien
24	443.5	57.4	115	1	KV2A_HUMAN	P01614 homo sapien
25	439.5	56.9	112	1	KV2C_HUMAN	P01616 homo sapien
26	438	56.7	248	2	Q65ZQ7	Q65zq7 mus sp. b3
27	436.5	56.5	237	2	Q7S236	Q7s236 xenopus lae
28	434	56.2	113	1	KV2G_MOUSE	P01631 mus musculus
29	433.5	56.2	236	2	Q7TS98	Q7ts98 mus musculus
30	433	56.1	133	1	KV2F_HUMAN	P06310 homo sapien
31	431.5	55.9	241	2	Q63ZX4	Q63zx4 mus musculus

32	427	55.3	112	2	Q6LEM8	Q6lem8 mus musculus
33	427	55.3	113	1	KV2E_MOUSE	P03976 mus musculus
34	427	55.3	113	1	KV2F_MOUSE	P01630 mus musculus
35	419	54.3	113	1	KV2B_HUMAN	P01615 homo sapien
36	415.5	53.8	114	2	Q9UL80	Q9ul80 homo sapien
37	403	52.2	112	1	KV2D_MOUSE	P01629 mus musculus
38	390.5	50.6	134	1	KV4C_HUMAN	P06314 homo sapien
39	385	49.9	113	1	KV2C_MOUSE	P01628 mus musculus
40	378	49.0	112	1	KV2A_MOUSE	P01626 mus musculus
41	376	48.7	133	1	KV4B_HUMAN	P06313 homo sapien
42	374.5	48.5	114	1	KV4A_HUMAN	P01625 homo sapien
43	372.5	48.3	108	1	KV1_CANPA	P01618 canis famil
44	364.5	47.2	111	1	KV3W_MOUSE	P01665 mus musculus
45	364.5	47.2	262	2	Q65ZII	Q65zii mus musculus

## ALIGNMENTS

### RESULT 1

ID	Q8NEK0	PRELIMINARY;	PRT;	239 AA.
AC	Q8NEK0;			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uadin T.B., Toehiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Iqbalano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fabey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences."			
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RC	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.			
RA	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC030814; AAH30814.1; -.			
DR	PIR; S23638; S23638.			
DR	PIR; S34091; S34091.			
DR	PIR; S40342; S40342.			
DR	PIR; S40357; S40357.			
DR	HSSP; P01834; 117Z.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig-cl.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	Pfam; PF07654; Cl-set; I.			
DR	SMART; SM00406; IGv; I.			
DR	PROSITE; PS50835; IG_LIKE; 2.			

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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;

Query Match      84.3%; Score 651; DB 2; Length 239;
Best Local Similarity 84.5%; Pred. No. 2.5e-57;
Matches 125; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 VTQSPLSLSTVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPOLLIIYEA FNRESGV 60
Db 24 MTQSPFLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPOLLIIYLGSNRASGV 83
QY 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQSIELPFTFGGTKVBIKRTVAAPSFI 120
Db 84 PDRFSGSGSGTDFTLKISKVEAEDVGIYVCMQGLQTPQTGGTKVEIKRTVAAPSFI 143
QY 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 144 PPSDEQLKSGTASVVCLLNNFYPRKERV 171

RESULT 2
Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC034142; AAH34142.1; -.
DR HSSP; P01837; 1KB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003596; Ig v.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 189D4DD8BB781BC4 CRC64;

Query Match      82.6%; Score 637.5; DB 2; Length 240;
Best Local Similarity 82.6%; Pred. No. 5.7e-56;
Matches 123; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 1 VTQSPLSLSTVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPOLLIIYEA FNRESGV 60
Db 24 MAQSPLSLSTVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPOLLIIYWGNSRASGV 83
QY 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQSIELPFTFGGTKVBIKRTVAAPSFI 119
Db 84 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQALQTPPTFGGTKLEIKRTVAAPSFI 143
QY 120 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 144 PPSDEQLKSGTASVVCLLNNFYPRKERV 172

RESULT 3
Q6P491 PRELIMINARY; PRT; 239 AA.
AC Q6P491;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC063599; AAH63599.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
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DR SMART: SM00406; IGV: 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match
Best Local Similarity 80.4%; Score 621; DB 2; Length 239;
Matches 119; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGPPASISCKSSQSLHSDGKTYLYWYLPKPGPPQLLIYEAFNRFSGV 60
Db 24 MTQTPSLSPVTLGPPASISCKSSQSLHSDGKTYLYWYLPKPGPPQLLIYKISNRFSGV 83

Qy 61 PDRFSGSGSGTDFTLKISRVAEDVGLYVCMQSLVLTFTFGGKTKVEIKRTVAAPSPVIF 120
Db 84 PDRFSGSGAGTDFTLKISRVAEDVGLYVCMQSHFPRFTFGGTRVEIKRTVAAPSPVIF 143

Qy 121 PPSDEQLKSGTASVVCLLNFPYPRKRV 148
Db 144 PPSDEQLKSGTASVVCLLNFPYPRKRV 171

RESULT 4
Q8TCD0 PRELIMINARY; PRT; 239 AA.
ID Q8TCD0
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Jordan A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; 117Z.
InterPro; IPR007110; Ig-like.
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DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV: 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match
Best Local Similarity 78.6%; Score 607; DB 2; Length 239;
Matches 116; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGPPASISCKSSQSLHSDGKTYLYWYLPKPGPPQLLIYEAFNRFSGV 60
Db 24 MTQTPSLSPVTLGPPASISCKSSQSLHSDGKTYLYWYLPKPGPPQLLIYKISNRDSGV 83

Qy 61 PDRFSGSGSGTDFTLKISRVAEDVGLYVCMQSLVLTFTFGGKTKVEIKRTVAAPSPVIF 120
Db 84 PDRFSGSGSGTDFTLKISRVAEDVGLYVCMQSHFPRFTFGGTRVEIKRTVAAPSPVIF 143

Qy 121 PPSDEQLKSGTASVVCLLNFPYPRKRV 148
Db 144 PPSDEQLKSGTASVVCLLNFPYPRKRV 171

RESULT 5
Q65ZC0 PRELIMINARY; PRT; 219 AA.
ID Q65ZC0
AC Q65ZC0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kappa light chain C region (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
recognizing a defined linear epitope of Chironomus thummi major
allergen Chi t 1.";
RL Int. Arch. Allergy Immunol. 110:348-353 (1996).
DR EMBL; Z37499; CA85724.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV: 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON TER 1 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match
Best Local Similarity 73.8%; Score 570; DB 2; Length 219;
Matches 109; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGPPASISCKSSQSLHSDGKTYLYWYLPKPGPPQLLIYEAFNRFSGV 60
Db 4 MTQSPSLSVSLGDAQSISCRSSQSLVHTNGNTYLHWYLPKPGSLKLLIIVSNRFSGV 63
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Db      24 LTQSPGTLSPGERATLSRASQSL----SSSYLAWYQQKPGQAPRLIIYGVSRATGI 79
Qy      61 PDRFSGSGGDTFTLKISRVEAEDVGLYYCMQ-SIELPFTFGGKTKVEIKRTVAAPS VFI 119
Db      80 PDRFSGSGGDTFTLTISRLSPEDPAVYCCQYGTSGRBITFGQGRLLDIKRTVAAPS VFI 139
Qy      120 FPPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db      140 FPPSDEQLKSGTASVVCLLNNFYPREAKV 168

RESULT 8
ID Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;

Query Match 65.7%; Score 507.5; DB 2; Length 236;
Best Local Similarity 66.4%; Pred. No. 7, 1e-43;
Matches 99; Conservative 23; Mismatches 22; Indels 5; Gaps 2;

Qy 1 VTQSPSLSVTFPGQPASISCKSSQLHSDGKTYLYWYLOKPGQPQLLIYEAENRFGV 60

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Db      24 LTQSPGTLSPGERATLSRASQTVFSS----HLAWYQQKPGQAPRLIIYGVSRATGI 79
Qy      61 PDRFSGSGGDTFTLKISRVEAEDVGLYYCMQSIETP-FTFGGKTKVEIKRTVAAPS VFI 119
Db      80 PDRFSGSGGDTFTLTITRLPEPDAVYFCQYGTSPSLTFGGGTRVEIKRTVAAPS VFI 139
Qy      120 FPPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db      140 FPPSDEQLKSGTASVVCLLNNFYPREAKV 168

RESULT 9
ID Q6PJF2 PRELIMINARY; PRT; 235 AA.
AC Q6PJF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 65.3%; Score 504; DB 2; Length 235;
Best Local Similarity 65.5%; Pred. No. 1, 6e-42;
Matches 97; Conservative 22; Mismatches 25; Indels 4; Gaps 1;

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QY 1 VTQSPLSVTPGQASISCKSSQSLHSDGKTYLYWLKQPGPPOLLIIYAFNRFSV 60  
 Db 24 LTQSPATLSVPGERATLSRASQISINN---SSAYLAWYQKPGQAPRLMFGSSRATGI 79  
 QY 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 120  
 Db 80 PDRFSGSGGTDFTLKISRLEPEDFAVYYCQYQSSQGTGPGTKVDIKRTVAAPSVFIF 139  
 QY 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148  
 Db 140 PPSDEQLKSGTASVVCLLNNFYPRKAV 167

## RESULT 10

Q6GMW0 Q6GMW0 PRELIMINARY; PRT; 235 AA.  
 ID Q6GMW0 AC Q6GMW0  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073792; AAH73792.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 235 AA; 25765 MW; 4360C36BD4133F5 CRC64;

Query Match 64.2%; Score 496; DB 2; Length 235;  
 Best Local Similarity 64.4%; Pred. No. 1e-41;  
 Matches 96; Conservative 27; Mismatches 20; Indels 6; Gaps 2;

QY 1 VTQSPLSVTPGQASISCKSSQSLHSDGKTYLYWLKQPGPPOLLIIYAFNRFSV 60  
 Db 24 MTQSPATLSVPGERATLSRASQISINN---LAWYQQRPGQAPRELLIYGASSRVGTI 78  
 QY 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVFI 119  
 Db 79 PGRFSGSGGTEFTLSTISLSQSDFAVYFCQYNDWLLYTFGQGTLEIKRTVAAPSVFI 138  
 QY 120 PPSDEQLKSGTASVVCLLNNFYPRKERV 148  
 Db 139 PPSDEQLKSGTASVVCLLNNFYPRKAV 167

## RESULT 11

Q6GMX0 Q6GMX0 PRELIMINARY; PRT; 236 AA.  
 ID Q6GMX0 AC Q6GMX0  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073775; AAH73775.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 64.2%; Score 495.5; DB 2; Length 236;  
 Best Local Similarity 65.5%; Pred. No. 1.2e-41;

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Matches 97; Conservative 15; Mismatches 31; Indels 5; Gaps 1;
Qy 1 VTQSPLSVTPGPAPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIIYEAFFRSGV 60
Db MTQSPSSLSASVGRVITTCRASQSI-----NNTLWYQLKPGKAPNLLIYAASLSQSGV 80
Qy 61 PDPSGSGSGDFTLTKISRVEAEADVGLYCMQSIETELPFTGGGTVKVEIKRTVAAPSVFIF 120
Db PPSRFGSGSGDFTLTKISRVEAEADVGLYCMQSIETELPFTGGGTVKVEIKRTVAAPSVFIF 140
Qy 121 PPSDEQLKSGTASVVCLLNNFYPKERV 148
Db PPSDEQLKSGTASVVCLLNNFYPKERV 168
RESULT 12
Q72473
ID Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RC Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS0290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
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Query Match 63.9%; Score 493.5; DB 2; Length 234;
Best Local Similarity 66.2%; Pred. No. 1.8e-41;
Matches 98; Conservative 15; Mismatches 30; Indels 5; Gaps 1;
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Qy 1 VTQSPLSVTPGPAPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIIYEAFFRSGV 60
Db MTQSPSSLSASVGRVITTCRASQSI-----GSLAWYQKPGKAPQQLIIYAASLQSGV 78
Qy 61 PDPSGSGSGDFTLTKISRVEAEADVGLYCMQSIETELPFTGGGTVKVEIKRTVAAPSVFIF 120
Db PPSRFGSGSGDFTLTKISRVEAEADVGLYCMQSIETELPFTGGGTVKVEIKRTVAAPSVFIF 138
Qy 121 PPSDEQLKSGTASVVCLLNNFYPKERV 148
Db PPSDEQLKSGTASVVCLLNNFYPKERV 166
RESULT 13
Q6GMX8
ID Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC Q6GMX8
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IGV; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS0290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
```

```
Query Match 63.9%; Score 493.5; DB 2; Length 236;
Best Local Similarity 64.9%; Pred. No. 1.8e-41;
Matches 96; Conservative 19; Mismatches 28; Indels 5; Gaps 1;
```





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 68.6168 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-36  
Perfect score: 772  
Sequence: 1 VTQSPLSLSTPGQPASISC.....SGTASVCLLNFFPKERV 148

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	772	100.0	148	2 AAY34315	Aay34315 IgG antib
2	704	91.2	168	8 ADK52426	Adk52426 Human ant
3	679.5	88.0	238	2 AAR93554	Aar93554 Monoclonal
4	662	85.8	241	3 AAY96303	Aay96303 Human IGF
5	661	85.6	247	5 ABG70338	Abg70338 Human MDD
6	657	85.1	238	8 ADL93653	Adl93653 Human CD4
7	656	85.0	238	8 ADL93649	Adl93649 Human CD4
8	653	84.6	238	8 ADL93654	Adl93654 Human CD4
9	652	84.5	219	6 ABP58286	Abp58286 Humanised
10	652	84.5	238	6 ABP58288	Abp58288 Humanised
11	650	84.2	238	8 ADL93650	Adl93650 Human CD4
12	649	84.1	239	3 AAY82611	Aay82611 Human PTH
13	649	84.1	239	7 ADL23139	Adl23139 Mouse/hum
14	648	83.9	219	6 ABR39464	Abr39464 Humanised
15	648	83.9	219	6 ABU08310	Abu08310 Humanised
16	648	83.9	219	6 ABR39792	Abr39792 Humanised
17	648	83.9	219	6 ABB80108	Abb80108 Light cha
18	648	83.9	219	7 ADE94065	Ade94065 Humanised
19	648	83.9	219	8 ADN61713	Adn61713 Humanised
20	648	83.9	238	4 AAU07744	Aau07744 Humanised
21	648	83.9	238	6 ABR39842	Abr39842 Humanised
22	647	83.8	219	8 ADR16817	Adr16817 Human bre
23	647	83.8	238	4 AAB72235	Aab72235 Humanised
24	647	83.8	238	4 AAB72231	Aab72231 Humanised
25	647	83.8	238	4 AAB72227	Aab72227 Humanised

26	647	83.8	238	4 AAB72233	Aab72233 Humanised
27	644	83.4	239	3 AAY82615	Aay82615 Human PTH
28	643	83.3	239	2 AAW71876	Aaw71876 Anti-huma
29	643	83.3	239	2 AAW71878	Aaw71878 Anti-huma
30	643	83.3	239	3 AAB12913	Aab12913 Anti-huma
31	643	83.3	239	3 AAB12915	Aab12915 Anti-huma
32	643	83.3	239	7 ADE28461	Ade28461 Human ant
33	641	83.0	239	7 ADE28421	Ade28421 Human ant
34	640	82.9	219	7 ADJ32138	Adj32138 Human int
35	639.5	82.8	175	8 ADK52414	Adk52414 Human ant
36	639	82.8	239	2 AAW71879	Aaw71879 Anti-huma
37	639	82.8	239	2 AAW71877	Aaw71877 Anti-huma
38	639	82.8	239	3 AAB12914	Aab12914 Anti-huma
39	639	82.8	239	3 AAB12916	Aab12916 Anti-huma
40	639	82.8	239	7 ADE28405	Ade28405 Human ant
41	638.5	82.7	237	8 ADL93658	Adl93658 Human CD4
42	638.5	82.7	237	8 ADL93651	Adl93651 Human CD4
43	638	82.6	239	7 ADE28465	Ade28465 Human ant
44	637	82.5	238	2 AAW14937	Aaw14937 Murine an
45	637	82.5	238	2 AAW14942	Aaw14942 3F4 Human

ALIGNMENTS

RESULT 1  
AAY34315  
ID AAY34315 standard; protein; 148 AA.  
XX AC AAY34315;  
XX DT 19-NOV-1999 (first entry)  
XX DE IGG antibody 2.4.4 kappa chain sequence.  
XX KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX OS Homo sapiens.  
XX PN WO9945031-A2.  
XX PD 10-SEP-1999.  
XX PF 03-MAR-1999; 99WO-US004583.  
XX PR 03-MAR-1998; 98US-00034607.  
XX PR 03-FEB-1999; 99US-00244253.  
(ABGE-) ABGENIX INC.  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
FI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX WPI; 1999-540816/45.  
N-PSDB; AAZ20416.  
PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX Claim 61; Fig 30; 245pp; English.  
CC This sequence represents the kappa chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
 XX  
 SQ Sequence 148 AA;

Query Match 100.0%; Score 772; DB 2; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 2.le-54;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQSPLSLVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIYEAFNRESGV 60  
 DB 1 VTQSPLSLVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIYEAFNRESGV 60  
 QY 61 PDRFSGSGSGTDFTLKISRVEADVGLIYCMQSIELPFTFGGKTVEIKETVAAPSVFIF 120  
 DB 61 PDRFSGSGSGTDFTLKISRVEADVGLIYCMQSIELPFTFGGKTVEIKETVAAPSVFIF 120  
 QY 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148  
 DB 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148

RESULT 2  
 ADK52426  
 ID ADK52426 standard; protein; 168 AA.  
 XX AC ADK52426;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Human anti-MCP-1 variable region light chain #33.  
 XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;  
 KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoiatic;  
 KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;  
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;  
 KW anti-MCP-1; heavy chain; light chain.  
 XX OS Homo sapiens.  
 XX PN W02004016769-A2.  
 XX PD 26-FEB-2004.  
 XX PF 19-AUG-2003; 2003WO-US026232.  
 XX PR 19-AUG-2002; 2002US-0404802P.  
 XX PA (ABGE-) ABGENIX INC.  
 XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;  
 PI Bhakta S;  
 XX DR WPI; 2004-203794/19.  
 XX DR N-PSDB; ADK52425.  
 XX PT New human monoclonal antibody that binds to monocyte chemo-attractant  
 PT protein-1 and is immobilized on an insoluble matrix; useful for  
 PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,  
 PT rheumatoid arthritis or psoriasis.  
 XX PS Claim 2; SEQ ID NO 132; 154pp; English.  
 XX CC The present invention relates to a human monoclonal antibody that binds  
 CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful  
 CC for the preparation of a medicament useful for treating neoplastic or  
 CC inflammatory conditions. The neoplastic disease is selected from breast  
 CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
 CC pancreatic cancer or prostate cancer. The inflammatory condition is  
 CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,  
 CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The  
 CC antibodies are also useful for diagnosing the above diseases. It is also

CC useful for the determining the level of MCP-1 and MCP-1 family members in  
 CC patient samples. The present sequence represents a human anti-MCP-1  
 CC variable region light chain sequence.  
 XX  
 SQ Sequence 168 AA;

Query Match 91.2%; Score 704; DB 8; Length 168;  
 Best Local Similarity 89.9%; Pred. No. 6.9e-49;  
 Matches 133; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 VTQSPLSLVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIYEAFNRESGV 60  
 DB 16 MTQTPLSLVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIYEAFNRESGV 75  
 QY 61 PDRFSGSGSGTDFTLKISRVEADVGLIYCMQSIELPFTFGGKTVEIKETVAAPSVFIF 120  
 DB 76 PDRFSGSGSGTDFTLKISRVEADVGLIYCMQSIELPFTFGGKTVEIKETVAAPSVFIF 135  
 QY 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148  
 DB 136 PPSDEQLKSGTASVVCLLNNFYPREAKV 163

RESULT 3  
 AAR93554  
 ID AAR93554 standard; protein; 238 AA.  
 XX AC AAR93554;  
 XX DT 20-AUG-1996 (first entry)  
 XX DE Monoclonal antibody DNA light chain against 65 kD hCMV antigen.  
 XX KW Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;  
 KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /note= "Signal peptide"  
 FT Protein 21..238  
 FT /note= "Mature light chain"  
 XX PN JP08038178-A.  
 XX PD 13-FEB-1996.  
 XX PF 20-FEB-1995; 95JP-00030742.  
 XX PR 18-FEB-1994; 94JP-00021628.  
 XX PA (TANA/) TANAKA H.  
 PA (NISON) NISSHINBO IND INC.  
 XX DR WPI; 1996-154852/16.  
 DR N-PSDB; AAT18060.  
 XX PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -  
 PT produced by primer amplification, used in the diagnosis of hCMV  
 PT infection.  
 XX PS Claim 5; Page 19; 22pp; Japanese.  
 XX CC The sequences given in AAR93553-54 represent the heavy and light chains  
 CC respectively of a monoclonal antibody against a 65 kD antigen of human  
 CC cytomegalovirus (hCMV). The DNA's encoding these sequences were amplified  
 CC using the sequences given in AAT18040-58. The monoclonal antibody may be  
 CC used in the diagnosis of hCMV  
 XX SQ Sequence 238 AA;

Query Match 88.0%; Score 679.5; DB 2; Length 238;



Best Local Similarity 88.5%; Pred. No. 9,1e-47;  
Matches 131; Conservative 8; Mismatches 8; Indels 1; Gaps 1;  
Qy 1 VTQSPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGPPQLLIYEAFNRPSGV 60  
Db 24 MTQTPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGPPQLLIYEVSNRPSGV 83  
Qy 61 PDRFSGSGSGDFTLKISRVEAEDVGLYVCMQSTELPFTFGGKTKVEIKRTVAAPSVFIP 120  
Db 84 PDRFSGSGSGDFTLKISRVEAEDVGLYVCMQSTELPFTFGGKTKVEIKRTVAAPSVFIP 142  
Qy 121 PPSDEQLKSGTASVVCLLNNFYPKERV 148  
Db 143 PPSDEQLKSGTASVVCLLNNFYPKERV 170  
RESULT 4  
ID AAY96303 standard; protein; 241 AA.  
XX AAY96303;  
AC AAY96303;  
DT 16-AUG-2000 (first entry)  
XX Human IGFAM-15 immunoglobulin.  
DE Human; immunoglobulin; IGFAM-15; IGFAM; immune disorder; cancer;  
KW infection; inflammation; haematopoiesis; AIDS; allergy.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT Peptide 1..20  
FT Protein 21..241 /label= signal\_peptide  
FT Protein 21..241 /label= IGFAM-15  
FT Domain 36..115  
FT Domain 154..223 /label= Ig\_domain  
FT Domain 154..223 /label= Ig\_domain  
XX WO20029583-A2.  
XX 25-MAY-2000.  
XX 19-NOV-1999; 99WO-US027566.  
XX 19-NOV-1998; 98US-00195853.  
XX 22-DEC-1998; 98US-0113635P.  
XX 07-APR-1999; 99US-0128194P.  
XX (INCY-) INCYTE PHARM INC.  
XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;  
PI Lu DAM, Lal P, Hillman JL, Yang J;  
XX WPI; 2000-387796/33.  
DR N-PSDB; AAA27395.  
XX Immunoglobulin superfamily proteins, the agonist and antagonist of the  
PT protein is useful for preventing and treating disorders associated with  
PT altered levels of the protein such as cancer, immune system disorders.  
XX Claim 1; Page 89-90; 105pp; English.  
XX The present sequence is the human immunoglobulin superfamily protein  
CC IGFAM-15. Its gene was isolated from a cDNA library of colon tissue. It  
CC is expressed in reproductive, gastrointestinal, haematopoietic and immune  
CC and cardiovascular tissue, where cancer and inflammation are common. The  
CC gene, protein, its antibodies, agonists and antagonists are suitable for  
CC diagnosing and treating many diseases, including cancer, immune system  
CC disorders (such as inflammation, AIDS, allergies, anaemia, Crohn's  
CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's

CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, CC systemic lupus erythematosus and ulcerative colitis), complications of CC cancer, haemodialysis and extracorporeal circulation, trauma and CC haematopoietic cancer (such as leukaemia) and infections caused by CC bacteria, viruses, fungi or parasites  
XX Sequence 241 AA;  
Query Match 85.8%; Score 662; DB 3; Length 241;  
Best Local Similarity 83.3%; Pred. No. 2.3e-45;  
Matches 125; Conservative 17; Mismatches 6; Indels 2; Gaps 1;  
Qy 1 VTQSPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGPPQLLIYEAFNRPSGV 60  
Db 24 LTQTPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGPPQLLIYEVSNRPSGV 83  
Qy 61 PDRFSGSGSGDFTLKISRVEAEDVGLYVCMQSTELPFTFGGKTKVEIKRTVAAPSVF 118  
Db 84 PDRFSGSGSGDFTLKISRVEAEDVGLYVCMQSTELPFTFGGKTKVEIKRTVAAPSVF 143  
Qy 119 IFPPSDEQLKSGTASVVCLLNNFYPKERV 148  
Db 144 IFPPSDEQLKSGTASVVCLLNNFYPKERV 173  
RESULT 5  
ID ABG70338 standard; protein; 247 AA.  
XX ABG70338;  
AC ABG70338;  
DT 21-OCT-2002 (first entry)  
XX Human MDDT protein Incyte ID No: LI:1171219.2.orf3:2001JAN12.  
XX Human; molecule for disease detection and treatment; MDDT; cancer;  
KW cell proliferative disorder; arteriosclerosis; cirrhosis; asthma;  
KW autoimmune disorder; inflammatory disorder; Crohn's disease;  
KW multiple sclerosis; cytostatic; antiarteriosclerotic; antiinflammatory;  
KW hepatotropic; immunosuppressive; antiasthmatic.  
XX Homo sapiens.  
XX WO200255738-A2.  
XX 18-JUL-2002.  
XX 09-JAN-2002; 2002WO-US001008.  
XX 12-JAN-2001; 2001US-0261622P.  
XX 16-JAN-2001; 2001US-0261865P.  
XX 17-JAN-2001; 2001US-0262208P.  
XX 17-JAN-2001; 2001US-0262209P.  
XX 17-JAN-2001; 2001US-0262326P.  
XX 19-JAN-2001; 2001US-0263063P.  
XX 19-JAN-2001; 2001US-0263065P.  
XX 19-JAN-2001; 2001US-0263329P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Panzer SR, Lincoln SE, Altus CM, Dufour GE, Hillman JL, Jones AL;  
PI Dam TC, Liu TF, Harris B, Flores V, Daffo A, Marwaha R, Chen AJ;  
PI Chang SC, Gerstein EH, Peralta CH, David MH, Lewis SA;  
XX WPI; 2002-590679/63.  
DR N-PSDB; ABS51811.  
XX New disease detection and treatment molecule (MDDT) polynucleotides and  
PT polypeptides, useful in diagnosing, studying, preventing or treating  
PT diseases associated with MDDT expression, e.g. autoimmune or inflammatory  
PT disorders.  
XX

PS Claim 27; Page 125-126; 129pp; English.  
 XX The present invention relates to the isolation of novel human molecules  
 CC for disease detection and treatment (MDDT), and the polynucleotide  
 CC sequences (mdt) encoding them. The MDDT polypeptides may be used to  
 CC screen for molecules that bind to, or are bound by the encoded  
 CC polypeptides, and to develop a transcript image of a tissue or cell type.  
 CC Probes comprising at least 20 nucleotides of the mdt polynucleotide may  
 CC be used to assess the toxicity of a test compound. The MDDT polypeptides  
 CC and mdt polynucleotides are useful in the diagnosis, study, prevention  
 CC and treatment of diseases associated with the expression of molecules for  
 CC disease detection and treatment. Such disorders include cell  
 CC proliferative disorders (e.g. arteriosclerosis, cirrhosis, or cancers),  
 CC and autoimmune/inflammatory disorders (e.g. asthma, Crohn's disease, or  
 CC multiple sclerosis). The mdt polynucleotides may also be used as  
 CC molecule markers in microarrays, and in somatic or germline gene  
 CC therapy. ABG70306-ABG70341 represent the MDDT proteins of the invention  
 XX  
 SQ Sequence 247 AA;

Query Match 85.6%; Score 661; DB 5; Length 247;  
 Best Local Similarity 84.5%; Pred. No. 2.9e-45;  
 Matches 125; Conservative 12; Mismatches 11; Indels 0; Gaps 0;  
 Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYAFNRFSGV 60  
 Db 32 MTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYLGSSRASGV 91  
 Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIETLPTFGGGTKVEIKRTVAAPSVPFIF 120  
 Db 92 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIETLPTFGGGTKVEIKRTVAAPSVPFIF 151  
 Qy 121 PPSDEQLKSGTASVVCLLNNFPYPRKERV 148  
 Db 152 PPSDEQLKSGTASVVCLLNNFPYPRKERV 179

RESULT 6  
 ADL93653  
 ID ADL93653 standard; protein; 238 AA.  
 AC ADL93653;  
 XX  
 XX 17-JUN-2004 (first entry)  
 DT  
 DE Human CD44-binding antibody light chain BE-D7-kappa-light SEQ ID NO:148.  
 XX human; CD44; light chain immunoglobulin variable domain;  
 KW heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;  
 KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
 KW dermatological; vasotropic; neuroprotective; antibody therapy;  
 KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
 KW graft versus host response; multiple sclerosis; neoplastic disorder;  
 KW cancer; antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2004024750-A2.  
 XX  
 XX 25-MAR-2004.  
 XX  
 XX 15-SEP-2003; 2003WO-US029318.  
 XX  
 XX 13-SEP-2002; 2002US-0410758P.  
 XX 09-MAY-2003; 2003US-0469123P.  
 XX  
 XX (DYAX-) DYAX CORP.  
 XX  
 XX Rondon IJ, Edge A, Baribault Kent R;  
 XX  
 XX WPI; 2004-270003/25.  
 XX  
 XX New protein comprising a light chain (LC) immunoglobulin variable domain

PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
 PT useful for preparing a composition for treating inflammatory or  
 PT neoplastic disorders.  
 XX  
 XX Disclosure; SEQ ID NO 148; 128pp; English.  
 PS  
 CC The invention relates to a novel isolated protein comprising a light  
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
 CC immunoglobulin variable domain sequence that form an antigen binding site  
 CC with binding affinity for the human CD44 extracellular domain and where  
 CC CD83 of the LC variable domain sequence. A protein of the invention has  
 CC cytotstatic, antiinflammatory, immunosuppressive, antiarthritic,  
 CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,  
 CC and may have a use in antibody therapy. The protein is useful for  
 CC preparing a composition for treating inflammatory disorders, e.g.,  
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
 CC multiple sclerosis or neoplastic disorder, which is a malignant or  
 CC metastatic cancer. The present sequence represents a human CD44-binding  
 CC antibody light chain.  
 XX  
 SQ Sequence 238 AA;

Query Match 85.1%; Score 657; DB 8; Length 238;  
 Best Local Similarity 85.1%; Pred. No. 5.8e-45;  
 Matches 126; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
 Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYAFNRFSGV 60  
 Db 23 MTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYLGSSRASGV 82  
 Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIETLPTFGGGTKVEIKRTVAAPSVPFIF 120  
 Db 83 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIETLPTFGGGTKVEIKRTVAAPSVPFIF 142  
 Qy 121 PPSDEQLKSGTASVVCLLNNFPYPRKERV 148  
 Db 143 PPSDEQLKSGTASVVCLLNNFPYPRKERV 170

RESULT 7  
 ADL93649  
 ID ADL93649 standard; protein; 238 AA.  
 AC ADL93649;  
 XX  
 XX 17-JUN-2004 (first entry)  
 DT  
 DE Human CD44-binding antibody light chain HAE-A3-kappa-light SEQ ID NO:144.  
 XX human; CD44; light chain immunoglobulin variable domain;  
 KW heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;  
 KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
 KW dermatological; vasotropic; neuroprotective; antibody therapy;  
 KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
 KW graft versus host response; multiple sclerosis; neoplastic disorder;  
 KW cancer; antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2004024750-A2.  
 XX  
 XX 25-MAR-2004.  
 XX  
 XX 15-SEP-2003; 2003WO-US029318.  
 XX  
 XX 13-SEP-2002; 2002US-0410758P.  
 XX 09-MAY-2003; 2003US-0469123P.  
 XX  
 XX (DYAX-) DYAX CORP.  
 XX  
 XX Rondon IJ, Edge A, Baribault Kent R;  
 XX  
 XX WPI; 2004-270003/25.

XX New protein comprising a light chain (LC) immunoglobulin variable domain  
 PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
 PT useful for preparing a composition for treating inflammatory or  
 PT neoplastic disorders.  
 XX Disclosure; SEQ ID NO 144; 128pp; English.  
 XX  
 CC The invention relates to a novel isolated protein comprising a light  
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
 CC immunoglobulin variable domain sequence that form an antigen binding site  
 CC with binding affinity for the human CD44 extracellular domain and where  
 CC CDR3 of the LC variable domain sequence. A protein of the invention has  
 CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,  
 CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,  
 CC and may have a use in antibody therapy. The protein is useful for  
 CC preparing a composition for treating inflammatory disorders, e.g.,  
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
 CC multiple sclerosis or neoplastic disorder, which is a malignant or  
 CC metastatic cancer. The present sequence represents a human CD44-binding  
 CC antibody light chain.  
 XX Sequence 238 AA;  
 SQ  
 Query Match 85.0%; Score 656; DB 8; Length 238;  
 Best Local Similarity 85.1%; Pred. No. 7e-45;  
 Matches 126; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 VTQPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPQLLIYEAFNRSGV 60  
 DB 23 MTQSPSLPVTTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPQLLIYLSNRASGV 82  
 QY 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQSIELPFTFGGKTKVEIKRTVAAPSVPFIF 120  
 DB 83 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQALQTPPTFGGKTKVEIKRTVAAPSVPFIF 142  
 QY 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148  
 DB 143 PPSDEQLKSGTASVVCLLNNFYPRKRV 170  
 RESULT 8  
 ID ADL93654 standard; protein; 238 AA.  
 AC ADL93654;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Human CD44-binding antibody light chain BE-H10-kappa-light SEQ ID NO:149.  
 XX  
 KW human; CD44; light chain immunoglobulin variable domain;  
 KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;  
 KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
 KW dermatological; vasotropic; neuroprotective; antibody therapy;  
 KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
 KW graft versus host response; multiple sclerosis; neoplastic disorder;  
 KW cancer; antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004024750-A2.  
 XX  
 PD 25-MAR-2004.  
 PF 15-SEP-2003; 2003WO-US029318.  
 XX  
 PR 13-SEP-2002; 2002US-0410758P.  
 PR 09-MAY-2003; 2003US-0469123P.  
 XX  
 PA (DYAX-) DYAX CORP.  
 XX  
 FI Rondon IJ, Edge A, Baribault Kent R;

XX WPI; 2004-270003/25.  
 XX  
 PT New protein comprising a light chain (LC) immunoglobulin variable domain  
 PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
 PT useful for preparing a composition for treating inflammatory or  
 PT neoplastic disorders.  
 XX Disclosure; SEQ ID NO 149; 128pp; English.  
 XX  
 CC The invention relates to a novel isolated protein comprising a light  
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
 CC immunoglobulin variable domain sequence that form an antigen binding site  
 CC with binding affinity for the human CD44 extracellular domain and where  
 CC CDR3 of the LC variable domain sequence. A protein of the invention has  
 CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,  
 CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,  
 CC and may have a use in antibody therapy. The protein is useful for  
 CC preparing a composition for treating inflammatory disorders, e.g.,  
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
 CC multiple sclerosis or neoplastic disorder, which is a malignant or  
 CC metastatic cancer. The present sequence represents a human CD44-binding  
 CC antibody light chain.  
 XX Sequence 238 AA;  
 SQ  
 Query Match 84.6%; Score 653; DB 8; Length 238;  
 Best Local Similarity 84.5%; Pred. No. 1.2e-44;  
 Matches 125; Conservative 11; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 VTQPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPQLLIYEAFNRSGV 60  
 DB 23 MTQSPSLPVTTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPQLLIYLSNRASGV 82  
 QY 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQSIELPFTFGGKTKVEIKRTVAAPSVPFIF 120  
 DB 83 PDRFSGSGSGTDFTLKISRVEAEDVGLYVCMQALQTPPTFGGKTKVEIKRTVAAPSVPFIF 142  
 QY 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148  
 DB 143 PPSDEQLKSGTASVVCLLNNFYPRKRV 170  
 RESULT 9  
 ID ABP58286 standard; protein; 219 AA.  
 AC ABP58286;  
 XX  
 DT 23-OCT-2003 (revised)  
 DT 31-MAR-2003 (first entry)  
 XX  
 DE Humanised 10D5 antibody light chain.  
 XX  
 KW Monoclonal antibody; 10D5; complementarity determining region; CDR;  
 KW mouse; human; humanised antibody; antibody; Alzheimer's disease;  
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; neurotropic.  
 XX  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..113  
 FT /note= "light chain variable region"  
 FT Region 24..39  
 FT /note= "CDR1"  
 FT Region 55..61  
 FT /note= "CDR2"  
 FT Region 94..102  
 FT /note= "CDR3"  
 XX  
 FN WO200288307-A2.

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XX PD 07-NOV-2002.
XX FH
XX PF
XX PR 26-APR-2002; 2002WO-US011854.
XX PA 30-APR-2001; 2001US-0287653P.
XX PI (ELIL ) LILLY & CO ELI.
XX PI Hinton PR, Vasquez M;
XX DR WPI; 2003-183836/18.
XX PT New humanized 10D5 antibody, useful for the manufacture of a medicament
XX PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
XX PT disease or cerebral amyloid angiopathy.
XX PS Claim 5; Page 9-10; 52pp; English.
XX PD
XX CC The present sequence is the protein sequence of the light chain of a
XX CC humanised antibody of the present invention. In the variable portion, the
XX CC complementarity determining regions (CDRs) originate from murine
XX CC monoclonal antibody 10D5 and the framework region originates from human
XX CC germline Vk segment DPK18 and J segment Jk4. Novel humanised antibodies
XX CC of the invention have CDRs from 10D5 and human framework sequences. These
XX CC humanised antibodies have binding affinities (affinity and epitope
XX CC location) approximately the same as those of the mouse 10D5 antibody. The
XX CC invention includes antibodies, single chain antibodies, and their
XX CC fragments, as well as nucleotide sequences, vectors, transformed host
XX CC cells, and methods of using the humanised antibody to treat, prevent,
XX CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
XX CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
XX CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
XX CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
XX CC OS field)
XX SQ Sequence 219 AA;
Query Match 84.5%; Score 652; DB 6; Length 219;
Best Local Similarity 83.1%; Pred. No. 1.3e-44;
Matches 123; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
Qy 1 VTQSPSLSVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIVAFNRFSGV 60
Db 4 MTQSPSLPVTGLGQPASISCRSSQNIHSNGNTYLEWYLOKPGQSPRLLIYKVSNRFSGV 63
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVEIF 120
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVEIF 123
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 124 PPSDEQLKSGTASVVCLLNNFYPRKERV 151
RESULT 10
ABP58288
ID ABP58288 standard; protein; 238 AA.
XX AC ABP58288;
XX XX
XX DT 23-OCT-2003 (revised)
XX DT 31-MAR-2003 (first entry)
XX XX
XX DE Humanised 10D5 antibody light chain.
XX KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
XX KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
XX KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Chimeric.
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XX Key Location/Qualifiers
XX FH Peptide 1..19
XX FT /label= Signal_peptide
XX FT Peptide 20..238
XX FT /label= Mature_protein
XX FT /note= "the mature light chain is claimed in Claim 5"
XX FT Region 20..132
XX FT /note= "light chain variable region, claimed in Claim 4"
XX FT Region 43..58
XX FT /note= "CDR1"
XX FT Region 74..80
XX FT /note= "CDR2"
XX FT Region 113..121
XX FT /note= "CDR3"
XX PN WO200288307-A2.
XX XX
XX PD 07-NOV-2002.
XX XX
XX PF 26-APR-2002; 2002WO-US011854.
XX PR 30-APR-2001; 2001US-0287653P.
XX PA (ELIL ) LILLY & CO ELI.
XX PI Hinton PR, Vasquez M;
XX DR WPI; 2003-183836/18.
XX DR N-PSDB; ABZ24638, ABZ24640.
XX PT New humanized 10D5 antibody, useful for the manufacture of a medicament
XX PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
XX PT disease or cerebral amyloid angiopathy.
XX PS Disclosure; Page 13; 52pp; English.
XX XX
XX CC The present sequence is the protein sequence of the light chain of a
XX CC humanised antibody of the present invention. In the variable portion, the
XX CC complementarity determining regions (CDRs) originate from murine
XX CC monoclonal antibody 10D5 and the framework region originates from human
XX CC germline Vk segment DPK18 and J segment Jk4. Novel humanised antibodies
XX CC of the invention have CDRs from 10D5 and human framework sequences. These
XX CC humanised antibodies have binding affinities (affinity and epitope
XX CC location) approximately the same as those of the mouse 10D5 antibody. The
XX CC invention includes antibodies, single chain antibodies, and their
XX CC fragments, as well as nucleotide sequences, vectors, transformed host
XX CC cells, and methods of using the humanised antibody to treat, prevent,
XX CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
XX CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
XX CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
XX CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
XX CC OS field)
XX SQ Sequence 238 AA;
Query Match 84.5%; Score 652; DB 6; Length 238;
Best Local Similarity 83.1%; Pred. No. 1.5e-44;
Matches 123; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
Qy 1 VTQSPSLSVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIVAFNRFSGV 60
Db 23 MTQSPSLPVTGLGQPASISCRSSQNIHSNGNTYLEWYLOKPGQSPRLLIYKVSNRFSGV 82
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVEIF 120
Db 83 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVEIF 142
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 143 PPSDEQLKSGTASVVCLLNNFYPRKERV 170
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RESULT 11	
ADL93650	
ID	ADL93650 standard; protein; 238 AA.
XX	
AC	ADL93650;
XX	
XX	
DT	17-JUN-2004 (first entry)
XX	
DE	Human CD44-binding antibody light chain HAE-G2-kappa-light SEQ ID NO:145.
XX	
KW	human; CD44; light chain immunoglobulin variable domain;
KW	heavy chain immunoglobulin variable domain; immunoglobulin; cytosolic;
KW	antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
KW	dermatological; vasotropic; neuroprotective; antibody therapy;
KW	inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW	graft versus host response; multiple sclerosis; neoplastic disorder;
KW	cancer; antibody.
XX	
OS	Homo sapiens.
XX	
PN	WO2004024750-A2.
XX	
PD	25-MAR-2004.
XX	
PF	15-SEP-2003; 2003WO-US029318.
XX	
PR	13-SEP-2002; 2002US-0410758P.
PR	09-MAY-2003; 2003US-0469123P.
XX	
PA	(DYAX-) DYAX CORP.
XX	
PI	Rondon J, Edge A, Baribault Kent R;
XX	
DR	WPI; 2004-270003/25.
XX	
PT	New protein comprising a light chain (LC) immunoglobulin variable domain
PT	sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT	useful for preparing a composition for treating inflammatory or
PT	neoplastic disorders.
XX	
PS	Disclosure; SEQ ID NO 145; 128pp; English.
XX	
CC	The invention relates to a novel isolated protein comprising a light
CC	chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC	immunoglobulin variable domain sequence that form an antigen binding site
CC	with binding affinity for the human CD44 extracellular domain and where
CC	CDR3 of the LC variable domain sequence. A protein of the invention has
CC	cytosolic, antiinflammatory, immunosuppressive, antiarthritic,
CC	antirheumatic, dermatological, vasotropic, and neuroprotective activity,
CC	and may have a use in antibody therapy. The protein is useful for
CC	preparing a composition for treating inflammatory disorders, e.g.,
CC	rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC	multiple sclerosis or neoplastic disorder, which is a malignant or
CC	metastatic cancer. The present sequence represents a human CD44-binding
CC	antibody light chain.
XX	
SQ	Sequence 238 AA;
	Query Match 84.2%; Score 650; DB 8; Length 238;
	Best Local Similarity 83.8%; Pred. No. 2.1e-44;
	Matches 124; Conservative 12; Mismatches 12; Indels 0; Gaps 0
Qy	1 VTQSPSLSVTPCOPASISCKSSQSLHSDGKTYLYWYLOKPGOPOLLIVAFNRSVG 60
Db	23 MTQSPSLVPTGEPASISCRSSQSLHSGNYLDWYLOKPGOSPQLIYLGNSRAGV 82
Qy	61 PDRFSGSGGTFTLKISRVEADVGLYYCMQSIELPFTFGGKTKVIEKRTVAAPSVFIF 120
Db	83 PDRFSGSGGTFTLKISRVEADVGVYCMQALQPTWTFGGKTKLIEKRTVAAPSVFIF 142
Qy	121 PPSDEOLKSGTASVVCLLNNFYPRKRV 148
Db	143 PPSDEOLKSGTASVVCLLNNFYPRKV 170



CC antibody 266 has. The method or the anti-Abeta antibody is useful in  
CC preparing a medicament for treating cognitive symptoms or reducing  
CC disease progression in a subject having a condition or disease associated  
CC with Abeta. The condition or disease is Alzheimer's disease, Down's  
CC syndrome, cerebral amyloid angiopathy, vascular dementia, or mild  
CC cognitive impairment. The present sequence represents a humanised anti-  
CC Abeta antibody 266 light chain  
XX  
SQ Sequence 219 AA;

Query Match 83.9%; Score 648; DB 6; Length 219;  
Best Local Similarity 83.1%; Pred. No. 2.8e-44;  
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;  
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Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
4 MTQSPLSLPVTLGPPASISCKSSQSLIYSDGNAYLHWFLOKPGQSPRLLIYKVSNRFSGV 63  
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGSKVEIKRTVAAPSVPFIF 120  
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64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCSQSTHVPMTFGGSKVEIKRTVAAPSVPFIF 123  
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124 PPSDEQLKSGTASVVCLLNFPYPRKAV 151

RESULT 15  
ABU08310  
ID ABU08310 standard; protein; 219 AA.  
XX  
AC ABU08310;  
XX  
DT 22-MAY-2003 (first entry)  
XX  
DE Humanised 266 antibody light chain.  
XX  
KW Mouse; cognition; Abeta peptide associated disorder; anti-Abeta antibody;  
KW cognitive impairment; Alzheimer's disease; Down's syndrome;  
KW cerebral amyloid angiopathy; vascular dementia; neurotropic;  
KW mild cognitive impairment; antibody 266; light chain; humanised; mutant;  
KW muten.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
FN WO2003015691-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US021323.  
XX  
PR 17-AUG-2001; 2001US-0313222P.  
PR 28-MAY-2002; 2002US-0383846P.  
XX  
PA (ELIL ) LILLY & CO ELI.  
XX  
PI Bales KR, Dodart JF, Paul SM;  
XX  
DR WPI; 2003-268234/26.  
XX

Effecting rapid improvement of cognition in a subject having Alzheimer's  
disease, Down's syndrome, cerebral amyloid angiopathy, or mild cognitive  
impairment, comprises administering anti-A beta antibody.  
Disclosure; Page 20-21; 85pp; English.

The present invention relates to a method for effecting rapid improvement  
of cognition in a subject having a condition or disease related to the  
Abeta peptide. The method comprises administering an anti-Abeta antibody.  
The method is useful for treating cognitive impairments associated with  
Abeta peptide including those involved in Alzheimer's disease, Down's  
syndrome, cerebral amyloid angiopathy, certain vascular dementia, and

CC certain forms of mild cognitive impairment. The anti-Abeta antibody is  
CC useful for preparing a medicament for effecting rapid improvement in  
CC cognition in a subject having Alzheimer's disease, Down's syndrome,  
CC cerebral amyloid angiopathy, or mild cognitive impairment. The present  
CC sequence represents a preferred light chain for a humanised 266 antibody  
XX  
SQ Sequence 219 AA;

Query Match 83.9%; Score 648; DB 6; Length 219;  
Best Local Similarity 83.1%; Pred. No. 2.8e-44;  
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 VTQSPLSLVTGPPASISCKSSQSLHSDGKTYLYVWYLOKPGQPPQLLIYEAFNRFSGV 60  
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
4 MTQSPLSLPVTLGPPASISCKSSQSLIYSDGNAYLHWFLOKPGQSPRLLIYKVSNRFSGV 63  
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGSKVEIKRTVAAPSVPFIF 120  
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCSQSTHVPMTFGGSKVEIKRTVAAPSVPFIF 123  
Qy 121 PPSDEQLKSGTASVVCLLNFPYPRKERV 148  
Db :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
124 PPSDEQLKSGTASVVCLLNFPYPRKAV 151

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Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	661	85.6	247	US-10-466-164-69	Sequence 69, Appl
2	657	85.1	238	US-10-663-244-148	Sequence 148, App
3	656	85.0	238	US-10-663-244-144	Sequence 144, App
4	653	84.6	238	US-10-663-244-149	Sequence 149, App
5	650	84.2	238	US-10-663-244-145	Sequence 145, App
6	649	84.1	239	US-10-404-724-12	Sequence 12, Appl
7	649	84.1	239	US-10-816-276-8	Sequence 8, Appl
8	648	83.9	219	US-10-226-435A-11	Sequence 11, Appl
9	648	83.9	219	US-10-487-322-11	Sequence 11, Appl
10	647	83.8	219	US-10-698-041-4	Sequence 4, Appl
11	644	83.4	173	US-10-309-762-175	Sequence 175, App
12	643	83.3	239	US-10-292-088-40	Sequence 40, Appl
13	641	83.0	239	US-10-292-088-32	Sequence 32, Appl

14	640	82.9	219	10	US-09-972-656-92	Sequence 92, Appl
15	639	82.8	239	15	US-10-292-088-16	Sequence 16, Appl
16	638.5	82.7	237	16	US-10-663-244-146	Sequence 146, App
17	638.5	82.7	237	16	US-10-663-244-153	Sequence 153, App
18	638	82.6	239	15	US-10-292-088-56	Sequence 56, Appl
19	636	82.4	238	16	US-10-663-244-147	Sequence 147, App
20	636	82.4	239	15	US-10-292-088-8	Sequence 8, Appl
21	636	82.4	239	15	US-10-292-088-80	Sequence 80, Appl
22	636	82.4	239	15	US-10-292-088-102	Sequence 102, App
23	634	82.1	239	10	US-09-992-600A-8	Sequence 8, Appl
24	634	82.1	239	10	US-09-924-340-8	Sequence 8, Appl
25	634	82.1	239	10	US-09-992-095B-8	Sequence 8, Appl
26	634	82.1	239	10	US-09-999-570-8	Sequence 8, Appl
27	634	82.1	239	14	US-10-000-489-8	Sequence 8, Appl
28	634	82.1	239	14	US-10-000-986-8	Sequence 8, Appl
29	634	82.1	239	14	US-10-154-678-8	Sequence 8, Appl
30	634	82.1	239	15	US-10-404-724-45	Sequence 45, Appl
31	634	82.1	239	15	US-10-404-724-49	Sequence 49, Appl
32	634	82.1	239	17	US-10-816-276-41	Sequence 41, Appl
33	634	82.1	239	17	US-10-816-276-45	Sequence 45, Appl
34	634	82.1	239	17	US-10-838-854-8	Sequence 8, Appl
35	633.5	82.1	220	9	US-09-822-698A-24	Sequence 24, Appl
36	632.5	81.9	237	16	US-10-663-244-152	Sequence 152, App
37	632	81.9	239	15	US-10-404-724-47	Sequence 47, Appl
38	632	81.9	239	17	US-10-816-276-43	Sequence 43, Appl
39	628	81.3	239	15	US-10-108-260A-4028	Sequence 4028, App
40	626	81.1	239	9	US-09-758-173-6	Sequence 6, Appl
41	626	81.1	239	9	US-09-948-429B-6	Sequence 6, Appl
42	626	81.1	239	13	US-10-124-905-6	Sequence 6, Appl
43	626	81.1	239	14	US-10-124-807-6	Sequence 6, Appl
44	626	81.1	239	14	US-10-291-532-6	Sequence 41, Appl
45	626	81.1	239	15	US-10-404-724-41	

#### ALIGNMENTS

#### RESULT 1

US-10-466-164-69  
; Sequence 69, Application US/10466164  
; Publication No. US20040058365A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE CORPORATION; PANZER, Scott R.;  
; APPLICANT: LINCOLN, Stephen E.; ALTUS, Christina M.;  
; APPLICANT: DUFOUR, Gerard E.; JACKSON, Jennifer L.;  
; APPLICANT: JONES, Anissa L.; DAM, Tam C.;  
; APPLICANT: LIU, Tommy F.; HARRIS, Bernard;  
; APPLICANT: FLORES, Vincent Z.; DAPPO, Abel;  
; APPLICANT: MARWAHA, Rakesh; CHEN, Alice J.;  
; APPLICANT: CHANG, Simon C.; GERSTIN, Jr., Edward H.;  
; APPLICANT: PERALTA, Careyna H.; DAVID, Marie H.;  
; APPLICANT: LEWIS, Samantha A.  
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT  
; FILE REFERENCE: PT-1215 PCT  
; CURRENT APPLICATION NUMBER: US/10/466,164  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: PCT/US02/01008  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: US 60/261,865  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/263,065  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US 60/263,329  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US 60/262,209  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US 60/262,208  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US 60/262,326  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US 60/263,063  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: US 60/261,622

```
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 69
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058365A1 LI:1171219.2.orf3.2001JAN12
US-10-666-164-69

Query Match      85.6%; Score 661; DB 15; Length 247;
Best Local Similarity 84.5%; Pred. No. 2.4e-44;
Matches 125; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYEAFNRFSGV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
32 MTQSPFLSLVTPGEPASISCRSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYLGSSRASGV 91
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
92 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 151
Qy 121 PPSDEQLKSGTASVVCLLNFPYPRKERV 148
Db 152 PPSDEQLKSGTASVVCLLNFPYPRKERV 179

RESULT 2
US-10-663-244-148
; Sequence 148, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-148

Query Match      85.1%; Score 657; DB 16; Length 238;
Best Local Similarity 85.1%; Pred. No. 4.9e-44;
Matches 126; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYEAFNRFSGV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 MTQSPFLSLVTPGEPASISCRSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYLGSSRASGV 82
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 142
Qy 121 PPSDEQLKSGTASVVCLLNFPYPRKERV 148
Db 143 PPSDEQLKSGTASVVCLLNFPYPRKERV 170

RESULT 3
US-10-663-244-149
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-149

Query Match      84.6%; Score 653; DB 16; Length 238;
Best Local Similarity 84.5%; Pred. No. 1e-43;
Matches 125; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYEAFNRFSGV 60
```

```
US-10-663-244-144
; Sequence 144, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-144

Query Match      85.0%; Score 656; DB 16; Length 238;
Best Local Similarity 85.1%; Pred. No. 5.8e-44;
Matches 126; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYEAFNRFSGV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 MTQSPFLSLVTPGEPASISCRSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYLGSSRASGV 82
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 142
Qy 121 PPSDEQLKSGTASVVCLLNFPYPRKERV 148
Db 143 PPSDEQLKSGTASVVCLLNFPYPRKERV 170

RESULT 4
US-10-663-244-149
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-149

Query Match      84.6%; Score 653; DB 16; Length 238;
Best Local Similarity 84.5%; Pred. No. 1e-43;
Matches 125; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYEAFNRFSGV 60
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; ORGANISM: Homo Sapiens
US-10-404-724-12

Query Match      84.1%; Score 649; DB 15; Length 239;
Best Local Similarity 83.1%; Pred. No. 2.1e-43;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLPTVTPGPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYEAFNRFSGV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKVEIKRTVAAPSVFIF 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
143 PPSDEQLKSGTASVVCLLNNFYPREAKV 170

RESULT 5
US-10-663-244-145
; Sequence 145, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-145

Query Match      84.2%; Score 650; DB 16; Length 238;
Best Local Similarity 83.8%; Pred. No. 1.7e-43;
Matches 124; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLPTVTPGPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYEAFNRFSGV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 MTQSPLSLPTVTPGPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYLGSRASGV 82
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKVEIKRTVAAPSVFIF 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKVEIKRTVAAPSVFIF 142
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
143 PPSDEQLKSGTASVVCLLNNFYPREAKV 170

RESULT 6
US-10-404-724-12
; Sequence 12, Application US/10404724
; Publication No. US20030203447A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 13698US01
; CURRENT APPLICATION NUMBER: US/10/404,724
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
```

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; ORGANISM: Homo Sapiens
US-10-404-724-12

Query Match      84.1%; Score 649; DB 15; Length 239;
Best Local Similarity 83.1%; Pred. No. 2.1e-43;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLPTVTPGPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYEAFNRFSGV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
24 MTQSPLSLPTVTPGPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYQMSNRASGV 83
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKVEIKRTVAAPSVFIF 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 PDRFSGSGGTDFTLKISRVEAEDVGLYYCAQNLPRFTFGGKVEIKRTVAAPSVFIF 143
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
144 PPSDEQLKSGTASVVCLLNNFYPREAKV 171

RESULT 7
US-10-816-276-8
; Sequence 8, Application US/10816276
; Publication No. US20050005097A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Human Engineered to Antibodies to Ep-CAM
; FILE REFERENCE: 14923US02
; CURRENT APPLICATION NUMBER: US/10/816,276
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: 60/459,334
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-816-276-8

Query Match      84.1%; Score 649; DB 17; Length 239;
Best Local Similarity 83.1%; Pred. No. 2.1e-43;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLPTVTPGPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYEAFNRFSGV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
24 MTQSPLSLPTVTPGPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYQMSNRASGV 83
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKVEIKRTVAAPSVFIF 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 PDRFSGSGGTDFTLKISRVEAEDVGLYYCAQNLPRFTFGGKVEIKRTVAAPSVFIF 143
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
144 PPSDEQLKSGTASVVCLLNNFYPREAKV 171

RESULT 8
US-10-226-435A-11
; Sequence 11, Application US/10226435A
; Publication No. US20040043418A1
; GENERAL INFORMATION:
; APPLICANT: ELI LILLY AND COMPANY
; TITLE OF INVENTION: Humanized Antibodies that Sequester Amyloid Beta Peptide
; FILE REFERENCE: 8792/293
; CURRENT APPLICATION NUMBER: US/10/226,435A
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/06191
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,601
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/254,465
```

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; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/254,498
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibodies
US-10-226-435A-11

Query Match      83.9%; Score 648; DB 15; Length 219;
Best Local Similarity 83.1%; Pred. No. 2.3e-43;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLSTVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEA FNRFSGV 60
Db 4 MTQSPLSLPTVLGQPASISCKSSQSLIYSDGNAYLHWFLOKPGQSPRLIIYKVS NRFSGV 63

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 120
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 124 PPSDEQLKSGTASVVCLLNNFYPRKERV 151

RESULT 9
US-10-487-322-11
; Sequence 11, Application US/10487322
; Publication No. US2004019289A1
; GENERAL INFORMATION:
; APPLICANT: ELI LILLY AND COMPANY
; TITLE OF INVENTION: ANTI-AB ANTIBODIES
; FILE REFERENCE: X-15113
; CURRENT APPLICATION NUMBER: US/10/487,322
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: 60/313,234
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(219)
; OTHER INFORMATION: HUMANIZED ANTIBODY LIGHT CHAIN
US-10-487-322-11

Query Match      83.9%; Score 648; DB 16; Length 219;
Best Local Similarity 83.1%; Pred. No. 2.3e-43;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLSTVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEA FNRFSGV 60
Db 4 MTQSPLSLPTVLGQPASISCKSSQSLIYSDGNAYLHWFLOKPGQSPRLIIYKVS NRFSGV 63

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 120
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 124 PPSDEQLKSGTASVVCLLNNFYPRKERV 151
```

```
RESULT 10
US-10-698-041-4
; Sequence 4, Application US/10698041
; Publication No. US20040151724A1
; GENERAL INFORMATION:
; APPLICANT: Coronella-Wood, Julia
; TITLE OF INVENTION: Antibody Fab Fragments Specific for Breast Cancer
; FILE REFERENCE: 5051.057
; CURRENT APPLICATION NUMBER: US/10/698,041
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 60/423,052
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-041-4

Query Match      83.8%; Score 647; DB 16; Length 219;
Best Local Similarity 83.1%; Pred. No. 2.7e-43;
Matches 123; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSLSTVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEA FNRFSGV 60
Db 4 MTQSPLSLPTVLGQPASISCKSSQSLHSDGKTYLYWYLOKPGQSPOLLIIYLGFN RASGV 63

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 120
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 124 PPSDEQLKSGTASVVCLLNNFYPRKERV 151

RESULT 11
US-10-309-762-175
; Sequence 175, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Gudas, Jean
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ARGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-175

Query Match      83.4%; Score 644; DB 15; Length 173;
Best Local Similarity 81.8%; Pred. No. 3.7e-43;
Matches 121; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSLSTVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEA FNRFSGV 60
Db 20 MTQTPSSPVLTLGQPASISCKRASQSLVHSDGNTYLSLQRPQGPORLLIYKIS NRFSGV 79

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 120
Db 80 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 139
```

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148  
Db 140 PPSDEQLKSGTASVVCLLNNFYPRKRV 167

RESULT 12  
US-10-292-088-40  
; Sequence 40, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-088-40

Query Match 83.3%; Score 643; DB 15; Length 239;  
Best Local Similarity 83.1%; Pred. No. 6.1e-43;  
Matches 123; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 60  
Db 24 MTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYLSNRASGV 83

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFGGTTKVEIKRTVAAPSVPFIF 120  
Db 84 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFGGTTKVEIKRTVAAPSVPFIF 143

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148  
Db 144 PPSDEQLKSGTASVVCLLNNFYPRKRV 171

RESULT 13  
US-10-292-088-32  
; Sequence 32, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-088-32

Query Match 83.0%; Score 641; DB 15; Length 239;  
Best Local Similarity 81.8%; Pred. No. 8.8e-43;  
Matches 121; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 60  
Db 24 MTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYLSNRASGV 83

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFGGTTKVEIKRTVAAPSVPFIF 120  
Db 84 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFGGTTKVEIKRTVAAPSVPFIF 143

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148  
Db 144 PPSDEQLKSGTASVVCLLNNFYPRKRV 171

RESULT 14  
US-09-972-656-92  
; Sequence 92, Application US/09972656  
; Publication No. US20030099647A1  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Tsai, Mei-Mei  
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
; TITLE OF INVENTION: Neutralizing Activity  
; FILE REFERENCE: A-799  
; CURRENT APPLICATION NUMBER: US/09/972,656  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 92  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-656-92

Query Match 82.9%; Score 640; DB 10; Length 219;  
Best Local Similarity 81.8%; Pred. No. 9.7e-43;  
Matches 121; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 60  
Db 4 MHTPLSSPVLTPGPASISCKSSQSLHSDGNTYLSMLHQRPGQPPRLLIYKISNRFSGV 63

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFGGTTKVEIKRTVAAPSVPFIF 120  
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFGGTTKVEIKRTVAAPSVPFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148  
Db 124 PPSDEQLKSGTASVVCLLNNFYPRKRV 151

RESULT 15  
US-10-292-088-16  
; Sequence 16, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-292-088-16

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Query Match      82.8%; Score 639; DB 15; Length 239;
Best Local Similarity 83.1%; Pred No. 1.3e-42;
Matches 123; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEA FNRFSGV 60
   :|||||:|||||:|||||:|||||:|:|||||:|||||:|||||:|||||
Db 24 MTQSPLSLVTPGPAPASISCRSSQSLIYSNGYNFLDWYLOKPGQSPQLLIYLGSNRASGV 83

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGGTKVEIKRTVAAPSVFIF 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQALQTPRTFGQGTKVEIKRTVAAPSVFIF 143

Qy 121 PPSDEQLKSGTASVVCILNNFYPRKERV 148
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 144 PPSDEQLKSGTASVVCILNNFYPREAKV 171
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Search completed: March 8, 2005, 07:05:56  
Job time : 78.5397 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.2736 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-36  
Perfect score: 772  
Sequence: 1 VTQSPLSLVTPGPASISCSQSLLHSDGKTYLYWYLOKPGQPQLLIYEAFNRFSGV 148

Scoring table: -BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	634	82.1	239	4	US-10-000-489-8
2	626	81.1	239	3	US-08-487-550-6
3	626	81.1	239	4	US-09-526-098-6
4	626	81.1	239	4	US-09-383-916-6
5	613	79.4	238	4	US-09-698-705-10
6	610	79.0	133	4	US-09-472-087-26
7	610	79.0	133	4	US-09-472-087-116
8	606	78.5	218	4	US-09-698-705-12
9	604	78.2	242	1	US-08-398-613A-56
10	604	78.2	242	1	US-08-398-612A-56
11	604	78.2	242	1	US-08-398-611A-56
12	604	78.2	242	2	US-08-491-334A-56
13	604	78.2	242	3	US-09-027-449-42
14	604	78.2	242	3	US-08-804-444A-42
15	604	78.2	242	3	US-09-026-985-42
16	604	78.2	242	4	US-09-121-952A-42
17	604	78.2	242	4	US-09-234-340A-42
18	583	75.5	139	4	US-09-472-087-25
19	583	75.5	139	4	US-09-472-087-114
20	572	74.1	216	4	US-09-254-180C-132
21	572	74.1	216	4	US-09-254-180C-183
22	569	73.7	173	5	PCT-US91-02942-3
23	569	73.7	173	5	PCT-US91-02945-3
24	565	73.2	238	3	US-09-192-545-4
25	565	73.2	242	3	US-09-027-449-62
26	565	73.2	242	3	US-09-026-985-62
27	565	73.2	242	4	US-09-121-952A-62

28	565	73.2	242	4	US-09-234-340A-62	Sequence 62, Appl
29	564	73.1	242	3	US-09-027-449-51	Sequence 51, Appl
30	564	73.1	242	3	US-08-804-444A-51	Sequence 51, Appl
31	564	73.1	242	3	US-09-026-985-51	Sequence 51, Appl
32	564	73.1	242	4	US-09-121-952A-51	Sequence 51, Appl
33	564	73.1	242	4	US-09-234-340A-51	Sequence 51, Appl
34	563	72.9	219	3	US-09-027-449-72	Sequence 72, Appl
35	563	72.9	219	3	US-09-026-985-72	Sequence 72, Appl
36	563	72.9	219	4	US-09-121-952A-72	Sequence 72, Appl
37	563	72.9	219	4	US-09-234-340A-72	Sequence 72, Appl
38	563	72.9	242	3	US-09-027-449-56	Sequence 56, Appl
39	563	72.9	242	3	US-08-804-444A-56	Sequence 56, Appl
40	563	72.9	242	3	US-09-026-985-56	Sequence 56, Appl
41	563	72.9	242	4	US-09-121-952A-56	Sequence 56, Appl
42	563	72.9	242	4	US-09-234-340A-56	Sequence 56, Appl
43	558	72.3	222	4	US-09-479-614-26	Sequence 26, Appl
44	558	72.3	242	4	US-09-479-614-20	Sequence 20, Appl
45	556	72.0	216	4	US-09-254-180C-182	Sequence 182, App

ALIGNMENTS

RESULT 1  
US-10-000-489-8  
; Sequence 8, Application US/10000489  
; Patent No. 6794363  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CONAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.US6.DIV  
; CURRENT APPLICATION NUMBER: US/10/000.489  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: US 09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: JPatent  
; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
US-10-000-489-8

Query Match 82.1%; Score 634; DB 4; Length 239;  
Best Local Similarity 81.8%; Pred No. 1.7e-57;  
Matches 121; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy	1	VTQSPLSLVTPGPASISCSQSLLHSDGKTYLYWYLOKPGQPQLLIYEAFNRFSGV 60
Db	24	MTQSPFLPVTGPSPASISCSQSLLHSDGKTYLYWYLOKPGQPQLLIYLGSNRAGV 83
Qy	61	PDRFSGSGSGTDFTLKISRVEAEDVGLYCMQSTELPFTGGGTVKVKRTPAAPSVEIF 120
Db	84	PDRFSGSGSGTDFTLKISRVEAEDVGLYCMQSTELPFTGGGTVKVKRTPAAPSVEIF 143
Qy	121	PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db	144	PPSDEQLKSGTASVVCLLNNFYPRKRV 171

```
RESULT 2
US-08-487-550-6
; Sequence 6, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-6

Query Match      81.1%; Score 626; DB 3; Length 239;
Best Local Similarity 80.4%; Pred. No. 1.1e-56;
Matches 119; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEAAPNSGV 60
Db 24 MTQSPLSLPTPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRDGV 83

Qy 61 PDRFSGSGGTDFTLKISRVEADVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVPF 120
Db 84 PDRFSGSGAGTDFTLKISAVEADVGVYFCQGTRTPPTFGGKTKVEIKRTVAAPSVPF 143

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 144 PPSDEQLKSGTASVVCLLNNFYPREKV 171

RESULT 3
US-09-526-098-6
; Sequence 6, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
```

```
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-526-098-6

Query Match      81.1%; Score 626; DB 4; Length 239;
Best Local Similarity 80.4%; Pred. No. 1.1e-56;
Matches 119; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEAAPNSGV 60
Db 24 MTQSPLSLPTPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRDGV 83

Qy 61 PDRFSGSGGTDFTLKISRVEADVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVPF 120
Db 84 PDRFSGSGAGTDFTLKISAVEADVGVYFCQGTRTPPTFGGKTKVEIKRTVAAPSVPF 143

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 144 PPSDEQLKSGTASVVCLLNNFYPREKV 171

RESULT 4
US-09-383-916-6
; Sequence 6, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/383,916

FILING DATE: 26-AUG-1999

CLASSIFICATION:

PRIOR APPLICATION DATA: US 08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-383-916-6

Query Match 81.1%; Score 626; DB 4; Length 239;

Best Local Similarity 80.4%; Pred. No. 1.1e-56;

Matches 119; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRSGV 60

Db 24 MTQSPLSLPITPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYKVNRSQGV 83

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYVYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 120

Db 84 PDRFSGSGAGTDFTLKISRVEAEDVGLYVYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 143

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148

Db 144 PPSDEQLKSGTASVVCLLNNFYPRKRV 171

RESULT 5

US-09-698-705-10

Sequence 10, Application US/09698705

Patent No. 6824780

GENERAL INFORMATION:

APPLICANT: Devaux, B.

APPLICANT: Keller, G.

APPLICANT: Koepfen, H.

APPLICANT: Lasky, L.

TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use

FILE REFERENCE: P1777R1

CURRENT APPLICATION NUMBER: US/09/698,705

PRIOR FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60/162,558

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60/182,872

PRIOR FILING DATE: 2000-02-16

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 10

LENGTH: 238

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: sequence is chimeric mouse/human

US-09-698-705-10

Query Match 79.4%; Score 613; DB 4; Length 238;

Best Local Similarity 77.0%; Pred. No. 2.5e-55;

Matches 114; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRSGV 60

Db 23 MTQAAPSVFVTPGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYRMSNLASGV 82

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYVYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 120

Db 83 PDRFSGSGGTAFTLIRISREAEADVGVYVCIQLHLEYPTFGGKTKLELKRVAAPSVFIF 142

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148

Db 143 PPSDEQLKSGTASVVCLLNNFYPRKRV 170

RESULT 6

US-09-472-087-26

Sequence 26, Application US/09472087

Patent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, EILLEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PF1

CURRENT APPLICATION NUMBER: US/09/472,087

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/113,647

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 26

LENGTH: 133

TYPE: PRT

ORGANISM: Homo sapiens

US-09-472-087-26

Query Match 79.0%; Score 610; DB 4; Length 133;

Best Local Similarity 86.5%; Pred. No. 2.5e-55;

Matches 115; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 12 PGQPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSVGPDRFSGSGSGT 71

Db 1 PGEPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYLGSRASVGPDRFSGSGSGT 60

Qy 72 DFTLKISRVEAEDVGLYVYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGT 131

Db 61 DFTLKISRVEAEDVGLYVYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGT 120

Qy 132 ASVVCLNNFYPR 144

Db 121 ASVVCLNNFYPR 133

RESULT 7

US-09-472-087-116

Sequence 116, Application US/09472087

Patent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, EILLEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PF1

CURRENT APPLICATION NUMBER: US/09/472,087

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/113,647

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 116
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-116

Query Match      79.0%; Score 610; DB 4; Length 133;
Best Local Similarity 86.5%; Pred. No. 2.5e-55;
Matches 115; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 12 PGQPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYEAFNRFGVDPDRFGSGSGT 71
Db 1 PGPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYLGSRASGVDPDRFGSGSGT 60

Qy 72 DFTLKISRVAEDVGLYYCMQSIELPFTFGGTVKRTVAAPSVFIPPSDEQLKSGT 131
Db 61 DFTLKISRVAEDVGLYYCMQSIELPFTFGGTVKRTVAAPSVFIPPSDEQLKSGT 120

Qy 132 ASVVCLLNFFPR 144
Db 121 ASVVCLLNFFPR 133

RESULT 8
US-09-698-705-12
; Sequence 12, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Laaky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P177R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-12

Query Match      78.5%; Score 606; DB 4; Length 218;
Best Local Similarity 79.7%; Pred. No. 1.2e-54;
Matches 118; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYEAFNRFGSV 60
Db 4 MTQTPLTSLVTIGQPASISCKSSQSLHSDGKTYLYWYLOKPGQPKRLIYVSTLDSGV 63

Qy 61 PDRFSGSGGTDFTLKISRVAEDVGLYYCMQSIELPFTFGGTVKRTVAAPSVFIF 120
Db 64 PDRFTGSGGTDFTLKISRVAEDVGLYYCMQSIELPFTFGGTVKRTVAAPSVFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNFFPRKERV 148
Db 124 PPSDEQLKSGTASVVCLLNFFPRKERV 151

RESULT 9
US-08-398-613A-56
; Sequence 56, Application US/08398613A
; Patent No. 5677426
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
{
```

```
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory I
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,613A
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 874P1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1489
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-398-613A-56

Query Match      78.2%; Score 604; DB 1; Length 242;
Best Local Similarity 76.4%; Pred. No. 2.1e-54;
Matches 113; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYEAFNRFGSV 60
Db 27 MTQTPLTSLPVSLGDAQASISCKSSQSLVHGIGNTVYLHWYLOKPGQPKRLIYKVSNRFGSV 86

Qy 61 PDRFSGSGGTDFTLKISRVAEDVGLYYCMQSIELPFTFGGTVKRTVAAPSVFIF 120
Db 87 PDRFSGSGGTDFTLKISRVAEDVGLYFCQSTHVLPTFGAGTKLEKRAVAAPTVFIF 146

Qy 121 PPSDEQLKSGTASVVCLLNFFPRKERV 148
Db 147 PPSDEQLKSGTASVVCLLNFFPRKERV 174

RESULT 10
US-08-398-612A-56
; Sequence 56, Application US/08398612A
; Patent No. 5686070
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
```

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;
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,612A
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-398-612A-56
;
;
; Query Match 78.2%; Score 604; DB 1; Length 242;
; Best Local Similarity 76.4%; Pred. No. 2.1e-54;
; Matches 113; Conservative 17; Mismatches 18; Indels 0; Gaps 0;
;
; QY 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIYEAFNRFSGV 60
; DB 27 MTQTPLSLVSLGDPQASISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNRFSGV 86
;
; QY 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGTTKVEIKRTVAAPSVPFIF 120
; DB 87 PDRFSGSGGTDFTLRISRVEAEDGLYFCQSQTHVPLTFGAGTKLELKRAVAAPTVPFIF 146
;
; QY 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
; DB 147 PPSSEQLKSGTASVVCLLNNFYPREAKV 174
;
;
; RESULT 11
; US-08-398-611A-56
; Sequence 56, Application US/08398611A
; Patent No. 5702946
;
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
; OF INFLAMMATORY DISORDERS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,334A
; FILING DATE: 27-Jun-1995
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
;
; ATTORNEY/AGENT INFORMATION:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,611A
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-398-611A-56
;
;
; Query Match 78.2%; Score 604; DB 1; Length 242;
; Best Local Similarity 76.4%; Pred. No. 2.1e-54;
; Matches 113; Conservative 17; Mismatches 18; Indels 0; Gaps 0;
;
; QY 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIYEAFNRFSGV 60
; DB 27 MTQTPLSLVSLGDPQASISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVSNRFSGV 86
;
; QY 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGTTKVEIKRTVAAPSVPFIF 120
; DB 87 PDRFSGSGGTDFTLRISRVEAEDGLYFCQSQTHVPLTFGAGTKLELKRAVAAPTVPFIF 146
;
; QY 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
; DB 147 PPSSEQLKSGTASVVCLLNNFYPREAKV 174
;
;
; RESULT 12
; US-08-491-334A-56
; Sequence 56, Application US/08491334A
; Patent No. 5874080
;
; GENERAL INFORMATION:
; APPLICANT: Hebert, Caroline A.
; APPLICANT: Kabakoff, Rhona C.
; APPLICANT: Moore, Mark W.
; TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
; DISORDERS AND ASTHMA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,334A
; FILING DATE: 27-Jun-1995
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
;
; ATTORNEY/AGENT INFORMATION:
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Qy 121 PPSDEQLKSGTASVVCLNNFYPRKRV 148  
Db 147 PPSSEQLKSGTASVVCLNNFYPREAKV 174

## RESULT 15

US-09-026-985-42  
; Sequence 42, Application US/09026985  
; Patent No. 6133426  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,985  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-026-985-42

Query Match 78.2%; Score 604; DB 3; Length 242;  
Best Local Similarity 76.4%; Pred. No. 2.1e-54;  
Matches 113; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

Qy 1 VTQSPLSLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEAAPNRESGV 60  
Db 27 MTQTPSLPSVLGDSQASISCKSSQSLVHGIGNTYLHWYLOKPGSPKLLIYKVSNRSGV 86  
Qy 61 PDRFSGSGSGDFTLKISRVEAEVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVPFIF 120  
Db 87 PDRFSGSGSGDFTLRISRVEAEGLGYFCQSQSTHVPPLTFGAGTKLELKRAVAAPTVPFIF 146  
Qy 121 PPSDEQLKSGTASVVCLNNFYPRKRV 148  
Db 147 PPSSEQLKSGTASVVCLNNFYPREAKV 174

Search completed: March 8, 2005, 05:54:12  
Job time : 17.2736 secs

4

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 12.295 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-37

Perfect score: 912  
Sequence: 1 GEGLVKPGGSLRLSCAASGF.....SWNSGALTSGVHTFPAVLQ 173

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637.5	69.9	548	2	Ig epsilon chain C
2	637	69.8	213	2	Ig heavy chain (Ma
3	617	67.7	143	2	Ig heavy chain V r
4	601.5	66.0	254	2	Ig heavy chain V r
5	568.5	62.3	220	2	Ig heavy chain (Ma
6	568.5	62.3	444	2	monoclonal antibod
7	555.5	60.9	241	2	Ig heavy chain (DO
8	546	59.9	220	2	Ig gamma-1 heavy c
9	544	59.6	125	2	Ig heavy chain V r
10	528.5	57.9	469	2	Ig gamma-2a chain
11	517.5	56.7	141	2	Ig heavy chain V r
12	516	56.6	246	2	Ig gamma chain - m
13	516	56.6	446	2	Ig gamma-2a chain
14	515.5	56.5	470	2	Ig heavy chain pre
15	507	55.6	231	2	Ig gamma-2b chain
16	505.5	55.4	214	2	monoclonal antibod
17	501	54.9	221	2	Ig gamma-1 chain -
18	499.5	54.8	110	2	Ig heavy chain V r
19	497.5	54.6	147	2	Ig variable region
20	496.5	54.4	128	2	Ig heavy chain - h
21	496	54.4	119	2	Ig heavy chain V r
22	496	54.4	123	2	Ig heavy chain V r
23	495.5	54.3	112	2	Ig heavy chain pre
24	494	54.2	160	2	Ig heavy chain V r
25	491.5	53.9	120	2	Ig heavy chain V r
26	490	53.7	117	2	Ig heavy chain V r
27	490	53.7	119	2	Ig heavy chain V r
28	490	53.7	474	1	Ig gamma-2b chain
29	488.5	53.6	128	2	Ig heavy chain V r

RESULT 1  
S38864  
Ig epsilon chain C region - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-May-2001  
C/Accession: S38864  
R/Kipp, B.; Becker, W.; Schlaak, M.  
A/Description: Combination of a defined specificity and desired isotype by cloning of an  
submitted to the EMBL Data Library, November 1993  
A/Reference number: S38864  
A/Accession: S38864  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-548 <KIP>  
A/Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAAB1788.1; PID:g940782  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
F:353-421/Domain: immunoglobulin homology <IMM>

ALIGNMENTS

Query Match 69.9%; Score 637.5; DB 2; Length 548;  
Best Local Similarity 71.1%; Pred. No. 1.3e-41;  
Matches 123; Conservative 17; Mismatches 32; Indels 1; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNWVRQAPGKGLWVSSISSSSYIYADSVKGR 60  
Db 8 GGDVLPKPGGSLRLSCAASGLTFSSYGMWVRQIPDKRLWVATISSGGTYTYYPDSVKGR 67  
Qy 61 FTISRDNKNSLYLQMSLRADTAVYVCARDSSGWYEDYDYGQGLTVTVSSASTKGP 120  
Db 68 FTISRDNKNTLYLQMSLSKSDTAMYYCAKQGVSTM-IRPAYWGQGLTVTVSAGKTPP 126  
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYPPEPTVTSWNSGALTSGVHTFPAVLQ 173  
Db 127 SVYFLAPCSAAQTSMWTLGCLVKGYFPEPTVTWNSGSLSSGVHTFPAVLQ 179

RESULT 2  
S68213  
Ig heavy chain (Mab03-1) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 29-Jul-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C/Accession: S68213  
R/Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
FEBS Lett. 375, 273-276, 1995  
A/Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
A/Reference number: S68211; MUID:96085223; PMID:7498516  
A/Accession: S68213  
A/Status: preliminary; nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-213 <TAK>  
A/Cross-references: UNIPROT:Q91Z05; EMBL:D296667  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
F:137-201/Domain: immunoglobulin homology <IMM>

30	486.5	53.3	114	2	S31120	Ig heavy chain - h
31	486	53.3	568	2	A34891	Ig heavy chain pre
32	485	53.2	140	2	S31588	Ig heavy chain V r
33	484.5	53.1	249	2	S69340	Ig heavy chain VH1
34	483	53.0	119	2	D36005	Ig heavy chain V r
35	483	53.0	127	2	S38489	Ig heavy chain - h
36	483	53.0	138	2	S31666	Ig heavy chain V r
37	483	53.0	509	2	S17597	Ig delta chain (WI
38	483	53.0	549	2	S04845	Ig heavy chain pre
39	481.5	52.8	118	2	S31105	Ig heavy chain (su
40	481	52.7	152	2	B26471	Ig heavy chain pre
41	479.5	52.6	124	2	S20782	Ig heavy chain V r
42	479	52.5	119	2	S31108	Ig heavy chain - h
43	479	52.5	121	2	S36005	Ig heavy chain V r
44	478.5	52.5	475	2	S01321	Ig gamma-2b chain
45	478	52.4	123	2	S31114	Ig heavy chain - h

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Query Match 69.8%; Score 637; DB 2; Length 213;
Best Local Similarity 71.7%; Pred. No. 5.4e-42;
Matches 124; Conservative 18; Mismatches 27; Indels 4; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSSIIYYADSVKGR 60
Db 8 GGGVLQPGGSRKLLSCAASGFTFSFGMHVRQAPKLEWVAVISSGSSIIYYADTVKGR 67

Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYDWGQGTLLTVSSASTKGP 120
Db 68 FTISRDNKNTLFLQMTSLRSEDAMYYCAR---SWLLP-FDWGQGTLLTVSSAKTTPP 123

Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYRPPETVTSWNSGALTSVGHVTPPAVLQS 173
Db 124 SVFPLAPCGDITGSSVTLGCLVKGYFPEPVTVWNSGSLSSSSVHVPFALLQS 176

RESULT 3
S23624
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S23624
R/Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A/Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A/Reference number: S23623; MUID:92156804; PMID:1740665
A/Accession: S23624
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-143 <OLE>
A/Cross-references: EMBL:X59703; NID:g32012; PIDN:CAA42224.1; PID:g32013
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.7%; Score 617; DB 2; Length 143;
Best Local Similarity 89.3%; Pred. No. 1.2e-40;
Matches 125; Conservative 3; Mismatches 8; Indels 4; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSSIIYYADSVKGR 60
Db 8 GGGVLQPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSVISSSSIIYYADSVKGR 67

Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYDWGQGTLLTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMSLRAEDTAVYYCAR--SGYRG--DYWGQGTLLTVSSASTKGP 123

Qy 121 SVFPLAPCSRSTSESTAALG 140
Db 124 SVFPLAPCSRSTSGTAAALG 143

RESULT 4
B31790
Ig heavy chain V region (17/9) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997
C/Accession: B31790
R/Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A/Title: Preliminary crystallographic data, primary sequence, and binding data for an
A/Reference number: A92886; MUID:89034213; PMID:3182835
A/Accession: B31790
A/Molecule type: mRNA
A/Residues: 1-254 <SCH>
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.0%; Score 601.5; DB 2; Length 254;
Best Local Similarity 67.4%; Pred. No. 3.4e-39;
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Matches 122; Conservative 22; Mismatches 28; Indels 9; Gaps 5;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSSIIYYADSVKGR 60
Db 8 GGGVLQPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVAISGGGYIYPDSVKGR 67

Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYDWGQGTLLTVSSASTKGP 120
Db 68 FTISRDNKNTLYLQMSLSKSDSAMYYCAR-RERYDENGFAVWGQGTLLTVSSAAKTTP 126

Qy 121 SVFPLAPCSR--STSSSTAALGCLVKDYRPPETV--SW-----NSGALTSG-VHTFPAVLQ 172
Db 127 SVFPLAPVCGXDDTGGSSVTLGCLVKGYFPEPVTLTXWXXXNXXSGSLSSGXVHTFPAVLQ 186

Qy 173 s 173
Db 187 s 187

RESULT 5
S68211
Ig heavy chain (Mab13-1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000
C/Accession: S68211
R/Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A/Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A/Reference number: S68211; MUID:96085223; PMID:7498516
A/Accession: S68211
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-220 <TAK>
A/Cross-references: EMBL:D29669; NID:g473958; PIDN:BA06140.1; PID:g473959
A/Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequence
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F/136-200/Domain: immunoglobulin homology <IMM>

Query Match 62.3%; Score 568.5; DB 2; Length 220;
Best Local Similarity 64.8%; Pred. No. 1e-36;
Matches 113; Conservative 22; Mismatches 35; Indels 5; Gaps 4;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSIS-SSSSY-IYYADSVK 58
Db 4 GGGVLQPGNSLKLSCLTSGFTFSYRHMWLRQPGKLEWIAVITVKSVDNYGAKYAESVR 63

Qy 59 GRTFISRDNAKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYDWGQGTLLTVSSASTK 118
Db 64 GRTFISRDSDSKSVYLQMNRLREEDTATYYCCR--TPWVY-AMDCWGGQGTSVIVSSAKTT 120

Qy 119 GPSVFPLAPCSRSTSESTAALGCLVKDYRPPETVTSWNSGALTSVGHVHTFPAVLQS 173
Db 121 PPSVYPLAPGSAQAQTNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS 175

RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C/Accession: PC4436
R/Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.;
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A/Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A/Reference number: JCS810; MUID:98063277; PMID:9398605
A/Accession: PC4436
A/Molecule type: protein
A/Residues: 1-444 <AKA>
C/Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F/251-320/Domain: immunoglobulin homology <IMM>
F/22/Disulfide bonds: interchain (to 98) #status predicted
F/99/Disulfide bonds: interchain (to 109) #status predicted
```



Query Match 62.3%; Score 568.5; DB 2; Length 444;  
Best Local Similarity 64.6%; Pred. No. 2.1e-36;  
Matches 113; Conservative 22; Mismatches 35; Indels 5; Gaps 4;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYNNWVRQAPGKGLWVSSIS-SSSSV-IYYADSVK 58  
Db 8 GGGVLRPENSUKLSCLTSGFTFSYNNWVRQAPGKGLWIAIVIKSDNYGAKYASVR 67  
Qy 59 GRFTISRDNAKNSLYLQMSLRADTAIVYICARDSSGWYEDYFDYWGQGLTVTVSSASTK 118  
Db 68 GRFTISRDSSKSYLVQWNLREEDTATYYCCR--TPWVY-AMDCWGQTSVISSAKTT 124  
Qy 119 GPSVFPPLAPCSRSTSESTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQS 173  
Db 125 PPSVYPLAPGSAQTNSMTVLGCLVKGYFPPPTVTVSNWNSGSLSSGVHTFPAVLQS 179

RESULT 7  
S69131  
Ig heavy chain (DOT) - human (fragment)  
N:Alternate names: anti-riboflavin IgG Fd fragment  
C:Species: Homo sapiens (man)  
C:Date: 12-Feb-1998 #sequence\_revision 22-May-1998 #text\_change 21-Jan-2000  
C:Accession: S69131  
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.  
Eur. J. Biochem. 228, 886-893, 1995  
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins  
A:Reference number: S69130; MUID:95255298; PMID:7737190  
A:Accession: S69131  
A:Molecule type: protein  
A:Residues: 1-241 <STO>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid  
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAT>  
F:140-205/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 60.9%; Score 555.5; DB 2; Length 241;  
Best Local Similarity 62.9%; Pred. No. 1.1e-35;  
Matches 105; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

Qy 7 PGGLRLSCAASGFTFSYNNWVRQAPGKGLWVSSISSSSSIIYYADSVKGFRTISRD 66  
Db 14 PGASVRISSCKASGAFENYIHWVRQAPGLGLEWGFNPVAGAV-SSEKFRDLVMSDD 72  
Qy 67 NAKNSLYLQMSLRADTAIVYICARDSSGWYEDYFDYWGQGLTVTVSSASTKGPSVPLA 126  
Db 73 TSANTVSNQLRLNSDDTGRIFCARVYDFQYGMWVGQGLTVTVSSASTKGPSVPLA 132  
Qy 127 PCSRSTSESTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQS 173  
Db 133 PCSRSTSESTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQS 179

RESULT 8  
A49444  
Ig gamma-1 heavy chain (New) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 16-Jul-1999  
C:Accession: A49444  
R:Saul, F.A.; Poljak, R.J.  
Proteins 14, 363-371, 1992  
A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A res  
A:Reference number: A49444; MUID:93066153; PMID:1438175  
A:Accession: A49444  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-220 <SAU>  
A:Note: this sequence modified after extraction from NCBI backbone  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin

F:137-202/Domain: immunoglobulin homology <IMM>

Query Match 59.9%; Score 546; DB 2; Length 220;  
Best Local Similarity 60.2%; Pred. No. 5.4e-35;  
Matches 109; Conservative 21; Mismatches 31; Indels 20; Gaps 4;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYNNWVRQAPGKGLWVSSISSSSSIIYYA----- 54  
Db 8 GPGVLRPSQSLTCTVSGTFSDDYYWVRQPPGRGLEWI-----GYFFYGTGTLTD 60  
Qy 55 DSVKGRFTISRDNAKNSLYLQMSLRADTAIVYICARD--SSGWYEDYFDYWGQGLTVTV 112  
Db 61 PSLRGRVTMLVNTSKNQFSLRLSSVTAADTAIVYCARNLIAAG-----IDWVGQGLTVTV 115  
Qy 113 SSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQ 172  
Db 116 SSASTKGPSVFPPLAPSKTSKSGTAAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPAVLQ 175

Qy 173 S 173

Db 176 S 176

RESULT 9

S30531

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C:Accession: S30531

R:Mariette, X.

submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30531

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-125 <MAR>

A:Cross-references: UNIPROT:Q9JUL91; EMBL:Z18317

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 59.6%; Score 544; DB 2; Length 125;

Best Local Similarity 89.8%; Pred. No. 4.2e-35;

Matches 106; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYNNWVRQAPGKGLWVSSISSSSSIIYYADSVKGR 60

Db 8 GGGVLRPFGSLRLSCAASGFTFSYNNWVRQAPGKGLWISYSSSSSTIIYYADSVKGR 67

Qy 61 FTISRDNAKNSLYLQMSLRADTAIVYICAR----DSSGWYEDYFDYWGQGLTVTVSS 114

Db 68 FTISRDNAKNSLYLQMSLRADTAIVYICARSRNYDSSGYSHYFDYWGQGLTVTVSS 125

RESULT 10

S37483

Ig gamma-2a chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S37483

R:Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A:Reference number: S37483

A:Accession: S37483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-469 <DUC>

A:Cross-references: EMBL:X70423; NID:9406252; PIDN:CAA49868.1; PID:9406253

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 528.5; DB 2; Length 469;

Best Local Similarity 56.1%; Pred. No. 2.6e-33;  
Matches 97; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

QY 1 GEGVLKPGGSLRLSCAAGTFFSSYSNNVVRQAPKGLEWVSSISSSSSYYIYADSVKGR 60

Db 27 GPVLVRFPGASVKISKASGTYFTDYINWVKRQPGQLRWIGWYIPASGNTKYNPKG 86

QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYICARDSSGWYEDFYWGQGTLLVTSSASTKGP 120

Db 87 ATLTVDTSSSTAYWQLSSLTSEDVAVFCAR-ANGATATLLDYWGQGTLLVTSSAKTAP 145

QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPAVLQS 173

Db 146 SVYPLAPVCGDTTGGSSVTLGCLVKGYFPEPVTLTWNSSLSGSGVHTFPAVLQS 198

## RESULT 11

S31669

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S31669

R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31669

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-141 <CUI>

A/Cross-references: EMBL:Z14212; NID:G30959; PIDN:CAAY78581.1; PID:G30960

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 56.7%; Score 517.5; DB 2; Length 141;

Best Local Similarity 89.7%; Pred. No. 5.2e-33;

Matches 104; Conservative 3; Mismatches 6; Indels 3; Gaps 2;

QY 1 GEGVLKPGGSLRLSCAAGTFFSSYSNNVVRQAPKGLEWVSSISSSSSYYIYADSVKGR 60

Db 27 GGLVLPKPGSLRLSCAAGTFFSSYSNNVVRQAPKGLEWVSSISSSSSYYIYADSVKGR 86

QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYICARDS--SGWYEDFYWGQGTLLVTSS 114

Db 87 FTISRDNKNSLYLQWNSLRAEDTAVYICARGHLTG-EKGYFLWGRGTLVTSS 141

## RESULT 12

S38950

Ig gamma chain - mouse

C/Species: Mus musculus (house mouse)

C/Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999

C/Accession: S38950

R/Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bit

Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993

A/Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha

A/Reference number: S38950; MUID:94128242; PMID:8297501

A/Accession: S38950

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-246 <KLE>

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin

F;137-201/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 56.6%; Score 516; DB 2; Length 246;

Matches 95; Conservative 32; Mismatches 42; Indels 4; Gaps 1;

QY 1 GEGVLKPGGSLRLSCAAGTFFSSYSNNVVRQAPKGLEWVSSISSSSSYYIYADSVKGR 60

Db 8 GPVLVRFPGASVKISKASGTYFTDYIHWVKRFGEGLEWIGWYIPGSGNTKYNPKG 67

QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYICARDSSGWYEDFYWGQGTLLVTSSASTKGP 120

Db 68 ATLTVDTSSSTAYWQLSSLTSEDVAVFCARGG----KFAMDYWGQGTSTVTSSAKTAP 123

QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPAVLQS 173

Db 124 SVYPLAPVCGDTTGGSSVTLGCLVKGYFPEPVTLTWNSSLSGSGVHTFPAVLQS 176

## RESULT 13

S40295

Ig gamma-2a chain (mAb735) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004

C/Accession: S40295

R/Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bit

submitted to the EMBL Data Library, January 1993

A/Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against

A/Reference number: S40295

A/Accession: S40295

A/Molecule type: protein

A/Residues: 1-446 <KLE>

A/Cross-references: UNIPROT:Q99L25

C/Genetics:

A/Map position: 12

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F;1-117/Domain: V-D-J region <VDJ>

F;118-446/Domain: C region <CHR>

F;118-214/Domain: C1 region <CH1>

F;215-230/Region: hinge

F;231-340/Domain: C2 region <CH2>

F;341-446/Domain: C3 region <CH3>

F;360-427/Domain: immunoglobulin homology <IMM>

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;22-96,144-199,261-321,367-425/disulfide bonds: #status predicted

F;132/disulfide bonds: interchain (to light chain) #status predicted

F;224,227,229/disulfide bonds: interchain #status predicted

F;237/binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 56.6%; Score 516; DB 2; Length 446;

Best Local Similarity 54.9%; Pred. No. 2.2e-32;

Matches 95; Conservative 32; Mismatches 42; Indels 4; Gaps 1;

QY 1 GEGVLKPGGSLRLSCAAGTFFSSYSNNVVRQAPKGLEWVSSISSSSSYYIYADSVKGR 60

Db 8 GPVLVRFPGASVKISKASGTYFTDYIHWVKRFGEGLEWIGWYIPGSGNTKYNPKG 67

QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYICARDSSGWYEDFYWGQGTLLVTSSASTKGP 120

Db 68 ATLTVDTSSSTAYWQLSSLTSEDVAVFCARGG----KFAMDYWGQGTSTVTSSAKTAP 123

QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPAVLQS 173

Db 124 SVYPLAPVCGDTTGGSSVTLGCLVKGYFPEPVTLTWNSSLSGSGVHTFPAVLQS 176

## RESULT 14

S22080

Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine

N/Alternate names: Ig gamma-1 chain C region (clone 8.10)

C/Species: Bos primigenius taurus (cattle)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C/Accession: S22080; S06610; A31303

R/Sanders, P.G.

submitted to the EMBL Data Library, November 1991

A/Reference number: S22080

A/Accession: S22080

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-470 <SAN>

Query Match	55.6%; Score 507; DB 2; Length 231;
Best Local Similarity	54.3%; Pred. No. 5.5e-32;
Matches	94; Conservative 31; Mismatches 46; Indels 2; Gaps 2;
Qy	1 GEGLVKPGGSLRLSCAASGTPFPSSYSNNWVROAPKGLEWVSISSSSSYYIYADSVKGR 60           : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :
Dd	8 GPGVLVAPSQSLSITCTVGSPFLSDYGVSIRIQPPKGLEWLGIWIAGGS-TFYNALKSR 66           : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :
Qy	61 FTISRDNAKNSLYLQMNSLRRAEDTAVYYCARDSSGWYEDFYDWGGQCTLVTVSSASTKGP 120   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :
Dd	67 LSINKONSKSQVFLLKNMSLHTDDTAIIYCYVKHEDR-YDWFYFDWGAGTTTVTSASAKTTP 125   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :
Qy	121 SVTFPLPCSRSTSESTAAALGLVKDYPPPEPVTVSNWSNGALTSGVHHTFPVQLQS 173   : :   : :   : :   : :   : :   : :   : :   : :
Dd	126 SVTFPLAPRCDDTTGGSSVFTLGCLVKGPPEPSTVTWNSSGLSSSVHHFFPALLOS 178   : :   : :   : :   : :   : :   : :   : :   : :

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 64.6068 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-37  
Perfect score: 912  
Sequence: 1 GEGLVKGGSLRLSCAASGF.....SWNSGALTGVHTFPVAVLQS 173

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	805	88.3	464	2 Q6MZU6	Q6mz6 homo sapien
2	785	86.1	470	2 Q6PJ44	Q6pja4 homo sapien
3	764.5	83.8	473	2 Q6MZV7	Q6mzv7 homo sapien
4	744	81.6	478	2 Q6PI81	Q6pi81 homo sapien
5	743.5	81.5	465	2 Q6P6C4	Q6p6c4 homo sapien
6	723	79.3	472	2 Q6N089	Q6n089 homo sapien
7	719.5	78.9	475	2 Q6MZQ6	Q6mzq6 homo sapien
8	715.5	78.5	544	2 Q6PJ95	Q6pj95 homo sapien
9	707	77.5	480	2 Q6N094	Q6n094 homo sapien
10	687	75.3	470	2 Q7Z5W1	Q7z5w1 homo sapien
11	686	75.2	466	2 Q6IN78	Q6in78 homo sapien
12	681.5	74.7	475	2 Q6GMW7	Q6gmw7 homo sapien
13	679	74.5	521	2 Q6N4Y9	Q6n4y9 homo sapien
14	676	74.1	466	2 Q6N096	Q6n096 homo sapien
15	670	73.5	493	2 Q68CN4	Q68cn4 homo sapien
16	641	70.3	417	2 Q6N093	Q6n093 homo sapien
17	639.5	70.1	473	2 Q6P055	Q6p055 homo sapien
18	638.5	70.0	473	2 Q6I205	Q6i205 mus musculus
19	635	69.6	482	2 Q7Z351	Q7z351 homo sapien
20	624.5	68.5	481	2 Q6N097	Q6n097 homo sapien
21	623.5	68.4	518	2 Q6N030	Q6n030 homo sapien
22	622.5	68.3	471	2 Q66K04	Q66k04 mus musculus
23	603	66.1	606	2 Q6GMV2	Q6gmv2 homo sapien
24	602.5	66.1	475	2 Q6N095	Q6n095 homo sapien
25	596	65.4	464	2 Q6PIP8	Q6pip8 mus musculus
26	592	64.9	458	2 Q65ZQ1	Q65zq1 homo sapien
27	591.5	64.9	469	2 Q7Z7P5	Q7z7p5 homo sapien
28	587.5	64.4	597	2 Q96BB9	Q96bb9 homo sapien
29	583	63.9	476	2 Q6GMX1	Q6gmx1 homo sapien
30	580.5	63.7	465	2 Q6GMX6	Q6gmx6 homo sapien
31	579.5	63.5	494	2 Q96K68	Q96k68 homo sapien

32	573	62.8	613	2 Q8WUK1	Q8wuk1 homo sapien
33	572.5	62.8	473	2 Q8TC63	Q8tc63 homo sapien
34	570	62.5	208	2 Q6ZP87	Q6zpb7 homo sapien
35	567	62.2	573	2 Q8WU38	Q8wu38 homo sapien
36	565	62.0	480	2 Q6PJF1	Q6pjf1 homo sapien
37	559	61.3	473	2 Q9D8L4	Q9d8l4 mus musculus
38	557	61.1	476	2 Q6MZX7	Q6mzx7 homo sapien
39	539.5	59.2	463	2 Q99LC4	Q99lc4 mus musculus
40	536.5	58.8	487	2 Q99KA4	Q99ka4 mus musculus
41	534.5	58.6	465	2 Q6PJB2	Q6pjb2 mus musculus
42	533.5	58.5	593	2 Q6INM5	Q6inm5 xenopus lae
43	529	58.0	493	2 Q6GMX2	Q6gmx2 homo sapien
44	527	57.8	614	2 Q6DDQ7	Q6ddq7 xenopus lae
45	526	57.7	472	2 Q6PJA7	Q6pja7 mus musculus

ALIGNMENTS

RESULT 1  
Q6MZU6 PRELIMINARY; PRT; 464 AA.  
AC Q6MZU6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686C15213.  
GN Name=DKFZp686C15213;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Bloeker H., Bocher M., Mewes H.W., Weil B., Amid C., Oeanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640874; CAB45931.1; -.  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2; 3.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein\_  
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 88.3%; Score 805; DB 2; Length 464;  
Best Local Similarity 91.4%; Pred. No. 1.2e-65;  
Matches 159; Conservative 2; Mismatches 9; Indels 4; Gaps 3;

Qy	1	GEGLVKGGSLRLSCAASGFTFSSYSMNVRQAPKGLEWVSSISS-SSSYIYVADSVKG	59
Db	27	GGGLVKPGGSLRLSCAASGFTFSSYSMNVRQAPKGLEWVSSFSRRGGSYEYVADSVKG	86
Qy	60	RFTISRDNKNSLYLQWNSLRADTAIVYICARDSSGWYDFYWGQGLTVTVSSASTKG	119
Db	87	RFTISRDNKNSLYLQWNSLRADTAIVYICARD-LGWFG--LDYWGQGLTVTVSSASTKG	143
Qy	120	PSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNMGALTSGLTSVHTFPVAVLQS	173
Db	144	PSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNMGALTSGLTSVHTFPVAVLQS	197

RESULT 2



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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC041037; AAH41037.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 81.6%; Score 744; DB 2; Length 478;
Best Local Similarity 80.1%; Pred. No. 5.1e-60;
Matches 145; Conservative 10; Mismatches 18; Indels 8; Gaps 1;

QY 1 GEGVLKPGSLRLSCAASGFTFSYSMNVRQAPGKLEWVSSISSSSYIYVADSVKGR 60
Db 27 GGGVLKPGSLRLSCAASGFTFSYSMNVRQAPGKLEWVSSISSSSYIYVADSVKGR 86
QY 61 FTISRDNAKNSLYLQMSRLRAEDTAVYICAREFESTMTNADYYFYFMDVWGKTTVV 112
Db 87 FTISRDNAKNSLYLQMSRLRAEDTAVYICAREFESTMTNADYYFYFMDVWGKTTVV 146
QY 113 SSASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQ 172
Db 147 SSASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQ 206
QY 173 S 173
Db 207 S 207

RESULT 5
Q6P6C4 PRELIMINARY; PRT; 465 AA.
AC Q6P6C4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC062335; AAH62335.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDD89348ADC37E6D CRC64;

Query Match 81.5%; Score 743.5; DB 2; Length 465;
Best Local Similarity 83.0%; Pred. No. 5.5e-60;
Matches 142; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

QY 3 GLVKPGSLRLSCAASGFTFSYSMNVRQAPGKLEWVSSISSSSYIYVADSVKGRFT 62
Db 29 GLVKPGSLRLSCAASGFTFSYSMNVRQAPGKLEWVSSISSSSYIYVADSVKGRFT 88
QY 63 ISRDNAKNSLYLQMSRLRAEDTAVYICARDSSGWYEDYFDYWGQGLTVTVSSASTKGPSV 122
Db 89 ISRDNAKNSLYLQMSRLRAEDTAVYICAREIPGG-RCFYDFWGHGTLTVTVSSASTKGPSV 147
QY 123 FPLAPCSRSTSESTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQ 173
Db 148 FPLAPCSRSTSESTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQ 198

RESULT 6
Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686p15220.
GN Name=DKFZp686p15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;

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RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RG The German Human cDNA Consortium;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BX640627; CAE45781.1; -.  
 DR HSP; P01861; IADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein\_  
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 79.3%; Score 723; DB 2; Length 472;  
 Best Local Similarity 81.1%; Pred. No. 4.3e-58;  
 Matches 142; Conservative 10; Mismatches 21; Indels 2; Gaps 1;  
 QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLWVSSISSSSIYYADSVKGR 60  
 DB 27 GGGVLQPGSLRLSCAASGFTFDYAHVVRQAPGKGLWVSGISWNSGSIAYADSVKGR 86  
 QY 61 FTISRDNKNSLYLQMSLRADDTAVYVCARD--SSGWYEDYFYWGQGLVTVSSASTK 118  
 DB 87 FTISRDNKNSLYLQMSLRADDTALYCAKEIGHNFYFYGMVWGQGLVTVSSASTK 146  
 QY 119 GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 173  
 DB 147 GPSVFPLAPSRKSTSGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 201

RESULT 7  
 Q6MZQ6 PRELIMINARY; PRT; 475 AA.  
 AC Q6MZQ6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein DKFZp686G11190.  
 GN Name=DKFZp686G11190;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human esophagus tumor;  
 RG The German Human cDNA Consortium;  
 RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
 RA Han M., Wiemann S.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BX640947; CAE45972.1; -.  
 DR HSP; P01861; IADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.

SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;  
 Query Match 78.9%; Score 719.5; DB 2; Length 475;  
 Best Local Similarity 78.5%; Pred. No. 9.1e-58;  
 Matches 142; Conservative 11; Mismatches 17; Indels 11; Gaps 2;  
 QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLWVSSISSSSIYYADSVKGR 60  
 DB 27 GGGVLQPGGSLRLSCAASGFTFRYAMVVRQAPGKGLWVSGISWNSGVTYADSVKGR 86  
 QY 61 FTISRDNKNSLYLQMSLRADDTAVYVCARDSSGWYED-----YFYWGQGLTVTV 112  
 DB 87 FTISGDIINTLYLQMSLRADDTAVYVCARD---YRDYQVSPAYWYFVWGRGTLVSV 143  
 QY 113 SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 172  
 DB 144 SAASTKGPSVFPLAPSRKSTSGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 203  
 QY 173 S 173  
 DB 204 S 204  
 RESULT 8  
 Q6PU95 PRELIMINARY; PRT; 544 AA.  
 ID Q6PU95  
 AC Q6PU95; 2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RP "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BC019046; AAH19046.1; -.  
 DR HSP; P01861; IADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.



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DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;

Query Match 78.5%; Score 715.5; DB 2; Length 544;
Best Local Similarity 78.1%; Pred. No. 2.5e-57;
Matches 139; Conservative 11; Mismatches 23; Indels 5; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSMNMVWVQAPGKGLWVSSISSSSYIYADSVKGR 60
Db 27 GGVVQPGSSRLSCAASGFTFSYSSMNMVWVQAPGKGLWVSSISSSSYIYADSVKGR 86
Qy 61 FTISRDNAKNSLYLQMNSLRAEDTAVYVCARDSSGWEY-----YFDYWGQGLTVVSSA 115
Db 87 FTISRDNSKNTLSLQMNSLRAEDTAVYVCARDSSGWEY-----YFDYWGQGLTVVSSA 146
Qy 116 STKGPSVPEPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 173
Db 147 STKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 204

RESULT 9
Q6N094 PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686001196.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human esophagus tumor;
RC The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAE45776.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match 77.5%; Score 707; DB 2; Length 480;
Best Local Similarity 74.1%; Pred. No. 1.3e-56;
Matches 137; Conservative 15; Mismatches 19; Indels 14; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSMNMVWVQAPGKGLWVSSISSSSYIYADSVKGR 60
Db 27 GGVVQPGSSRLSCAASGFTFSYSSMNMVWVQAPGKGLWVSSISSSSYIYADSVKGR 86
Qy 61 FTISRDNAKNSLYLQMNSLRAEDTAVYVCARDSSGWEY-----EDYFDYWGQGLT 108
Db 87 FTISRDNAKNSLYLQMNSLRAEDTAVYVCARDSSGWEY-----EDYFDYWGQGLT 144
Qy 109 LVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 168
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Db 145 LVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 204
Qy 169 AVLQS 173
Db 205 AVLQS 209

RESULT 10
Q7Z5W1 PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human esophagus tumor;
RC The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAE45776.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 75.3%; Score 687; DB 2; Length 470;
Best Local Similarity 77.6%; Pred. No. 8.8e-55;
Matches 135; Conservative 11; Mismatches 26; Indels 2; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSMNMVWVQAPGKGLWVSSISSSSYIYADSVKGR 60
Db 27 GGVVQPGGSLRLSCAASGFTFSYSSMNMVWVQAPGKGLWVSSISSSSYIYADSVKGR 85
Qy 61 FTISRDNAKNSLYLQMNSLRAEDTAVYVCARDSSGWEY-----DYFDYWGQGLTVVSSASTKG 119
Db 86 FTISRENKOSLYLQMNSLRAEDTAVYVCARDSSGWEY-----DYFDYWGQGLTVVSSASTKG 145
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QY 120 PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSVGHVHFFPAVLQ 173
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 146 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVGHVHFFPAVLQ 199
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDE81076E CRC64;

Query Match 75.2%; Score 686; DB 2; Length 466;
Best Local Similarity 79.7%; Pred. No. 1.1e-54;
Matches 141; Conservative 7; Mismatches 17; Indels 12; Gaps 3;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLVWSISSSSYI-----YYADS 56
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 GGGLIQFGSLITLSCAASGLTVSSNMVVRQAPGKGLVWSVL-----YIGGATYYADS 81
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 57 VKGRFTISRDNKNSLYLQMSLRADTAIVYCAR-----DSSGWEDYFDYWGQGLTVTVSSAS 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 82 VKGRFTISRDNKNSLYLQMSLRADTAIVYCAR---GNVVPAPMGQGLTVTVSSAS 138
117 TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSVGHVHFFPAVLQ 173
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 139 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVGHVHFFPAVLQ 195
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q6GNW7 PRELIMINARY; PRT; 475 AA.
AC Q6GNW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00407; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE5D736860F8 CRC64;

Query Match 74.7%; Score 681.5; DB 2; Length 475;
Best Local Similarity 76.4%; Pred. No. 2.9e-54;
Matches 136; Conservative 12; Mismatches 25; Indels 5; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLVWSISSSSYI-----YYADS 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 GGGLIQFGSLITLSCAASGLTVSSNMVVRQAPGKGLVWSISSENSTYYADSVKGR 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 FTISRDNKNSLYLQMSLRADTAIVYCAR-----DSSGWEDYFDYWGQGLTVTVSSA 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db 87 FTISRDNKNSLYLQWNSLKTDTTAVYCYVRDLEGAGKYDWDYFDIWRGILTVSSAS 146
Qy 116 STKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQS 173
Db 147 STKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQS 204

RESULT 13
Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AAH33178.1; -.
DR PIR; A60764; A60764.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D2D2E72D6CAA2 CRC64;

Query Match 74.5%; Score 679; DB 2; Length 521;
Best Local Similarity 75.7%; Pred. No. 54e-54;
Matches 134; Conservative 13; Mismatches 26; Indels 4; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVWVRAQPGKGLVWVSLMRDASSETAYAEFVQGR 58
Db 27 GGGVLVQPGGSLRLSCAASGFTVNNYWHVRVRAQPGKGLVWVSLMRDASSETAYAEFVQGR 86
Qy 59 GRFTISRDNKNSLYLQWNSLKTDTTAVYCYVRDLEGAGKYDWDYFDIWRGILTVSSAS 116
Db 27 GGGVLVQPGGSLRLSCAASGFTVNNYWHVRVRAQPGKGLVWVSLMRDASSETAYAEFVQGR 86
Qy 59 GRFTISRDNKNSLYLQWNSLKTDTTAVYCYVRDLEGAGKYDWDYFDIWRGILTVSSAS 116
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Db 87 GRFTILRDDSKNSVHLQWNSLKTDTTAVYCYVRDLEGAGKYDWDYFDIWRGILTVSSAS 146
Qy 117 TKGSVPFLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQS 173
Db 147 TKGSVPFLAPCSRSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQS 203

RESULT 14
Q6N096 PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686i115196.
GN Name=DKFZp686i115196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAB45774.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;

Query Match 74.1%; Score 676; DB 2; Length 466;
Best Local Similarity 77.5%; Pred. No. 9e-54;
Matches 134; Conservative 14; Mismatches 21; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVWVRAQPGKGLVWVSLMRDASSETAYAEFVQGR 60
Db 27 GGGVLVQPGGSLRLSCAASGFTVNNYWHVRVRAQPGKGLVWVSLMRDASSETAYAEFVQGR 86
Qy 61 FTISRDNKNSLYLQWNSLKTDTTAVYCYVRDLEGAGKYDWDYFDIWRGILTVSSASTKGP 120
Db 87 FTISRDNKNTLFLQSLSLRAEDTAVYCYVRDLEGAGKYDWDYFDIWRGILTVSSASTKGP 142
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQS 173
Db 143 SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQS 195

RESULT 15
Q68CN4 PRELIMINARY; PRT; 493 AA.
AC Q68CN4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686E23209 (Fragment).
GN Name=DKFZp686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 80.2075 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-37  
Perfect score: 912  
Sequence: 1 GEGLVKGGSLRLSCAASGF.....SWNSGALTGVHPTPAVLQS 173

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	912	100.0	173	2	AY34306 IgG antib
2	799.5	87.7	475	7	ADM47075 Mouse ant
3	798.5	87.6	443	2	AAM13564 Humanised
4	794	87.1	470	5	ABG77158 Germline
5	794	87.1	470	8	ADR28580 Human ant
6	793	87.0	465	7	ADN93783
7	791	86.7	444	6	ABR55342 Amino aci
8	788.5	86.5	468	8	ADL93666 Human CD4
9	785	86.1	469	8	ADL93669 Human CD4
10	780	85.5	469	8	ADL93662 Human CD4
11	778.5	85.4	473	5	ABG77162 Germline
12	778.5	85.4	473	8	ADR28584 Human ant
13	777.5	85.3	224	6	ABR01511 Human ant
14	777	85.2	224	7	ADJ32114 Human int
15	776.5	85.1	467	6	ABP71365 Anti-OPGL
16	776	85.1	470	5	ABG77157 Amino aci
17	776	85.1	470	8	ADR28579 Human ant
18	770.5	84.5	444	6	AAE35327 Humanised
19	770.5	84.5	444	6	AAE34876 BiWA4/8 a
20	770.5	84.5	444	8	ADL15443 Humanised
21	770.5	84.5	444	8	ADOC00851 Humanised
22	770	84.4	222	7	ADJ32120 Human int
23	770	84.4	470	5	ABG77161 Amino aci
24	770	84.4	470	8	ADR28583 Human ant
25	767	84.1	217	6	ABR01509 Human ant

26	767	84.1	249	6	ABR55323 Amino aci
27	767	84.1	484	6	ABR55341 Amino aci
28	766.5	84.0	449	5	AAO18400 Mature hu
29	766.5	84.0	697	8	ADQ07403 hCBEl1/hB
30	766.5	84.0	697	8	ADQ12180 Heavy cha
31	766.5	84.0	701	8	ADQ07409 hCBEl1 mo
32	766.5	84.0	701	8	ADQ12186 Heavy cha
33	766	84.0	451	8	ADH34584 008 heavy
34	765	83.9	463	8	ADL93665 Human CD4
35	764.5	83.8	222	6	ABR01515 Human ant
36	764.5	83.8	462	8	ADL93670 Human CD4
37	763.5	83.7	628	6	ABJ38670 Fab expre
38	763.5	83.7	638	6	ADA89103 Phage dis
39	763.5	83.7	638	6	ADA90139 Anti-Abet
40	763.5	83.7	638	6	ADA91410 Anti-Abet
41	763.5	83.7	747	7	ADG74355 MSPRO lig
42	763	83.7	217	6	ABR01504 Human ant
43	763	83.7	467	2	AAR80617 Anti-huma
44	762.5	83.6	466	8	ADL93667 Human CD4
45	760	83.3	221	6	ABR01534 Human ant

ALIGNMENTS

RESULT 1  
AAY34306  
ID AAY34306 standard; protein; 173 AA.  
XX  
AC AAY34306;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE IG antibody 2.1.1 heavy chain sequence.  
XX  
KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
OS Homo sapiens.  
XX  
PN WO9945031-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 03-MAR-1999; 99WO-US004583.  
XX  
PR 03-MAR-1998; 98US-00034607.  
PR 03-FEB-1999; 99US-00244253.  
PA (ABGE-) ABGENIX INC.  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX  
DR WPI; 1999-540816/45.  
XX N-PSDB; AAZ20407.  
PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancer, autoimmune diseases and inflammatory diseases.  
XX  
PS Claim 60; Fig 31; 245pp; English.  
XX  
CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAb) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 MAb  
CC by the IGM MAb ABX-CBL, providing that the antibody is not CBL1. The MAb  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic) and autoimmune diseases  
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
 XX  
 SQ Sequence 173 AA;  
 Query Match 100.0%; Score 912; DB 2; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-70;  
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVROAPGKGLWVSSISSSSSYYIYADSVKGR 60  
 DB 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVROAPGKGLWVSSISSSSSYYIYADSVKGR 60  
 QY 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDYFDYWGQGLTLVTVSSASTKGP 120  
 DB 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDYFDYWGQGLTLVTVSSASTKGP 120  
 QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQS 173  
 DB 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQS 173  
 RESULT 2  
 ADM47075  
 ID ADM47075 standard; protein; 475 AA.  
 XX  
 AC ADM47075;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Mouse anti-human G-CSF antibody heavy chain protein.  
 XX  
 KW methylotroph yeast; mammalian sugar chain; OCH1; alpha-1;  
 KW 6-mannosyl transferase; alpha-1; 2-mannosidase;  
 KW orotidin-5'-phosphate decarboxylase; URA3;  
 KW phosphoribosyl-amino-imidazole succinocarboxamide synthase; ADE1;  
 KW imidazole-glycerol-phosphate dehydratase; HIS3;  
 KW 3-isopropyl malate dehydrogenase; LEU2; proteinase A; proteinase B; PRB1;  
 KW PEP4; YPS1; KTR1; MN9; AOX; GAPDH; mannosyl transferase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; mannose glycoprotein.  
 XX  
 OS Mus sp.  
 XX  
 XX WO2003091431-A1.  
 XX  
 XX 06-NOV-2003.  
 XX  
 XX 28-APR-2003; 2003WO-JP005464.  
 XX  
 XX 26-APR-2002; 2002JP-00127677.  
 XX  
 XX (KIRI ) KIRIN BEER KK.  
 XX  
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 XX  
 XX Kobayashi K, Kitagawa Y, Kameda T, Kawashima N, Jigami Y;  
 XX Chiba Y;  
 XX  
 XX WPI; 2003-854401/79.  
 XX  
 XX Producing methylotroph yeast that expresses mammalian sugar chains by  
 XX disrupting the OCH1 gene and inserting an alpha-1,2-mannosidase gene.  
 XX  
 XX Example 28; SEQ ID NO 94; 247pp; Japanese.  
 XX  
 CC The invention relates to the production of a methylotroph yeast that  
 CC produces mammalian sugar chains, comprising disrupting the OCH1 gene in  
 CC the yeast that encodes for alpha-1,6-mannosyl transferase and inserting  
 CC and expressing the alpha-1,2-mannosidase gene. The specification also  
 CC includes DNA sequences encoding: (a) orotidin-5'-phosphate decarboxylase  
 CC (URA3); (b) phosphoribosyl-amino-imidazole succinocarboxamide synthase  
 CC (ADE1); (c) imidazole-glycerol-phosphate dehydratase (HIS3); (d) 3-  
 CC isopropyl malate dehydrogenase (LEU2); (e) alpha-1,6-mannosyl transferase  
 CC (OCH1); (f) proteinase A (PEP4); (g) proteinase B (PRB1); and (h)

CC aspartic protease (YPS1), mannosyl transferase (KTR1 or MN9), alcohol  
 CC oxidase (AOX) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene  
 CC sequences. The yeast is used for the production of human and mammalian  
 CC high mannose glycoproteins with high yield and purity. The method is also  
 CC useful for producing hybrid or complex sugar chains containing mammalian  
 CC type chains. This sequence represents a mouse anti-human G-CSF antibody  
 CC heavy chain used in the invention.  
 XX  
 SQ Sequence 475 AA;  
 Query Match 87.7%; Score 799.5; DB 7; Length 475;  
 Best Local Similarity 89.9%; Pred. No. 8.6e-60;  
 Matches 160; Conservative 1; Mismatches 12; Indels 5; Gaps 2;  
 QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVROAPGKGLWVSSISSSSSYYIYADSVKGR 60  
 DB 27 GGGLVKPGGSLRLSCAASGFTFSYSSNMVROAPGKGLWVSSISSSSSYYIYADSVKGR 86  
 QY 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDYFDYWGQGLTLVTVSSA 115  
 DB 87 FTISRDNKNSLYLQMSLRAEDTAVYYCARDRIIMVRGVYVYVGMVWGQGLTLVTVSSA 146  
 QY 116 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQS 173  
 DB 147 STKGPSVFPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQS 204  
 RESULT 3  
 AAW13564  
 ID AAW13564 standard; protein; 443 AA.  
 XX  
 AC AAW13564;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 03-JUN-1997 (first entry)  
 XX  
 DE Humanised anti-L-selectin antibody HuDreg 55 heavy chain.  
 XX  
 KW L-selectin; humanised antibody; HuDreg 55; acute organ damage;  
 KW organ failure; poly-trauma; haemorrhagic-traumatic shock.  
 XX  
 OS Mus; sp.  
 OS Homo sapiens.  
 OS Chimeric.  
 XX  
 XX WO9706822-A1.  
 XX  
 XX 27-FEB-1997.  
 XX  
 XX 14-AUG-1996; 96WO-US013152.  
 XX  
 XX 17-AUG-1995; 95EP-00112895.  
 XX 19-SEP-1995; 95EP-00114696.  
 XX 27-DEC-1995; 95US-00578953.  
 XX  
 XX (PROT-) PROTEIN DESIGN LABS INC.  
 XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 XX Haselbeck A, Schumacher G, Co M, Martin U;  
 XX  
 XX WPI; 1997-165036/15.  
 XX N-PSDB; AAT61281.  
 XX  
 XX Using anti-selectin antibody to prevent acute organ damage and multiple  
 XX organ failure - during extracorporeal circulation or following  
 XX polytrauma, e. g. haemorrhagic-traumatic shock.  
 XX  
 XX Disclosure; Page 34-36; 52pp; English.  
 XX  
 CC Humanised anti-L-selectin antibody HuDreg 55 comprises 2 heavy chains  
 CC each having the sequence given in AAW13564 and 2 light chains each having  
 CC the sequence given in AAW13563. These are encoded by the cDNA clones  
 CC given in AAT61281 and AAT61280. HuDreg 55 can be used to prevent multiple

CC organ failure associated with polytrauma and for the prevention of acute  
CC organ damage associated with extracorporeal blood circulation. The  
CC antibody inhibits interaction between the carbohydrate-recognising domain  
CC of the selectin and the corresponding cell surface receptor. (Updated on  
CC 17-OCT-2003 to standardise OS field)

XX Sequence 443 AA;

Query Match 87.6%; Score 798.5; DB 2; Length 443;  
Best Local Similarity 89.0%; Pred. NO. 9.6e-60;  
Matches 154; Conservative 8; Mismatches 6; Indels 5; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSSISSSSYIYYADSVKGR 60  
Db 8 GGGVLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSSISSSSYIYYADSVKGR 66  
Qy 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWEDYDYGQGLTVTVSSASTKGP 120  
Db 67 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWEDYDYGQGLTVTVSSASTKGP 122  
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173  
Db 123 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 175

#### RESULT 4

ABG77158  
ID ABG77158 standard; protein; 470 AA.

AC ABG77158;

DT 24-OCT-2002 (first entry)

DE Germline protein sequence of anti-IGF-IR antibody DP-47(3-23)/D6-19/JH6.

KW Insulin-like growth factor I receptor; antibody; human; cytostatic;  
KW osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour;  
KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;  
KW acromegaly; gigantism; psoriasis; atherosclerosis.

OS Homo sapiens.

FN WO200253596-A2.

PD 11-JUL-2002.

PF 20-DEC-2001; 2001WO-US051113.

PR 05-JAN-2001; 2001US-0259927P.

PA (PFIZ ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;

DR WPI; 2002-575410/61.

XX Novel humanized, chimeric monoclonal antibody that specifically binds to  
XX insulin-like growth factor I (IGF-I) receptor useful for inhibiting  
XX binding of IGF-I or IGF-II to receptor and for treating cancer in humans.

PS Disclosure; Fig 19B; 172pp; English.

XX This invention relates to a novel humanised, chimeric or human monoclonal  
XX antibody or its antigen binding portion that specifically binds to  
XX insulin-like growth factor I receptor (IGF-IR). The antibodies of the  
XX invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-  
XX IR and can inhibit in vivo tumour growth and IGF-IR tyrosine  
XX phosphorylation. The antibodies of the invention are useful for  
XX diagnosing the presence or location of an IGF-IR-expressing tumour in a  
XX subject. The antibody or its antigen-binding portion is also useful for  
XX treating cancer in a human. The method for this further involves an anti  
XX neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The

CC antibodies may also be useful for increasing IGF-IR activity and thus  
CC restoring IGF-IR activity in a condition characterised by low IGF-IR  
CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is  
CC also useful for inducing apoptosis of specific cells in a patient, and to  
CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,  
CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies  
CC minimise the immunogenic and allergic responses intrinsic to mouse or  
CC mouse-derivatised monoclonal antibodies and thus increase the efficacy  
CC and safety of the administered antibodies. The present sequence  
CC represents an anti-insulin-like growth factor I receptor antibody of the  
CC invention

XX Sequence 470 AA;

Query Match 87.1%; Score 794; DB 5; Length 470;  
Best Local Similarity 87.0%; Pred. NO. 2.5e-59;  
Matches 154; Conservative 8; Mismatches 11; Indels 4; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSSISSSSYIYYADSVKGR 60  
Db 27 GGGVLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSSISSSSYIYYADSVKGR 86  
Qy 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWEDYDYGQGLTVTVSSAS 116  
Db 87 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWEDYDYGQGLTVTVSSAS 146  
Qy 117 TKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173  
Db 147 TKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 203

#### RESULT 5

ADR28580  
ID ADR28580 standard; protein; 470 AA.

AC ADR28580;

XX 18-NOV-2004 (first entry)

DE Human anti-IGF-IR antibody DP-47(3-23)/D6-19/JH6 protein SEQ ID NO:46.

KW aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;  
KW T-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;  
KW neurodegenerative disorder; human;

KW anti-IGF-IR antibody; cytostatic; immunosuppressive; endocrine;  
KW vasotropic; neuroprotective; nootropic; antithyroid; vaccine;  
KW gene therapy.

OS Homo sapiens.

FN WO2004071529-A2.

PD 26-AUG-2004.

PF 03-FEB-2004; 2004WO-IB000366.

PR 13-FEB-2003; 2003US-0447353P.

PA (PFIZ ) PFIZER PROD INC.

XX Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;  
XX Cusmano JD, Guyot DJ, Page KL;

XX WPI; 2004-625776/60.

XX Treating or preventing aging or a disorder (e.g. multiple myeloma,  
XX autoimmune disease or neurodegenerative disorder) in humans comprises  
XX administering an amount of a human anti-insulin-like growth factor I  
XX receptor antibody.

PS Disclosure; SEQ ID NO 46; 105pp; English.

CC The present invention describes a method for treating or preventing aging  
CC or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus  
CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,  
CC ischaemia or neurodegenerative disorder) in a mammal. The method  
CC comprises administering to the mammal an amount of a human anti-insulin-  
CC like growth factor I receptor (IGF-IR) antibody. Also described is a  
CC pharmaceutical composition for treating or preventing the above-mentioned  
CC disorder in a mammal, comprising an amount of the human anti-IGF-IR  
CC antibody and a pharmaceutical carrier. The composition has cytostatic,  
CC immunosuppressive, endocrine, vasotropic, neuroprotective, and  
CC antithyroid activities, and can be used in vaccines and in gene therapy.  
CC The method and composition are useful for preventing or treating aging or  
CC a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus  
CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,  
CC ischaemia or neurodegenerative disorder) in mammals, such as humans. The  
CC human IGF-IR antibody is used in preparing a composition for the  
CC treatment or prevention of the above-mentioned disorders. The present  
CC sequence represents a human anti-IGF-IR antibody heavy chain amino acid  
CC sequence, which is used in the exemplification of the present invention.  
XX  
SQ Sequence 470 AA;

Query Match 87.1%; Score 794; DB 8; Length 470;  
Best Local Similarity 87.0%; Pred. No. 2.5e-59;  
Matches 154; Conservative 8; Mismatches 11; Indels 4; Gaps 2;  
  
Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSVMWVRQAPGKGLWVSSISSSSYIYADSVKGR 60  
Db 27 GGGVLPQGGSLRLSCAASGFTFSYSSVMWVRQAPGKGLWVSSISSSSYIYADSVKGR 86  
Qy 61 FTISRDNAKNSLYLQMNSLAIEDTAVYICARD--SSGWYEDYF---DYWGQGLTVTVSSAS 116  
Db 87 FTISRDNSKNTLYLQMNSLAIEDTAVYICAKYSSGWYIYVYGVMDVWGQGLTVTVSSAS 146  
Qy 117 TKGPSVFLPACSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 173  
Db 147 TKGPSVFLPACSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 203

RESULT 6  
ADD93783  
ID ADD93783 standard; protein; 465 AA.  
AC ADD93783;  
DT 29-JAN-2004 (first entry)  
XX Monoclonal antibody 20.13.3 heavy chain.  
KW Monoclonal antibody; antibody; antiasthmatic; antiallergic;  
KW antiinflammatory; immunosuppressive; dermatological;  
KW gastrointestinal-gen.; antihelminthic; cytostatic; ophthalmological;  
KW bronchodilator; interleukin-5; human; gene therapy.  
OS Homo sapiens.

PH Key Location/Qualifiers  
FT Peptide 1..19  
FT Protein /note= "Signal peptide"  
FT Protein /note= "Mature protein"  
FT Region 20..138  
FT Region /note= "Variable region"  
FT Misc-difference 50..127  
FT Region /note= "Region specifically described in Claim 1"  
FT Region 50..54  
FT Region /note= "CDR1"  
FT Region 69..85  
FT Region /note= "CDR2"  
FT Region 118..127  
FT Region /note= "CDR3"  
FT Region 139..236  
FT Region /note= "CH1 region"

FT Region 237..248  
FT Region /note= "Hinge region"  
FT Region 249..358  
FT Region /note= "CH2 region"  
FT Region 359..465  
FT Region /note= "CH2 region"  
XX WO2003085089-A2.  
XX 16-OCT-2003.  
XX 27-MAR-2003; 2003WO-US0009260.  
XX 29-MAR-2002; 2002US-0369044P.  
XX (SCHE ) SCHERING CORP.  
XX (ABGE-) ABGENIX INC.  
XX Greenfeder S, Corvalan J;  
XX WPI; 2003-804302/75.  
XX N-PSDB; ADD93782.  
XX New antibody or its antigen-binding fragment that specifically binds  
FT interleukin-5, useful for diagnosing, treating or preventing a condition  
FT associated with undesired interleukin-5 activity, e.g. asthma or allergic  
FT rhinitis.  
XX Claim 1; Page 25; 75pp; English.

XX The present sequence is the protein sequence of the heavy chain of anti-  
CC human interleukin-5 (IL-5) human monoclonal antibody (Mab) 20.13.3. To  
CC obtain this IgG4 Mab, XenoMouse (TM) were immunised with human IL-5.  
CC Spleen and/or lymph nodes were then fused with myeloma P3-X63-Ag8 653 or  
CC myeloma NSO-bcl2 cells, and hybridomas were screened by ELISA for the  
CC presence of human IgG/kappa specific for IL-5. Nucleotides comprising the  
CC present sequence, or nucleotides 1-707, 1102-1137, 1256-1585, 1683-2002,  
CC 58-709, and 148-381 of it, are claimed and used in methods of the  
CC invention. The invention relates to antibodies or their antigen-binding  
CC fragments that specifically bind IL-5. Human anti-IL-5 antibodies are  
CC provided, including chimeric, bispecific, derivatised, single chain  
CC antibodies or portions of fusion proteins, and methods of making anti-IL-  
CC 5 antibodies, pharmaceutical compositions comprising these antibodies and  
CC methods of using the antibodies and compositions for diagnosis and  
CC treatment. The invention also provides gene therapy methods using nucleic  
CC acids encoding the heavy and/or light chain molecules that comprise the  
CC human anti-IL-5 antibodies, and transgenic animals. The antibodies can be  
CC used to prevent or inhibit a condition or disorder characterised by  
CC undesired IL-5 activity, including asthma, asthma exacerbations, asthma  
CC worsening episodes, chronic pneumonia, allergic rhinitis, perennial  
CC allergic rhinitis, allergic bronchopulmonary aspergillosis,  
CC hyper-eosinophilia, Churg-Strauss syndrome, atopic dermatitis, onchocercal  
CC dermatitis, episodic angioedema, eosinophilic myalgia syndrome, coeliac  
CC disease, eosinophilic gastroenteritis, helminth infections, Hodgkin's  
CC disease, nasal polyps, Loeffler's syndrome, urticaria, hypereosinophilic  
CC bronchitis, arteritis nodosa, sinusitis, chronic sinusitis, eosinophilic  
CC oesophagitis, allergic eosinophilic oesophagitis, or allergic  
CC conjunctivitis, by decreasing or inhibiting the infiltration of  
CC eosinophils into affected tissue. The antibodies are also useful for  
CC preventing or inhibiting an IL-5 mediated allergic response in a subject  
CC or an IL-5 mediated event, such as eosinophil proliferation, maturation,  
CC survival, activation, migration into the bloodstream, adhesion to  
CC endothelium, infiltration into tissues, pulmonary oedema,  
CC bronchoconstriction, airway hyperresponsiveness, pulmonary eosinophilia  
CC or neutrophilia, cutaneous eosinophilia, or airway epithelial damage (all  
CC claimed).

XX SQ Sequence 465 AA;

Query Match 87.0%; Score 793; DB 7; Length 465;  
Best Local Similarity 87.3%; Pred. No. 3e-59;  
Matches 151; Conservative 9; Mismatches 11; Indels 2; Gaps 1;



Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSMMVWRQAPGKGLWVSSISSSSYIYADSVKGR 60  
 Db 27 GGGVLVQPGGSLRLSCAASGFTFSYSSMMVWRQAPGKGLWVSSISSSSYIYADSVKGR 86  
 Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWEDYFDYWGQGTFLVTVSSASTKGP 120  
 Db 87 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWEDYFDYWGQGTFLVTVSSASTKGP 144  
 Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQS 173  
 Db 145 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQS 197

RESULT 7  
 ABR55342  
 ID ABR55342 standard; protein; 444 AA.  
 XX AC ABR55342;  
 XX DT 29-JUL-2003 (first entry)  
 XX DE Amino acid sequence of a grafted VH chain for anti-KDR antibody.  
 XX KW Antibody; kinase insert domain-containing receptor; KDR; antibody VR165;  
 KW complementarity determining region; vascular endothelial growth factor;  
 KW CDR; VEGF; inflammation; psoriasis; rheumatoid arthritis; tumour.  
 XX OS Synthetic.  
 XX PN WO2003031475-A2.  
 XX PD 17-APR-2003.  
 XX PF 10-OCT-2002; 2002WO-GB004619.  
 XX PR 10-OCT-2001; 2001GB-00024317.  
 XX PA (CELL-) CELTECH R & D LTD.  
 XX PI Popplewell AG, Tickle SP, Zinkewich-Peotti K, Morrison RK;  
 XX WPI; 2003-441133/41.  
 XX DR Novel antibody molecules having specificity for human kinase insert  
 PT domain-containing receptors, useful for treating inflammation, psoriasis,  
 PT rheumatoid arthritis, tumor growth and metastasis.  
 XX PS Claim 16; Fig 21; 57pp; English.  
 XX CC The specification describes an antibody molecule which has specificity  
 CC for human kinase insert domain-containing receptor (KDR). The antibody  
 CC comprises complementarity determining regions (CDRs) from the heavy and  
 CC light chain variable domains of the murine monoclonal antibody VR165.  
 CC This antibody is specific for human KDR. The antibody of the invention  
 CC blocks vascular endothelial growth factor (VEGF) binding to KDR.  
 CC Antibodies of the invention are useful for treating a pathology in which  
 CC VEGF and/or KDR are implicated, and in the manufacture of a medicament  
 CC for the treatment of a pathology in which VEGF and/or KDR are implicated.  
 CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour  
 CC growth or metastasis. The present sequence represents a grafted VH chain,  
 CC comprising a VR165 CDR regions and a human framework. It is used to  
 CC produce antibody molecules of the invention  
 SQ Sequence 444 AA;

Query Match 86.7%; Score 791; DB 6; Length 444;  
 Best Local Similarity 87.9%; Pred. No. 4.2e-59;  
 Matches 152; Conservative 6; Mismatches 11; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSMMVWRQAPGKGLWVSSISSSSYIYADSVKGR 60  
 Db 8 GGGVLVQPGGSLRLSCAASGFTFSYSSMMVWRQAPGKGLWVSSISSSSYIYADSVKGR 67

Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWEDYFDYWGQGTFLVTVSSASTKGP 120  
 Db 68 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWEDYFDYWGQGTFLVTVSSASTKGP 123  
 Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQS 173  
 Db 124 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQS 176

RESULT 8  
 ADL93666  
 ID ADL93666 standard; protein; 468 AA.  
 XX AC ADL93666;  
 XX DT 17-JUN-2004 (first entry)  
 XX DE Human CD44-binding antibody heavy chain HAB-B8-heavy SEQ ID NO:161.  
 XX KW human; CD44; light chain immunoglobulin variable domain;  
 KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;  
 KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
 KW dermatological; vasotropic; neuroprotective; antibody therapy;  
 KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
 KW graft versus host response; multiple sclerosis; neoplastic disorder;  
 KW cancer; antibody.  
 XX OS Homo sapiens.  
 XX PN WO2004024750-A2.  
 XX PD 25-MAR-2004.  
 XX PF 15-SEP-2003; 2003WO-US029318.  
 XX PR 13-SEP-2002; 2002US-0410758P.  
 XX PR 09-MAY-2003; 2003US-0469123P.  
 XX PA (DYAX-) DYAX CORP.  
 XX PI Rondon IJ, Edge A, Baribault Kent R;  
 XX WPI; 2004-270003/25.  
 XX DR New protein comprising a light chain (LC) immunoglobulin variable domain  
 PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
 PT useful for preparing a composition for treating inflammatory or  
 PT neoplastic disorders.  
 XX PS Disclosure; SEQ ID NO 161; 128pp; English.  
 XX CC The invention relates to a novel isolated protein comprising a light  
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
 CC immunoglobulin variable domain sequence that form an antigen binding site  
 CC with binding affinity for the human CD44 extracellular domain and where  
 CC CDR3 of the LC variable domain sequence. A protein of the invention has  
 CC antirheumatic, antiinflammatory, immunosuppressive, antiarthritic,  
 CC antineoplastic, dermatological, vasotropic, and neuroprotective activity,  
 CC and may have a use in antibody therapy. The protein is useful for  
 CC preparing a composition for treating inflammatory disorders, e.g.,  
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
 CC multiple sclerosis or neoplastic disorder, which is a malignant or  
 CC metastatic cancer. The present sequence represents a human CD44-binding  
 CC antibody heavy chain.  
 XX SQ Sequence 468 AA;

Query Match 86.5%; Score 788.5; DB 8; Length 468;  
 Best Local Similarity 88.1%; Pred. No. 7.3e-59;  
 Matches 155; Conservative 5; Mismatches 11; Indels 5; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSMMVWRQAPGKGLWVSSISSSSYIYADSVKGR 60  
 Db 1 GGGVLVQPGGSLRLSCAASGFTFSYSSMMVWRQAPGKGLWVSSISSSSYIYADSVKGR 67

Db 27 GGGVLQPGGSLRLSCAASGFTFSYMSWVRQAPGKGLEWVSSIGSPGGQTRYADSVKGR 86  
 Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCAR---DSSGWYEDYDYGQGLTLVTSSAST 117  
 Db 87 FTISRDNKNSLYLQMSLRAEDTAVYYCARDYDSSGY--SYFDYWGQGLTQVTSSAST 144  
 Qy 118 KGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPPTVTVSNWNSGALTSVGHHTFPAVLQS 173  
 Db 145 KGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPPTVTVSNWNSGALTSVGHHTFPAVLQS 200

RESULT 9  
 ADL93669  
 ID ADL93669 standard; protein; 469 AA.  
 XX  
 AC ADL93669;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Human CD44-binding antibody heavy chain HAE-H-H10-heavy SEQ ID NO:164.  
 XX  
 KW human; CD44; light chain immunoglobulin variable domain;  
 KW heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;  
 KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
 KW dermatological; vasotropic; neuroprotective; antibody therapy;  
 KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
 KW graft versus host response; multiple sclerosis; neoplastic disorder;  
 KW cancer; antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004024750-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 XX 15-SEP-2003; 2003WO-US029318.  
 XX  
 PF 13-SEP-2002; 2002US-0410758P.  
 PR 09-MAY-2003; 2003US-0469123P.  
 XX  
 XX (DYAX-) DYAX CORP.  
 XX  
 XX Rondon IJ, Edge A, Baribault Kent R;  
 XX  
 XX WPI; 2004-270003/25.  
 XX  
 DR New protein comprising a light chain (LC) immunoglobulin variable domain  
 PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
 PT useful for preparing a composition for treating inflammatory or  
 PT neoplastic disorders.  
 XX  
 PS Disclosure; SEQ ID NO 164; 128pp; English.  
 XX  
 CC The invention relates to a novel isolated protein comprising a light  
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
 CC immunoglobulin variable domain sequence that form an antigen binding site  
 CC with binding affinity for the human CD44 extracellular domain and where  
 CC CDR3 of the LC variable domain sequence. A protein of the invention has  
 CC cytotstatic, antiinflammatory, immunosuppressive, antiarthritic,  
 CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,  
 CC and may have a use in antibody therapy. The protein is useful for  
 CC preparing a composition for treating inflammatory disorders, e.g.,  
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
 CC multiple sclerosis or neoplastic disorder, which is a malignant or  
 CC metastatic cancer. The present sequence represents a human CD44-binding  
 CC antibody heavy chain.  
 XX  
 SQ Sequence 469 AA;

Query Match 86.1%; Score 785; DB 8; Length 469;  
 Best Local Similarity 87.0%; Pred. No. 1.5e-58;  
 Matches 154; Conservative 7; Mismatches 10; Indels 6; Gaps 2;

Qy 1 GEGVLKPGGSLRLSCAASGFTFSYMSWVRQAPGKGLEWVSSISSSSYIYADSVKGR 60  
 Db 27 GGGVLQPGGSLRLSCAASGFTFSYMSWVRQAPGKGLEWVSSISGGGLTDYADSVKGR 86  
 Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWY---DYFDYWGQGLTLVTSSAS 116  
 Db 87 FTISRDNKNSLYLQMSLRAEDTAVYYCARD--GYDSSGYEGFDYWGQGLTLVTSSAS 144  
 Qy 117 TKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPPTVTVSNWNSGALTSVGHHTFPAVLQS 173  
 Db 145 TKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPPTVTVSNWNSGALTSVGHHTFPAVLQS 201

RESULT 10  
 ADL93662  
 ID ADL93662 standard; protein; 469 AA.  
 XX  
 AC ADL93662;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Human CD44-binding antibody heavy chain HAE-H10-heavy SEQ ID NO:157.  
 XX  
 KW human; CD44; light chain immunoglobulin variable domain;  
 KW heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;  
 KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
 KW dermatological; vasotropic; neuroprotective; antibody therapy;  
 KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
 KW graft versus host response; multiple sclerosis; neoplastic disorder;  
 KW cancer; antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004024750-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 XX 15-SEP-2003; 2003WO-US029318.  
 XX  
 PF 13-SEP-2002; 2002US-0410758P.  
 PR 09-MAY-2003; 2003US-0469123P.  
 XX  
 XX (DYAX-) DYAX CORP.  
 XX  
 XX Rondon IJ, Edge A, Baribault Kent R;  
 XX  
 XX WPI; 2004-270003/25.  
 XX  
 DR New protein comprising a light chain (LC) immunoglobulin variable domain  
 PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
 PT useful for preparing a composition for treating inflammatory or  
 PT neoplastic disorders.  
 XX  
 PS Disclosure; SEQ ID NO 157; 128pp; English.  
 XX  
 CC The invention relates to a novel isolated protein comprising a light  
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
 CC immunoglobulin variable domain sequence that form an antigen binding site  
 CC with binding affinity for the human CD44 extracellular domain and where  
 CC CDR3 of the LC variable domain sequence. A protein of the invention has  
 CC cytotstatic, antiinflammatory, immunosuppressive, antiarthritic,  
 CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,  
 CC and may have a use in antibody therapy. The protein is useful for  
 CC preparing a composition for treating inflammatory disorders, e.g.,  
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
 CC multiple sclerosis or neoplastic disorder, which is a malignant or  
 CC metastatic cancer. The present sequence represents a human CD44-binding  
 CC antibody heavy chain.  
 XX  
 SQ Sequence 469 AA;

Query Match 85.5%; Score 780; DB 8; Length 469;  
 Best Local Similarity 86.4%; Pred. No. 3.9e-58;

Matches 153; Conservative 8; Mismatches 10; Indels 6; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVWRAQPGKLEWVSSISSSSSYIYADSVKGR 60  
Db 27 GGLLVQPGGSLRLSCAASGFTFSYSSNMVWRAQPGKLEWVSSISSSSSYIYADSVKGR 86  
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYVCARDSSGWYE----DYFDYWGQGTTLVTVSSAS 116  
Db 87 FTISRDNKNSLYLQMSLRAEDTAVYVCARDSSGWYE----DYFDYWGQGTTLVTVSSAS 144  
Qy 117 TKGPSVPLPACSRSTSESTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQ 173  
Db 145 TKGPSVPLPACSRSTSESTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQ 201

RESULT 11  
ABG77162  
ID ABG77162 standard; protein; 473 AA.  
XX  
AC ABG77162;  
XX  
DT 24-OCT-2002 (first entry)  
XX  
DE Germline protein sequence of anti-IGF-1R antibody DP-35(3-11)/D3-3/JH6.  
XX  
KW Insulin-like growth factor I receptor; antibody; human; cytostatic;  
KW osteopathic; antiatherosclerotic; antiporiatic; IGF-1R; tumour;  
KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;  
KW acromegaly; gigantism; psoriasis; atherosclerosis.  
XX  
OS Homo sapiens.  
XX  
FN WO200253596-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-US051113.  
XX  
PR 05-JAN-2001; 2001US-0259927P.  
XX  
PA (PFIZ ) PFIZER INC.  
PA (ABGE-) ABGENIX INC.  
XX  
FI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;  
XX  
DR WPI; 2002-575410/61.  
XX  
XX Novel humanized, chimeric monoclonal antibody that specifically binds to  
PT insulin-like growth factor I (IGF-I) receptor useful for inhibiting  
PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.  
XX  
PS Disclosure; Fig 19D; 172pp; English.

XX This invention relates to a novel humanised, chimeric or human monoclonal  
CC antibody or its antigen binding portion that specifically binds to  
CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the  
CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-  
CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine  
CC phosphorylation. The antibodies of the invention are useful for  
CC diagnosing the presence or location of an IGF-IR-expressing tumour in a  
CC subject. The antibody or its antigen-binding portion is also useful for  
CC treating cancer in a human. The method for this further involves an anti  
CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The  
CC antibodies may also be useful for increasing IGF-IR activity and thus  
CC restoring IGF-IR activity in a condition characterised by low IGF-IR  
CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is  
CC also useful for inducing apoptosis of specific cells in a patient, and to  
CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,  
CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies  
CC minimise the immunogenic and allergic responses intrinsic to mouse or  
CC mouse-derived monoclonal antibodies and thus increase the efficacy  
CC and safety of the administered antibodies. The present sequence  
CC represents an anti-insulin-like growth factor I receptor antibody of the

CC invention  
XX  
SQ Sequence 473 AA;  
Query Match 85.4%; Score 778.5; DB 5; Length 473;  
Best Local Similarity 86.1%; Pred. No. 5.3e-58;  
Matches 155; Conservative 5; Mismatches 13; Indels 7; Gaps 2;  
Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVWRAQPGKLEWVSSISSSSSYIYADSVKGR 60  
Db 27 GGLLVKPGGSLRLSCAASGFTFSYSSNMVWRAQPGKLEWVSSISSSSSYIYADSVKGR 86  
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYVCARDSSGWYE----DSSGWYEDYF--DYWGQGTTLVTVS 113  
Db 87 FTISRDNKNSLYLQMSLRAEDTAVYVCARDSSGWYE----DSSGWYEDYF--DYWGQGTTLVTVS 146  
Qy 114 SASTKGPSVPPLAPCSRSTSESTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQ 173  
Db 147 SASTKGPSVPPLAPCSRSTSESTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQ 206

RESULT 12  
ADR28584  
ID ADR28584 standard; protein; 473 AA.  
XX  
AC ADR28584;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human anti-IGF-1R antibody DP-35(3-11)/D3-3/JH6 protein SEQ ID NO:50.  
XX  
KW aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;  
KW T-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;  
KW neurodegenerative disorder; human;  
KW anti-insulin-like growth factor I receptor antibody;  
KW anti-IGF-1R antibody; cytostatic; immunosuppressive; endocrine;  
KW vasotropic; neuroprotective; nootropic; antithyroid; vaccine;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO2004071529-A2.  
XX  
PD 26-AUG-2004.  
XX  
PF 03-FEB-2004; 2004WO-IB000366.  
XX  
PR 13-FEB-2003; 2003US-0447353P.  
XX  
PA (PFIZ ) PFIZER PROD INC.  
XX  
FI Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;  
PI Cusmano JD, Guyot DJ, Page KL;  
XX  
XX WPI; 2004-625776/60.  
DR  
XX Treating or preventing aging or a disorder (e.g. multiple myeloma,  
PT autoimmune disease or neurodegenerative disorder) in humans comprises  
PT administering an amount of a human anti-insulin-like growth factor I  
PT receptor antibody.  
XX  
PS Disclosure; SEQ ID NO 50; 105pp; English.

XX The present invention describes a method for treating or preventing aging  
CC or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus  
CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,  
CC ischaemia or neurodegenerative disorder) in a mammal. The method  
CC comprises administering to the mammal an amount of a human anti-insulin-  
CC like growth factor I receptor (IGF-IR) antibody. Also described is a  
CC pharmaceutical composition for treating or preventing the above-mentioned  
CC disorder in a mammal, comprising an amount of the human anti-IGF-IR  
CC antibody and a pharmaceutical carrier. The composition has cytostatic,  
CC immunosuppressive, endocrine, vasotropic, neuroprotective, nootropic and

CC antithyroid activities, and can be used in vaccines and in gene therapy.  
 CC The method and composition are useful for preventing or treating aging or  
 CC a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus  
 CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,  
 CC ischaemia or neurodegenerative disorder) in mammals, such as humans. The  
 CC human IGF-IR antibody is used in preparing a composition for the  
 CC treatment or prevention of the above-mentioned disorders. The present  
 CC sequence represents a human anti-IGF-IR antibody heavy chain amino acid  
 CC sequence, which is used in the exemplification of the present invention.  
 XX  
 XX  
 XX Sequence 473 AA;

Query Match 85.4%; Score 778.5; DB 8; Length 473;  
 Best Local Similarity 86.1%; Pred. No. 5.3e-58;  
 Matches 155; Conservative 5; Mismatches 13; Indels 7; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSYYIYADSVKGR 60  
 DB 27 GGLVQPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSGSTYYIYADSVKGR 86  
 QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYYCAR----DSSGWYEDYP--DYWGQGTLLVTS 113  
 DB 87 FTISRDNKNSLYLQWNSLRAEDTAVYYCARVLRFLWLLYYIYGGNDYWGQGTLLVTS 146  
 QY 114 SASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173  
 DB 147 SASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 206

RESULT 13  
 ABR01511  
 ID ABR01511 standard; protein; 224 AA.  
 XX  
 AC ABR01511;  
 XX  
 DT 16-APR-2003 (first entry)  
 XX  
 DE Human anti-TIMP-1 antibody heavy chain #9.

XX Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;  
 KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;  
 KW variable light chain; cytotatic; nephrotropic; cardiant; liver fibrosis;  
 KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;  
 KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;  
 KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.  
 XX  
 OS Homo sapiens.

XX WO200286085-A2.  
 XX  
 XX 31-OCT-2002.  
 XX  
 XX 24-APR-2002; 2002WO-US012801.  
 XX  
 XX 24-APR-2001; 2001US-0285683P.  
 XX  
 XX (FARB ) BAYER CORP.  
 PA (MORP-) MORPHOSYS AG.  
 XX  
 XX Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;  
 PI  
 XX WPI; 2003-129114/12.  
 DR N-PSDB; ABZ74782.

XX  
 XX New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies,  
 PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1  
 PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung  
 PT cancer.  
 XX  
 XX Claim 20; Page 153-154; 228pp; English.

XX The invention relates to a novel purified preparation of a human  
 CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)

CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP  
 CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a  
 CC variable light chain (VLC)DR3 region. An antibody preparation of the  
 CC invention has hepatotropic, cytotatic, nephrotropic and cardiant  
 CC activity. The human antibody is useful for decreasing an MMP-inhibiting  
 CC activity of a TIMP-1. It is especially useful for ameliorating the  
 CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,  
 CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus  
 CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary  
 CC fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The  
 CC antibody is also useful for detecting a TIMP-1 in a test preparation, or  
 CC in diagnosing a disorder in which a TIMP-1 level is elevated. The  
 CC sequences shown in ABR01502-ABR01545 represent the heavy chain regions of  
 CC a human anti-TIMP-1 antibody of the invention  
 XX  
 XX Sequence 224 AA;

Query Match 85.3%; Score 777.5; DB 6; Length 224;  
 Best Local Similarity 86.7%; Pred. No. 2.7e-58;  
 Matches 150; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSYYIYADSVKGR 60  
 DB 8 GGLVQPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSAISGGSTYYIYADSVKGR 67  
 QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYYCARDSSGWYEDYFYWGQGTLLVTSASSTKGP 120  
 DB 68 FTISRDNKNSLYLQWNSLRAEDTAVYYCARLDT-YYPDLFDYWGQGTLLVTSASSTKGP 126  
 QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173  
 DB 127 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 179

RESULT 14  
 ADJ32114  
 ID ADJ32114 standard; protein; 224 AA.

XX AC ADJ32114;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human interferon-gamma antibody heavy chain amino acid sequence SeqID68.  
 XX  
 KW antibody; antigen binding domain; interferon-gamma; INF-gamma;  
 KW antagonist antibody; antiinflammatory; immunosuppressive;  
 KW autoimmune disease; inflammatory condition; human; heavy chain.  
 XX  
 OS Homo sapiens.

XX US2003099647-A1.  
 XX  
 XX 29-MAY-2003.  
 XX  
 XX 05-OCT-2001; 2001US-00972656.  
 XX  
 XX 05-OCT-2001; 2001US-00972656.  
 XX  
 XX (DESH/) DESHPANDE R V.  
 PA (TSAI/) TSAI M.

XX Deshpande RV, Tsai M;  
 XX  
 XX WPI; 2003-696068/66.  
 DR N-PSDB; ADJ32113.

XX New antibody or antigen binding domain, or its fragment, variant or  
 PT derivative, which binds to an interferon-gamma protein, useful for  
 PT preparing a composition for preventing or treating inflammatory or  
 PT autoimmune disorders.

XX Claim 10; SEQ ID NO 68; 113pp; English.

CC This invention relates to a novel antibody or antigen binding domain, or  
 CC its fragment, variant or derivative, which binds to an interferon-gamma  
 CC (INF-gamma) protein, and is an antagonist antibody. The invention may be  
 CC useful for the development of compounds with an antiinflammatory or  
 CC immunosuppressive activity through action as interferon-gamma agonists. A  
 CC composition containing the antibody is useful for preventing or treating  
 CC an autoimmune disease and an inflammatory condition. The present sequence  
 CC is that of an antibody heavy chain of a human IFN-gamma antibody which  
 CC may be part of the invention.

XX SQ Sequence 224 AA;

Query Match 85.2%; Score 777; DB 7; Length 224;  
 Best Local Similarity 85.5%; Pred. No. 3e-58;  
 Matches 148; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLVWVSSISSSSSYYIYADSVKGR 60  
 Db 8 GGLVQPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLVWVSAISGSGSTYYADSVKGR 67  
 Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120  
 Db 68 FTISRDNKNSLYLQMSLRAEDTAVYYCARDRVGYSSSLDYWGQGLTVTVSSASTKGP 127  
 Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173  
 Db 128 SVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180

# RESULT 15

ABP71365  
 ID ABP71365 standard; protein; 467 AA.

XX AC ABP71365;

XX DT 28-APR-2003 (first entry)

XX DE Anti-OPGL-1 antibody heavy chain.

XX KW Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;  
 XX antiarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.

XX OS Mus musculus.

Key	Location/Qualifiers
Peptide	1..19
Region	/note= "IgG2 signal peptide"
Region	20..141
Region	/note= "variable region"
Region	142..467
Region	/note= "constant region"

XX WO2003002713-A2.

XX PD 09-JAN-2003.

XX PF 25-JUN-2002; 2002WO-US020181.

XX PR 26-JUN-2001; 2001US-0301172P.

XX PA (ABGE-) ABGENIX INC.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Martin FH, Corvalan JR, Davis GC;

XX DR WPI; 2003-210262/20.

XX DR N-PSDB; ABZ59147.

XX PT New antibodies that interact with osteoprotegerin ligands, useful for  
 PT treating osteopenic disorders, e.g. osteoporosis, bone loss from  
 PT arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and  
 PT osteonecrosis.

XX

PS Claim 1; Fig 2; 144pp; English.

XX The invention relates to antibodies that interact with osteoprotegerin  
 CC ligands (OPGL). The antibody is useful for detecting the level of OPGL in  
 CC a biological sample. The antibody, or the pharmaceutical composition  
 CC comprising the antibody, is also useful for treating osteopenic disorder,  
 CC an inflammatory condition with attendant bone loss, an autoimmune  
 CC condition with attendant bone loss in a patient or rheumatoid arthritis  
 CC in a patient. In particular, the antibody or composition is useful for  
 CC treating bone diseases, e.g. osteoporosis, bone loss from arthritis,  
 CC Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's  
 CC syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, Menkes'  
 CC syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or  
 CC osteonecrosis. The present sequence represents an anti-OPGL-1 antibody  
 CC heavy chain

XX SQ Sequence 467 AA;

Query Match 85.1%; Score 776.5; DB 6; Length 467;  
 Best Local Similarity 84.8%; Pred. No. 7.7e-58;  
 Matches 151; Conservative 7; Mismatches 11; Indels 9; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLVWVSSISSSSSYYIYADSVKGR 60  
 Db 27 GGLVQPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLVWVSGITSGSGSTYYADSVKGR 86  
 Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSS-----GWYEDYFDYWGQGLTVTVSSA 115  
 Db 87 FTISRDNKNSLYLQMSLRAEDTAVYYCARDPGTTVMSW----FDPWGQGLTVTVSSA 142  
 Qy 116 STKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173  
 Db 143 STKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 200

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Job time : 82.2075 secs

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OM protein - protein search, using sw model

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Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9:	/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10:	/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11:	/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	798.5	87.6	443	9	US-09-917-410-4
2	794	87.1	470	15	US-09-917-410-4
3	793	87.0	465	14	US-10-038-591-46
4	788.5	86.5	468	16	US-10-038-591-46
5	785	86.1	469	16	US-10-038-591-46
6	780	85.5	469	16	US-10-038-591-46
7	778.5	85.4	473	15	US-10-038-591-46
8	777.5	85.3	224	16	US-10-038-591-46
9	777	85.2	224	10	US-09-972-656-68
10	776.5	85.1	467	15	US-10-038-591-46
11	776	85.1	470	15	US-10-038-591-46
12	770.5	84.5	444	14	US-10-038-591-46
13	770.5	84.5	444	16	US-10-038-591-46

14	770.5	84.5	444	16	US-10-645-215-74
15	770	84.4	222	10	US-09-972-656-74
16	770	84.4	470	15	US-10-038-591-49
17	767	84.1	217	16	US-10-128-520-146
18	766.5	84.0	663	15	US-10-412-406-32
19	766.5	84.0	4852	15	US-10-412-406-33
20	765	83.9	463	16	US-10-663-244-160
21	764.5	83.8	222	16	US-10-128-520-152
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23	763	83.7	217	16	US-10-128-520-141
24	762.5	83.6	466	16	US-10-663-244-162
25	760	83.3	221	16	US-10-128-520-171
26	759.5	83.3	220	16	US-10-128-520-154
27	759.5	83.3	220	16	US-10-128-520-156
28	759.5	83.3	464	16	US-10-663-244-156
29	758.5	83.2	218	16	US-10-128-520-144
30	758.5	83.2	367	15	US-10-045-674-453
31	758.5	83.2	368	11	US-09-837-306-196
32	756.5	82.9	222	16	US-10-128-520-145
33	756.5	82.9	445	14	US-10-320-231A-79
34	756	82.9	451	9	US-09-822-698A-26
35	755.5	82.8	464	16	US-10-663-244-158
36	754.5	82.7	462	16	US-10-663-244-155
37	753.5	82.6	460	16	US-10-663-244-159
38	753	82.6	217	16	US-10-128-520-140
39	753	82.6	217	16	US-10-128-520-142
40	753	82.6	451	14	US-10-153-382-17
41	752.5	82.5	446	15	US-10-408-901-38
42	750.5	82.3	224	16	US-10-128-520-150
43	750	82.2	449	9	US-09-736-371B-21
44	750	82.2	449	15	US-10-463-442-21
45	748.5	82.1	463	14	US-10-153-382-13

ALIGNMENTS

RESULT 1  
US-09-917-410-4  
; Sequence 4, Application US/09917410  
; Patent No. US20020098183A1  
; GENERAL INFORMATION:  
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;  
; CO, Man S.  
; TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF  
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR  
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER  
; EXTRACORPOREAL BLOOD CIRCULATION  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Computer Disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII, WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/917,410  
; FILING DATE: 26-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/578,953  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: EP 95 114 969.9  
; FILING DATE: 19-Sep-95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. US20020098183Alman D.  
; REGISTRATION NUMBER: 30,946





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; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-161

Query Match      86.5%; Score 788.5; DB 16; Length 468;
Best Local Similarity 88.1%; Pred. No. 1.8e-46;
Matches 155; Conservative 5; Mismatches 11; Indels 5; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSSISSSSYIYYADSVKGR 60
Db 27 GGGVLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKGLWVSSIGPSGGQTRYADSVKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVVYCAR--DSSGWEDYFDYWGQGLTVTVSSAST 117
Db 87 FTISRDNKNSLYLQMNLSRAEDTAVVYCARDYDSSG--SYFDYWGQGLTVTVSSAST 144
QY 118 KGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 173
Db 145 KGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 200

RESULT 5
US-10-663-244-164
; Sequence 164, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-164

Query Match      86.1%; Score 785; DB 16; Length 469;
Best Local Similarity 87.0%; Pred. No. 3.2e-46;
Matches 154; Conservative 7; Mismatches 10; Indels 6; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSSISSSSYIYYADSVKGR 60
Db 27 GGGVLVQPGGSLRLSCAASGFTFSYPLMSWVRQAPGKGLWVSSISGGLTDYADSVKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVVYCARDSSGWYE----DYFDYWGQGLTVTVSSAS 116
Db 87 FTISRDNKNSLYLQMNLSRAEDTAVVYCARD--GYDSSGVEGFDYWGQGLTVTVSSAS 144
QY 117 TKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 173
Db 145 TKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 201

; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-164

Query Match      86.1%; Score 785; DB 16; Length 469;
Best Local Similarity 87.0%; Pred. No. 3.2e-46;
Matches 154; Conservative 7; Mismatches 10; Indels 6; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSSISSSSYIYYADSVKGR 60
Db 27 GGGVLVQPGGSLRLSCAASGFTFSYPLMSWVRQAPGKGLWVSSISGGLTDYADSVKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVVYCARDSSGWYE----DYFDYWGQGLTVTVSSAS 116
Db 87 FTISRDNKNSLYLQMNLSRAEDTAVVYCARD--GYDSSGVEGFDYWGQGLTVTVSSAS 144
QY 117 TKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 173
Db 145 TKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 201
```

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RESULT 6
US-10-663-244-157
; Sequence 157, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-157

Query Match      85.5%; Score 780; DB 16; Length 469;
Best Local Similarity 86.4%; Pred. No. 7e-46;
Matches 153; Conservative 8; Mismatches 10; Indels 6; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSSISSSSYIYYADSVKGR 60
Db 27 GGGVLVQPGGSLRLSCAASGFTFSYPLMSWVRQAPGKGLWVSSISGGLTDYADSVKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVVYCARDSSGWYE----DYFDYWGQGLTVTVSSAS 116
Db 87 FTISRDNKNSLYLQMNLSRAEDTAVVYCARD--GYDSSGVEGFDYWGQGLTVTVSSAS 144
QY 117 TKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 173
Db 145 TKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 201

RESULT 7
US-10-038-591-50
; Sequence 50, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvahan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-50

Query Match      85.4%; Score 778.5; DB 15; Length 473;
Best Local Similarity 86.1%; Pred. No. 8.9e-46;
Matches 155; Conservative 5; Mismatches 13; Indels 7; Gaps 2;
```

QY	1	GGGLVKPGSLRLSCAASGFTSSYMNWVRQAPFGKLEHWVSSISSSSSVITYYADSVKGR	60
Db	27	GGGLVKPGSLRLSCAASGFTSSYMNWVRQAPFGKLEHWVSSISSSSGTITYYADSVKGR	86
QY	61	FTISRDNAKNSLYLQMNSLRRAEDTAVYYCAR---DSSGGWYDYF--DYWGQGTLLVTVYS	113
Db	87	FTISRDNAKNSLYLQMNSLRRAEDTAVYYCARVLFLEWLLYYYYYGMVWGQGTITVTVYS	146
QY	114	SASTKGPSVFPLAPCSRSTSTSTAALGCLVKDYPPEPVTVSMNSGALTSGVHTFPAVLQS	173
Db	147	SASTKGPSVFPLAPCSRSTSTSTAALGCLVKDYPPEPVTVSMNSGALTSGVHTFPAVLQS	206

```

RESULT 8
US-10-128-520-148
; Sequence 148, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-148

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RESULT 9
US-09-972-656-68
; Sequence 68, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-68

Query Match      85.2%; Score 777; DB 10; Length 224;
Best Local Similarity 85.5%; Pred. No. 5.6e-46;

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[illegible]

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RESULT 10
US-10-180-648-2
; Sequence 2, Application US/10180648
; Publication No. US20040033535A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvalan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPG
; FILE REFERENCE: 06843, 0049-00000
; CURRENT APPLICATION NUMBER: US/10/180,648
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/301,172
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-648-2

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RESULT 11
US-10-038-591-45
; Sequence 45, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-Pf2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-45

Query Match      85.1%; Score 776; DB 15; Length 470;
Best Local Similarity 83.7%; Pred. No. 1.3e-45;
Matches 149; Conservative 10; Mismatches 13; Indels 6; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYADSVKGR 60
Db 27 GGGLVQPGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYADSVKGR 86
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYICARDSSGWYEDYF-----DYWGQGLTVTVSSA 115
Db 87 FTISRDNKNSLYLQMSLRAEDTAVYICARDSSGWYEDYF-----DYWGQGLTVTVSSA 145
Qy 116 STKGPSVPEPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
Db 146 STKGPSVPEPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 203

RESULT 12
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6

Query Match      84.5%; Score 770.5; DB 14; Length 444;
Best Local Similarity 86.1%; Pred. No. 3e-45;
Matches 149; Conservative 5; Mismatches 12; Indels 7; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYADSVKGR 60
Db 8 GGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYADSVKGR 67
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYICARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMSLRAEDTAVYICARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
Db 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173

RESULT 13
US-10-704-522-6
; Sequence 6, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baumann, Michael
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and methods for treating cancer using
```

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; TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1414
; CURRENT APPLICATION NUMBER: US/10/704,522
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/429,516
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP 02024881
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-704-522-6

Query Match      84.5%; Score 770.5; DB 16; Length 444;
Best Local Similarity 86.1%; Pred. No. 3e-45;
Matches 149; Conservative 5; Mismatches 12; Indels 7; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYADSVKGR 60
Db 8 GGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYADSVKGR 67
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYICARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMSLRAEDTAVYICARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
Db 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173

RESULT 14
US-10-645-215-6
; Sequence 6, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10/645,215
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-645-215-6

Query Match      84.5%; Score 770.5; DB 16; Length 444;
Best Local Similarity 86.1%; Pred. No. 3e-45;
Matches 149; Conservative 5; Mismatches 12; Indels 7; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYADSVKGR 60
Db 8 GGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSYIYADSVKGR 67
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYICARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
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Db 68 FTISRDNKNSLYLQMNSLRAEDTAVYYCARQG-----LDYWGRTLVTVSSASTKGP 120
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173
Db 121 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173

RESULT 15
US-09-792-656-74
; Sequence 74, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-656-74

Query Match 84.4%; Score 770; DB 10; Length 222;
Best Local Similarity 88.4%; Pred. No. 1.7e-45;
Matches 153; Conservative 4; Mismatches 14; Indels 2; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMWVRQAPGKGLWVSSISSSSVIYYADSVKGR 60
Db 8 GGGLVKPGGSLRLSCAASGFTFSYSNMWVRQAPGKGLWVSSISSSSVIYYADSVKGR 67
Qy 61 FTISRDNKNSLYLQMNSLRAEDTAVYYCARDSSGWYEDYDWGQGTLVTVSSASTKGP 120
Db 68 FTISRDNKNTLYLQMNSLRAEDTAVYCA-DQMGTTISGN-DYWGQGTLVTVSSASTKGP 125
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173
Db 126 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 178
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Search completed: March 8, 2005, 07:05:57  
Job time : 92.8066 secs

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# OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 19.0225 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-37  
Perfect score: 912  
Sequence: 1 GEGLVKPGGSLRLSCAASGP.....SWNSGALTSGVHTPFAVLQS 173

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	798.5	83.6	443	5	PCT-US96-13152-4
2	763	81.7	467	1	US-08-704-744-81
3	753	82.6	451	4	US-09-472-087-70
4	748.5	82.1	463	4	US-09-472-087-4
5	748.5	82.1	463	4	US-09-472-087-68
6	748	82.0	225	4	US-09-456-090A-56
7	748	82.0	225	4	US-09-456-090A-60
8	748	82.0	225	4	US-09-456-090A-92
9	748	82.0	225	4	US-09-453-234-56
10	748	82.0	225	4	US-09-453-234-60
11	748	82.0	225	4	US-09-453-234-92
12	747	81.9	225	4	US-09-456-090A-68
13	747	81.9	225	4	US-09-453-234-68
14	745	81.7	225	4	US-09-456-090A-106
15	745	81.7	225	4	US-09-453-234-106
16	742.5	81.4	463	4	US-09-472-087-1
17	742.5	81.4	463	4	US-09-472-087-63
18	742.5	81.4	463	4	US-09-472-087-64
19	742	81.4	225	4	US-09-456-090A-94
20	742	81.4	225	4	US-09-453-234-94
21	742	81.4	464	4	US-09-472-087-2
22	742	81.4	464	4	US-09-472-087-66
23	741	81.2	225	4	US-09-456-090A-108
24	741	81.2	225	4	US-09-453-234-108
25	738.5	81.0	248	4	US-09-315-926A-80
26	737	80.8	225	4	US-09-456-090A-110
27	737	80.8	225	4	US-09-453-234-110

28 735 80.6 225 4 US-09-456-090A-102 Sequence 102, App  
29 735 80.6 225 4 US-09-453-234-102 Sequence 102, App  
30 734.5 80.5 167 4 US-09-472-087-74 Sequence 74, Appl  
31 734 80.5 470 4 US-09-859-053-32 Sequence 32, Appl  
32 734 80.5 470 4 US-09-859-053-36 Sequence 36, Appl  
33 732.5 80.3 174 4 US-09-472-087-12 Sequence 12, Appl  
34 730 80.0 225 4 US-09-456-090A-70 Sequence 70, Appl  
35 730 80.0 225 4 US-09-453-234-70 Sequence 70, Appl  
36 728.5 79.9 171 4 US-09-472-087-83 Sequence 83, Appl  
37 726.5 79.7 169 4 US-09-472-087-5 Sequence 5, Appl  
38 726.5 79.7 169 4 US-09-472-087-73 Sequence 73, Appl  
39 726 79.6 163 4 US-09-472-087-13 Sequence 13, Appl  
40 726 79.6 163 4 US-09-472-087-84 Sequence 84, Appl  
41 725 79.5 166 4 US-09-472-087-75 Sequence 75, Appl  
42 724 79.4 225 4 US-09-456-090A-100 Sequence 100, App  
43 724 79.4 225 4 US-09-453-234-100 Sequence 100, App  
44 720 78.9 225 4 US-09-456-090A-58 Sequence 58, Appl  
45 720 78.9 225 4 US-09-453-234-58 Sequence 58, Appl

## ALIGNMENTS

RESULT 1  
PCT-US96-13152-4  
; Sequence 4, Application PC/TUS9613152  
; GENERAL INFORMATION:  
; APPLICANT: Martin, Ulrich, et al.  
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Felfe & Lynch  
; ADDRESSEE: Attn: Norman D. Hanson  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Computer Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/13152  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/578,953  
; FILING DATE: 27-Dec-95  
; APPLICATION NUMBER: EP 95 112 895.8  
; FILING DATE: 17-Aug-95  
; APPLICATION NUMBER: EP 95 114 969.9  
; FILING DATE: 19-Sep-95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Norman D. Hanson  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 698-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 443  
; TYPE: amino acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US96-13152-4

Query Match 87.6%; Score 798.5; DB 5; Length 443;  
Best Local Similarity 89.0%; Pred. No. 2.8e-63;  
Matches 154; Conservative 8; Mismatches 6; Indels 5; Gaps 2;

[illegible]

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RESULT 2
US-08-704-744-81
; Sequence 81, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-704-744-81

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[illegible]

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Qy      121  SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 173
      |||||
Db      147  SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 199
      |||||

RESULT 3
US-09-472-087-70
; Sequence 70, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALLAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-70

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		Query Match	82.6%	Score 753;	DB 4;	Length 451;
		Best Local Similarity	83.6%;	Pred. No. 3.2e-59;		
		Matches 148;	Conservative	7;	Mismatches 18;	Indels 4; Gaps 1;
Qy	1	GEGLVKPGGSLRLSCAASGFTFSYSSNNVWQPAPKGLEWVSISLSSSSSYIYYADSVKGR	60			
		:   :	:	:	:	:
Dd	8	GGGVQPGSLRLSCAASGFTFSYGHHWVRPAPKGLEWVAVIWYDGSNKIYADSVKGR	67			
		:   :	:	:	:	:
Qy	61	FTISRDNAKNSLYLQNMSLRAEETAVYYCARDSSG----	116			
		:   :	:	:	:	:
Dd	68	FTISRDNKNLYLQNMSLRAEETAVYYCARDPRGATLYYYYGMVDWGQGTTVTVSAS	127			
		:   :	:	:	:	:
Qy	117	TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNNGALTSGVHTTFAVLQS	173			
		:   :	:	:	:	:
Dd	128	TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNNGALTSGVHTTFAVLQS	184			
		:   :	:	:	:	:

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RESULT 4
US-09-472-087-4
; Sequence 4, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOPFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-472-087-4
Query Match      82.1%; Score 748.5; DB 4; Length 463;
Best Local Similarity 84.4%; Pred. No. 8.4e-59;
Matches 146; Conservative 7; Mismatches 17; Indels 3; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAASGFTFSSYSNMWVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
DB 27 GGGVVEPGRSLRLSCAASGFTFSSYSNMWVRQAPGKGLEWVAVIWDGSKNHYADSAKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120
DB 87 FTISRDNKNSLYLQMNLSRAEDTAVYYCAR---AGLLGYFDYWGQGLTVTVSSASTKGP 143
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
DB 144 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 196

RESULT 5
US-09-472-087-68
; Sequence 68, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOPFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 68
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-68

Query Match      82.1%; Score 748.5; DB 4; Length 463;
Best Local Similarity 84.4%; Pred. No. 8.4e-59;
Matches 146; Conservative 7; Mismatches 17; Indels 3; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAASGFTFSSYSNMWVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
DB 27 GGGVVEPGRSLRLSCAASGFTFSSYSNMWVRQAPGKGLEWVAVIWDGSKNHYADSAKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120
DB 87 FTISRDNKNSLYLQMNLSRAEDTAVYYCAR---AGLLGYFDYWGQGLTVTVSSASTKGP 143
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
DB 144 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 196

RESULT 6
US-09-456-090A-56
; Sequence 56, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
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US-09-456-090A-56
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 56
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: MI-3H
US-09-456-090A-56

Query Match      82.0%; Score 748; DB 4; Length 225;
Best Local Similarity 83.8%; Pred. No. 3.9e-59;
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAASGFTFSSYSNMWVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
DB 8 GGGVVEPGRSLRLSCAASGFTFSSYSNMWVRQAPGKGLEWVTLITYDGDNKYYADSVKGR 67
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120
DB 68 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDGIG---YFDYWGQGLTVTVSSASTKGP 123
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
DB 124 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 176

RESULT 7
US-09-456-090A-60
; Sequence 60, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 60
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: MI-5H
US-09-456-090A-60

Query Match      82.0%; Score 748; DB 4; Length 225;
Best Local Similarity 83.8%; Pred. No. 3.9e-59;
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAASGFTFSSYSNMWVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
DB 8 GGGVVEPGRSLRLSCAASGFTFSSYSNMWVRQAPGKGLEWVTLITYDGDNKYYADSVKGR 67
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120
DB 68 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDGIG---YFDYWGQGLTVTVSSASTKGP 123
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
DB 124 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 176

RESULT 8
US-09-456-090A-92
; Sequence 92, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
```

; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS  
; FILE REFERENCE: 020015-000200US  
; CURRENT APPLICATION NUMBER: US/09/456,090A  
; CURRENT FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 92  
; LENGTH: 225  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M2-11H  
US-09-456-090A-92

Query Match 82.0%; Score 748; DB 4; Length 225;  
Best Local Similarity 83.8%; Pred. No. 3.9e-59;  
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;  
  
Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSGMWVRQAPGKGLWVSSISSSSIYYADSVKGR 60  
Db 8 GGGVQVQPSRLSLCAASGFTFSYGHMWVRQAPGKGLWVTLITYDGNKYADSVKGR 67  
  
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120  
Db 68 FTISRDNKNTLYLQMSLRAEDTAVYYCARDGIG----YFDYWGQGLTVTVSSASTKGP 123  
  
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173  
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 176

RESULT 9  
US-09-453-234-56  
; Sequence 56, Application US/09453234  
; Patent No. 6794132  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 56  
; LENGTH: 225  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-3H  
US-09-453-234-56

Query Match 82.0%; Score 748; DB 4; Length 225;  
Best Local Similarity 83.8%; Pred. No. 3.9e-59;  
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;  
  
Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSGMWVRQAPGKGLWVSSISSSSIYYADSVKGR 60  
Db 8 GGGVQVQPSRLSLCAASGFTFSYGHMWVRQAPGKGLWVTLITYDGNKYADSVKGR 67  
  
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120  
Db 68 FTISRDNKNTLYLQMSLRAEDTAVYYCARDGIG----YFDYWGQGLTVTVSSASTKGP 123  
  
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173  
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 176

Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 176  
  
RESULT 10  
US-09-453-234-60  
; Sequence 60, Application US/09453234  
; Patent No. 6794132  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 60  
; LENGTH: 225  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-5H  
US-09-453-234-60

Query Match 82.0%; Score 748; DB 4; Length 225;  
Best Local Similarity 83.8%; Pred. No. 3.9e-59;  
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;  
  
Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSGMWVRQAPGKGLWVSSISSSSIYYADSVKGR 60  
Db 8 GGGVQVQPSRLSLCAASGFTFSYGHMWVRQAPGKGLWVTLITYDGNKYADSVKGR 67  
  
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120  
Db 68 FTISRDNKNTLYLQMSLRAEDTAVYYCARDGIG----YFDYWGQGLTVTVSSASTKGP 123  
  
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173  
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 176

RESULT 11  
US-09-453-234-92  
; Sequence 92, Application US/09453234  
; Patent No. 6794132  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: GenPharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01  
; PRIOR FILING DATE: 1999-10-02  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 92  
; LENGTH: 225  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M2-11H  
US-09-453-234-92

Query Match 82.0%; Score 748; DB 4; Length 225;







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 7.17801 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-38

Perfect score: 522

Sequence: 1 LDQLTQSPSSLSASVGRV.....EDFATYYCQVNSYPFTFGP 101

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: Pirl.\*

2: Pirl2.\*

3: Pirl3.\*

4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	90.6	129	2 S40369	Ig kappa chain - h
2	466	89.3	107	2 I69017	anti-HIV1 envelope
3	466	89.3	117	2 C21056	Ig kappa chain pre
4	459	87.9	108	1 K1HUN	Ig kappa chain V-I
5	454	87.0	125	2 S40333	Ig kappa chain V-J
6	454	87.0	132	2 S40334	Ig kappa chain - h
7	453	86.8	107	2 S36264	Ig lambda chain V
8	451.5	86.5	107	2 S47183	Ig kappa chain - h
9	451	86.4	117	2 B21056	Ig kappa chain pre
10	451	86.4	117	2 S46376	Ig kappa chain V-J
11	446	85.4	117	1 K1HUI1	Ig kappa chain pre
12	446	85.4	125	2 S40349	Ig kappa chain V-J
13	444	85.1	108	2 B49047	Ig kappa chain V r
14	441	84.5	108	2 S19674	Ig kappa chain V r
15	441	84.5	123	2 S40331	Ig kappa chain - h
16	439.5	84.2	124	2 S40336	Ig kappa chain V-J
17	439	84.1	117	2 S46371	Ig kappa chain V-J
18	437	83.7	95	2 PH0866	Ig kappa chain pre
19	437	83.7	117	2 S21527	Ig kappa chain pre
20	437	83.7	127	2 S40367	Ig kappa chain V-J
21	436.5	83.6	108	2 S34007	Ig kappa chain V r
22	436.5	83.6	108	2 S30521	Ig kappa chain V r
23	436	83.5	131	2 S40352	Ig kappa chain V-J
24	434	83.1	128	2 S46372	Ig light chain var
25	433.5	83.0	107	1 K1HUR	Ig kappa chain V-I
26	433	83.0	108	2 S36277	Ig lambda chain V
27	433	83.0	125	2 S40353	Ig kappa chain V-J
28	433	83.0	127	2 S11240	Ig kappa chain V r
29	431	82.6	124	2 S40318	Ig kappa chain V r

RESULT 1  
S40369  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40369  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40369  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-129 <KLE>  
A:Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 473; DB 2; Length 129;  
Best Local Similarity 91.9%; Pred. No. 4.2e-34;  
Matches 91; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOQPKAPKSLIYAASSLSQGVPS 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 22 DIQWTQSPSSLSASVGRVITTCRAHVISHNLVWFQPKAPKSLIYAASSLSQGVPS 81  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Qy 62 KFSGSGSGTDTLTITISSLOPEDFATYYCQVNSYPFTFG 100  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 82 KFSGSGSGTDTLTITISSLOPEDFATYYCQVNSYPFTFG 120  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2  
I69017  
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (fr  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jan-2000  
C:Accession: I69017  
R:Chin, L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.  
Immunol. Lett. 44, 25-30, 1995  
A:Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a  
A:Reference number: I54563; MUID:95237884; PMID:7721339  
A:Accession: I69017  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-107 <RES>  
A:Cross-references: GB:S77140; NID:g913352; PIDN:AA834102.1; PID:g913353  
C:Genetics:  
A:Gene: Ig V kappa  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

ALIGNMENTS

Query Match 89.3%; Score 466; DB 2; Length 107;  
Best Local Similarity 89.9%; Pred. No. 1.4e-33;  
Matches 89; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 DIQLTQSPSSLASVGDVRVTITCRASQDISIYLAWFQORPGKAPKSLIYAASSLQSGVPS 61  
DB 1 DIQVTSFSSLASVGDVRVTITCRASHDIGSYLAWFQQEPAKESLIYAASSLQSGVPS 60  
QY 62 KFGSGSGDFTLTITSSLQPEDFATYYCCQNSYPFTFG 100  
DB 61 RFSGSGSGDFTLTITSSLQPEDFATYYCCQNSYPFTFG 99

RESULT 3  
C21056  
IG kappa chain precursor V region (HK137) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 21-Jan-2000  
C/Accession: C21056  
R/Bentley, D.L.; Rabbitts, T.H.  
Cell 32, 181-189, 1983  
A/Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated  
A/Reference number: A21056; MUID:83129397; PMID:6402305  
A/Accession: C21056  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-117 <BEN>  
A/Cross-references: GB:J00248; NID:G185991; PIDN:AAA59094.1; PID:G185992  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 466; DB 2; Length 117;  
Best Local Similarity 94.7%; Pred. No. 1.5e-33;  
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DIQLTQSPSSLASVGDVRVTITCRASQDISIYLAWFQORPGKAPKSLIYAASSLQSGVPS 61  
DB 23 DIQVTSFSSLASVGDVRVTITCRASQGISNYLAWFQORPGKAPKSLIYAASSLQSGVPS 82  
QY 62 KFGSGSGDFTLTITSSLQPEDFATYYCCQNSYP 96  
DB 83 RFSGSGSGDFTLTITSSLQPEDFATYYCCQNSYP 117

RESULT 4  
KI00EN  
IG kappa chain V-I region (Ban) - human  
C/Species: Homo sapiens (man)  
C/Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
C/Accession: A01878  
R/Dwulet, P.E.; O'Connor, T.P.; Benson, M.D.  
Mol. Immunol. 23, 73-78, 1986  
A/Title: Polymorphism in a kappa I primary (AL) amyloid protein (BAN).  
A/Reference number: A01878; MUID:86174817; PMID:3083240  
A/Accession: A01878  
A/Molecule type: protein  
A/Residues: 1-108 <DWU>  
A/Cross-references: UNIPROT:P04430  
C/Genetics:  
A/Genes: GDB:IGKV1  
A/Cross-references: GDB:136264  
A/Map position: 2p12-2p12  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: amyloid; heterotetramer; immunoglobulin  
F/1-23/Region: framework 1  
F/16-90/Domain: immunoglobulin homology <IMM>  
F/24-34/Region: complementarity-determining 1  
F/35-49/Region: framework 2  
F/50-56/Region: complementarity-determining 2  
F/57-88/Region: framework 3

F;89-97/Region: complementarity-determining 3  
F;98-107/Region: framework 4  
F;23-88/Distulfide bonds: #status predicted

Query Match 87.9%; Score 459; DB 1; Length 108;  
Best Local Similarity 87.9%; Pred.No.5.7e-33;  
Matches 87; Conservative 6; Mismatches 0; Gaps 0;

Qy 2 DIQLTQSPSLASVGRVTITCRASQDISIYLAWFQORPGKAPKSLIIYAASSLSQSGVPS 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 DIQLTQSPSLASVGRVTITCRASQSVYNYAVWFQKPKAPKSLIIDASTLQSGVPS 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 KFGSGSGTGDTFTTISLQPDEDPATYYCCQYNYPPTFG 100  
|||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 61 NFTGSGSGTDFTLTSSLPQDEPATYYCCQYNYPPTFG 99  
|||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5  
S40334  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40333  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40333  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-125 <KLE>  
A:Cross-references: EMBL:X72443; NID:g441354; PIDN:CAAS1111.1; PID:g441355  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 454; DB 2; Length 125;  
Best Local Similarity 85.9%; Pred.No.1.8e-32;  
Matches 85; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSLASVGRVTITCRASQDISIYLAWFQORPGKAPKSLIIYAASSLSQSGVPS 61  
|||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 19 DIQWTQSPSLASVGRVTITCRASQSISWLAIFYQQKFKAPKLLIKASSLESQGVPS 78  
|||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 KFGSGSGTGDTFTTISLQPDEDPATYYCCQYNYPPTFG 100  
|||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 79 RFSGSGSGTGDTFTTISLQPDDPATYYCCQYNYPPTFG 117  
|||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6  
S40334  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40334  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891; PMID:8258341  
A:Accession: S40334  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-132 <KLE>  
A:Cross-references: EMBL:X72444  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 454; DB 2; Length 132;  
Best Local Similarity 85.9%; Pred.No.1.9e-32;  
Matches 85; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSLASVGRVTITCRASQDISIYLAWFQORPGKAPKSLIIYAASSLSQSGVPS 61

```
Db      22 DIQTQSPFLSASIGDRVITTCRASQINSYLAWYQKPGKAPKLLIYVASTLSQGVPS 81
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 100
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      82 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36264
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36264
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID:g939919
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

      Query Match      86.8%; Score 453; DB 2; Length 107;
      Best Local Similarity 87.9%; Pred. No. 1.9e-32;
      Matches 87; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy      2 DIQTQSPSSLSASVGRVITTCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQGVPS 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EIVLTQSPSSLSASVGRVITTCRASQISSYLNWYQKPGKAPKLLIYAASSLSQGVPS 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 100
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 99
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
S47183
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47183
R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
A:Reference number: S47181
A:Accession: S47183
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <MCI>
A:Cross-references: EMBL:X79785; NID:g506424; PIDN:CAA56181.1; PID:g506425
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

      Query Match      86.5%; Score 451.5; DB 2; Length 107;
      Best Local Similarity 89.9%; Pred. No. 2.5e-32;
      Matches 89; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy      2 DIQTQSPSSLSASVGRVITTCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQGVPS 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 ETELQSPSSLSASVGRVITTCRASRGISYLAWFQKPGKAPKSLIYAASSLSQGVPS 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 100
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYP-QFG 98
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
```

```
B21056
Ig kappa chain precursor V region (HK134) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000
C:Accession: B21056
R:Bentley, D.L.; Rabbitts, T.H.
Cell 32, 181-189, 1983
A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicate
A:Reference number: A21056; MUID:83129397; PMID:6402305
A:Accession: B21056
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <BEN>
A:Cross-references: GB:K01323; NID:g185995; PIDN:AAAS8931.1; PID:g185996
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

      Query Match      86.4%; Score 451; DB 2; Length 117;
      Best Local Similarity 91.6%; Pred. No. 3e-32;
      Matches 87; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      2 DIQTQSPSSLSASVGRVITTCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQGVPS 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      23 DIQTQSPSSLSASVGRVITTCRASQGISSLAWYQKPEKAPKSLIYAASSLSQGVPS 82
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYP 96
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      83 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSYP 117
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
S46376
Ig kappa chain V-J region (T33-14) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46376; S38649
R:Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rear
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46376
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-references: EMBL:Z27177; NID:g415969; PIDN:CAA81701.1; PID:g415970
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-99/Domain: immunoglobulin homology <IMM>

      Query Match      86.4%; Score 451; DB 2; Length 117;
      Best Local Similarity 86.0%; Pred. No. 3e-32;
      Matches 86; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy      2 DIQTQSPSSLSASVGRVITTCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQGVPS 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      10 DIQTQSPSSVSASIGDRVITTCRASQISLWAWYQKPGKAPKLLIYAASSLSQGVPL 69
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 101
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      70 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSFPFG 109
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
K1HUI1
Ig kappa chain precursor V-1 region (HK101) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 09-Jul-2004
C:Accession: A01881; A21056
R:Bentley, D.L.; Rabbitts, T.H.
Nature 288, 730-733, 1980
A:Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa genes
A:Reference number: A93241; MUID:81098966; PMID:6779204
A:Accession: A01881
```

A;Molecule type: DNA  
A;Residues: 1-117 <BN2>  
A;Cross-references: UNIPROT:P01601; GB:V00558; GB:J00244; GB:J00246; NID:g33176; PIDN:CA  
A;Note: the sequence was determined from the germline gene  
R;Bentley, D.L.; Rabbitts, T.H.  
Cell 32, 181-189, 1983  
A;Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated  
A;Reference number: A21056; MUID:83129397; PMID:6402305  
A;Accession: A21056  
A;Molecule type: DNA  
A;Residues: 1-117 <BN2>  
A;Cross-references: GB:K01322; NID:g185993; PIDN:AAA58930.1; PID:g185994  
C;Genetics:  
A;Gene: GDB:IGKV1  
A;Cross-references: GDB:136264  
A;Map position: 2p12-2p12  
A;Introns: 19/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-117/Product: Ig kappa chain V-I region (HK101) #status predicted <MAT>  
F;38-112/Domain: immunoglobulin homology <IMM>  
F;45-110/Disulfide bonds: #status predicted

Query Match 85.4%; Score 446; DB 1; Length 117;  
Best Local Similarity 90.5%; Pred. No. 8.2e-32; Indels 0; Gaps 0;  
Matches 86; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQQTSPSSLSASVGRVVTITCRASQDISIYLAWFOQRPGKAPKSLIYAASSLSQGVPS 61  
Db 23 DIQQTSPSSLSASVGRVVTITCRASQDISIYLAWFOQRPGKAPKSLIYAASSLSQGVPS 82

Qy 62 KFSGSGGTDFTLTISSLPQEDFATYCCQYNSYP 96  
Db 83 RFGSGSGGTDFTLTISSLPQEDFATYCCQYNSYP 117

RESULT 12  
S40349  
Ig kappa chain V-J region - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C;Accession: S40349  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40349  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-125 <KLE>  
A;Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 85.4%; Score 446; DB 2; Length 125;  
Best Local Similarity 87.8%; Pred. No. 8.7e-32; Indels 0; Gaps 0;  
Matches 86; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 3 IQLTQSPSSLSASVGRVVTITCRASQDISIYLAWFOQRPGKAPKSLIYAASSLSQGVPSK 62  
Db 19 IQLTQSPSSLSASVGRVVTITCRASQDISIYLAWFOQRPGKAPKSLIYAASSLSQGVPSR 78

Qy 63 FSGSGSGGTDFTLTISSLPQEDFATYCCQYNSYPFTFG 100  
Db 79 FSGSGSGGTDFTLTISSLPQEDFATYCCQYNSYPFTFG 116

RESULT 13  
B49047

Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: B49047  
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.  
Eur. J. Immunol. 22, 2231-2236, 1992  
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes (C12.1).  
A;Reference number: A49047; MUID:92387224; PMID:1516616  
A;Accession: B49047  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-108 <VIC>  
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77  
A;Experimental source: thymic B lymphocytes  
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 444; DB 2; Length 108;  
Best Local Similarity 87.9%; Pred. No. 1.1e-31; Indels 0; Gaps 0;  
Matches 87; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 DIQQTSPSSLSASVGRVVTITCRASQDISIYLAWFOQRPGKAPKSLIYAASSLSQGVPS 61  
Db 1 DIQQTSPSSLSASVGRVVTITCRASQDISIYLAWFOQRPGKAPKSLIYAASSLSQGVPS 60

Qy 62 KFSGSGGTDFTLTISSLPQEDFATYCCQYNSYPFTFG 100  
Db 61 RFGSGSGGTDFTLTISSLPQEDFATYCCQYNSYPFTFG 99

RESULT 14  
S19674  
Ig kappa chain V region (clone alpha-TEL9) - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C;Accession: S19674  
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991  
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage lambda particles.  
A;Reference number: S19663; MUID:92085276; PMID:1748994  
A;Accession: S19674  
A;Molecule type: mRNA  
A;Residues: 1-108 <MAR>  
A;Cross-references: EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID:g1335386  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 441; DB 2; Length 108;  
Best Local Similarity 85.9%; Pred. No. 2e-31; Indels 0; Gaps 0;  
Matches 85; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 2 DIQQTSPSSLSASVGRVVTITCRASQDISIYLAWFOQRPGKAPKSLIYAASSLSQGVPS 61  
Db 1 EIVLTQSPSSLSASVGRVVTITCRASQDISIYLAWFOQRPGKAPKSLIYAASSLSQGVPS 60

Qy 62 KFSGSGGTDFTLTISSLPQEDFATYCCQYNSYPFTFG 100  
Db 61 RFGSGSGGTDFTLTISSLPQEDFATYCCQYNSYPFTFG 99

RESULT 15  
S40331  
Ig kappa chain - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40331  
R;Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891; PMID:8258341  
A;Accession: S40331

A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-123 <KLE>  
A;Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;32-106/Domain: immunoglobulin homology <IMM>  
  
Query Match 84.5%; Score 441; DB 2; Length 123;  
Best Local Similarity 87.9%; Pred. No. 2.3e-31;  
Matches 87; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 2 DIQLTQSPSSLASVSGDRVTITCRASODISYLAWFQORBCAPKSLIYAASSLQSGVPS 61  
Db 17 DIQMTQSPSSLASVSGDRVTITCRASQSSISYLNWYQQKPKAPKLIYAASSLQSGVPS 76  
  
Qy 62 KFGSGSGTDFTLTITSLQPEDFATYYCQQVNSYPFTFG 100  
Db 77 RFGSGSGTDFTLTITSLQPEDFATYYCQQSYSTPRTFG 115

Search completed: March 8, 2005, 06:39:30  
Job time : 7.22801 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 37.7184 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-38

Perfect score: 522

Sequence: 1 LDQLTQSPSLASVGDV.....EDFATYCCQNSVPTFGP 101

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_crembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	468	89.7	236	2	Q7Z3Y4	Q7Z3Y4	homo sapien
2	462	88.5	236	2	Q6GMX8	Q6GMX8	homo sapien
3	459	87.9	108	1	KV1V_HUMAN	P04430	homo sapien
4	457	87.5	108	2	Q9UL70	Q9UL70	homo sapien
5	452	86.6	236	2	Q6GMX9	Q6GMX9	homo sapien
6	446	85.4	117	1	KV1I_HUMAN	P01601	homo sapien
7	438	83.9	236	2	Q6PIH7	Q6PIH7	homo sapien
8	433.5	83.0	107	1	KVID_HUMAN	P01596	homo sapien
9	432	82.8	108	2	Q9UL77	Q9UL77	homo sapien
10	430	82.4	244	2	Q65ZC8	Q65ZC8	homo sapien
11	429	82.2	108	1	KV1Y_HUMAN	P80362	homo sapien
12	428	82.0	117	1	KV1J_HUMAN	P01602	homo sapien
13	427.5	81.9	107	2	Q66SA9	Q66SA9	homo sapien
14	427	81.8	108	1	KVIO_HUMAN	P01607	homo sapien
15	427	81.6	236	2	Q6GMW1	Q6GMW1	homo sapien
16	426	81.6	108	1	KV1S_HUMAN	P01611	homo sapien
17	425	81.4	108	1	KV1H_HUMAN	P01600	homo sapien
18	425	81.4	108	1	KV1P_HUMAN	P01608	homo sapien
19	422	80.8	240	2	Q65ZC9	Q65ZC9	homo sapien
20	421	80.7	108	1	KVIL_HUMAN	P01604	homo sapien
21	421	80.7	108	1	KV1L_HUMAN	P01610	homo sapien
22	420	80.5	236	2	Q6GMX0	Q6GMX0	homo sapien
23	419	80.3	108	1	KVIE_HUMAN	P01597	homo sapien
24	419	80.3	108	1	KVIG_HUMAN	P01599	homo sapien
25	417	79.9	129	1	KV1W_HUMAN	P04431	homo sapien
26	416.5	79.8	107	2	Q9UL81	Q9UL81	homo sapien
27	415	79.5	108	1	KV1B_HUMAN	P01594	homo sapien
28	415	79.5	108	1	KV1F_HUMAN	P01598	homo sapien
29	415	79.5	236	2	Q6PIT5	Q6PIT5	homo sapien
30	414	79.3	234	2	Q7Z473	Q7Z473	homo sapien
31	413	79.1	108	2	Q9UL79	Q9UL79	homo sapien

32	412	78.9	108	1	KV1M_HUMAN	P01605	homo sapien
33	406	77.8	108	1	KV1Q_HUMAN	P01609	homo sapien
34	403	77.2	129	1	KV1X_HUMAN	P04432	homo sapien
35	402	77.0	108	1	KV1A_HUMAN	P01593	homo sapien
36	402	77.0	108	1	KV1N_HUMAN	P01606	homo sapien
37	400	76.6	108	1	KV1K_HUMAN	P01603	homo sapien
38	399	76.4	116	2	Q96PF6	Q96PF6	homo sapien
39	396	75.9	236	2	Q6PIH4	Q6PIH4	homo sapien
40	395	75.7	108	1	KVIC_HUMAN	P01595	homo sapien
41	379.5	72.7	109	1	KV1T_HUMAN	P01612	homo sapien
42	372	71.3	108	2	Q9UL83	Q9UL83	homo sapien
43	372	71.3	112	1	KV1U_HUMAN	P01613	homo sapien
44	368	70.5	236	2	Q7TS98	Q7TS98	mus musculus
45	367	70.3	128	1	KV5E_MOUSE	P01637	mus musculus

#### ALIGNMENTS

RESULT 1  
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.  
AC Q7Z3Y4;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal Muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal Muscle;  
RA Strausberg R.;  
DR Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
EMBL: BC005332; AA05332.1; -.  
HSSP: P01834; 1HEZ.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003597; Ig cl.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF07654; Cl-set; 1.  
DR SMART: SM00406; Igv; 1.  
DR PROSITE: PS50835; IG\_LIKE; 2.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein\_  
SQ SEQUENCE 236 AA; 25702 MW; 7FBF4ED23084BC6 CRC64;

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Query Match      89.7%; Score 468; DB 2; Length 236;
Best Local Similarity 91.9%; Pred. No. 1.3e-40;
Matches 91; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRGKAPKSLIYAASSLSQGVPS 61
Db 23 DIQMTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRGKAPKSLIYAASSLSQGVPS 82

Qy 62 KFGSGSGTDTLTITISLQPEDPATYCCQYNSYPPTFG 100
Db 83 RFSGSGSGTDTLTITISLQPEDPATYCCQYNSYPPTFG 122

RESULT 2
Q6GMX8 ID Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC Q6GMX8,2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=4238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003596; Ig_MHC.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGL1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match      88.5%; Score 462; DB 2; Length 236;
Best Local Similarity 88.0%; Pred. No. 5.5e-40;
Matches 88; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRGKAPKSLIYAASSLSQGVPS 61
Db 23 DIQMTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRGKAPKSLIYAASSLSQGVPS 82

Qy 62 KFGSGSGTDTLTITISLQPEDPATYCCQYNSYPPTFG 100
Db 83 RFSGSGSGTDTLTITISLQPEDPATYCCQYNSYPPTFG 122

RESULT 3
KVIV HUMAN ID KVIV HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUEN.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match      87.9%; Score 459; DB 1; Length 108;
Best Local Similarity 87.9%; Pred. No. 4.7e-40;
Matches 87; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRGKAPKSLIYAASSLSQGVPS 61
Db 1 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRGKAPKSLIYAASSLSQGVPS 60

Qy 62 KFGSGSGTDTLTITISLQPEDPATYCCQYNSYPPTFG 100
Db 61 NFTGSGSGTDTLTITISLQPEDPATYCCQYNSYPPTFG 99

RESULT 4
Q9UL70 ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSP; P01607; LBWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON TER 1
FT NON TER 108
FT NON TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCA37 CRC64;

Query Match 87.5%; Score 457; DB 2; Length 108;
Best Local Similarity 88.0%; Pred. No. 7.6e-40;
Matches 88; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DIQQTQSPSSLSASVGRVTITCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQGVPS 61
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISNYLAWYQKPGKPKSLIYAASSLSQGVPS 60
Qy 62 KFGSGSGTDFTLTISLQPEDFATYCCQNSYPFTFG 101
Db 61 RFGSGSGTDFTLTISLQPEDVATYCCQNSAPRTFG 100

RESULT 5
ID Q6GMX9 PRELIMINARY; PRT; 236 AA.
AC Q6GMX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villaon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
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RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF7 CRC64;

Query Match 86.6%; Score 452; DB 2; Length 236;
Best Local Similarity 86.9%; Pred. No. 6e-39;
Matches 86; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DIQQTQSPSSLSASVGRVTITCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQGVPS 61
Db 23 DIQMTQSPSSLSASVGRVTITCRASQNSRWLAWYQQRPEKAPKSLIYATSSLHSGVPS 82
Qy 62 KFGSGSGTDFTLTISLQPEDFATYCCQNSYPFTFG 100
Db 83 RFGSGSGTDFTLTISLQPEDFATYCCQNTYPLTFG 121

RESULT 6
KVII HUMAN STANDARD; PRT; 117 AA.
ID P01601;
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HKI01 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RT kappa genes and a pseudogene.";
RL Nature 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305; DOI=10.1016/0092-8674(83)90508-1;
RA Bentley D.L., Rabbitts T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
RT recently duplicated human V kappa sequences have diverged by gene
RT conversion.";
RL Cell 32:181-189(1983).
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CC -----
DR EMBL; K01322; AAA58930.1; -.
DR EMBL; K01324; AAA58932.1; -.
DR EMBL; V00558; CAA23824.1; -.
DR PIR; A01881; KIHU11.
DR HSP; P01607; LBWW.
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```
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 >117 Ig kappa chain V-I region HK101.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 >117 Complementarity-determining-3.
FT DISULFID 45 110 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12799 MW; D7D0FF3718CEF587 CRC64;

Query Match 85.4%; Score 446; DB 1; Length 117;
Best Local Similarity 90.5%; Pred. No. 1.2e-38;
Matches 86; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
DB 23 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 82

QY 62 KFGSGSGTDFTLTISLSQPEDFATYCCQYNVSY 96
DB 83 RFGSGSGTDFTLTISLSQPEDFATYCCQYNVSY 117

RESULT 7
ID Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan T., Moore T., Max S.I., Wang J., Haieff F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozney K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
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RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; IAR2
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-set; 1.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGC1; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 83.9%; Score 438; DB 2; Length 236;
Best Local Similarity 86.9%; Pred. No. 1.7e-37;
Matches 86; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
DB 23 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 82

QY 62 KFGSGSGTDFTLTISLSQPEDFATYCCQYNVSYPTFG 100
DB 83 RFGSGSGTDFTLTISLSQPEDFATYCCQYNVSYPTFG 121

RESULT 8
KVLD_HUMAN STANDARD; PRT; 107 AA.
ID KVLD_HUMAN
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region CAR.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma
RT protein."
RL Eur. J. Biochem. 49:377-391(1974).
RC -I- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR HSSP; P80362; IWL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin V region.
FT CARBOHYD 28 107 N-linked (GlcNAc... ).
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Query Match 83.0%; Score 433.5; DB 1; Length 107;
Best Local Similarity 81.0%; Pred. No. 2.1e-37;
Matches 81; Conservative 14; Mismatches 4; Indels 1; Gaps 1;

QY 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
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Db 1 DIQWTQSPSTLSASVGRVAVITCRASQNISSWLAWYQKPKAPKVLIIYKSSSLESQVPS 60
Qy 62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 101
Db 61 RFGSGSGTDTFTLTISLQPEDFATYYCQQNTF-FTFGP 99

RESULT 9
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; AAD56273.1; -.
DR PIR: B49047; B49047.
DR PIR: S34083; S34083.
DR HSSP: P01607; 1BWW.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 82.8%; Score 432; DB 2; Length 108;
Best Local Similarity 85.9%; Pred. No. 3.1e-37;
Matches 85; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 2 DIQWTQSPSTLSASVGRVAVITCRASQNISSWLAWYQKPKAPKVLIIYKSSSLESQVPS 61
Db 1 DIQWTQSPSTLSASVGRVAVITCRASQNISSWLAWYQKPKAPKVLIIYKSSSLESQVPS 60

Qy 62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 100
Db 61 RFGSGSGTDTFTLTISLQPEDFATYYCQQSYSTWTFG 99

RESULT 10
Q65ZC8 PRELIMINARY; PRT; 244 AA.
AC Q65ZC8
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.S., Ming M.G., Winter G.;
RA "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
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DR EMBL: Y13057; CAA73500.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 244
FT NON_TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 82.4%; Score 430; DB 2; Length 244;
Best Local Similarity 80.8%; Pred. No. 1.2e-36;
Matches 80; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy 2 DIQWTQSPSTLSASVGRVAVITCRASQNISSWLAWYQKPKAPKVLIIYKSSSLESQVPS 61
Db 137 DIQWTQSPSTLSASVGRVAVITCRASQNISSWLAWYQKPKAPKVLIIYKSSSLESQVPS 196

Qy 62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 100
Db 197 RFGSGSGTDTFTLTISLQPEDFATYYCQQSYNPLTFG 235

RESULT 11
KVLY HUMAN STANDARD; PRT; 108 AA.
ID KVLY HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers."
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human kappa Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB: 1WTL; X-ray; A/B=1-108.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DOMAIN 108 107
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FT DISULFID 23 88 By similarity.
FT CONFLICT 30 31 TN -> SD (in Ref. 2).
FT STRAND 4 7
FT TURN 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT STRAND 60 61
FT TURN 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 98 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 82.2%; Score 429; DB 1; Length 108;
Best Local Similarity 81.8%; Pred. No. 6.3e-37;
Matches 81; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRGKAPKSLIYAASLSQGVPS 61
Db 1 DIQMTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRGKAPKSLIYGASILETGVPS 60

Qy 62 KFGSGSGTDFTLTISSLPQDEPATYCCQVNSYPTFG 100
Db 61 RFSGSGSGTDFTLTISSLPQDEPATYCCQVNTLPLTFG 99

RESULT 12
KV1IJ HUMAN
ID "KV1IJ_HUMAN STANDARD; PRT; 117 AA.
AC P01602;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region HK102 precursor (Fragment).
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
kappa genes and a pseudogene.";
RL Nature 288:730-733(1980).
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CC -----
DR EMBL; J00245; AAA59087.1; -.
DR EMBL; Z00001; CAA77292.1; -.
DR PIR; A01882; KIHUL2.
DR HSP; P01607; LEWV.
DR Genew; HGNC:5741; IGKV1-5.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
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DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 >117 Ig kappa chain V-I region HK102.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 >117 Complementarity-determining-3.
FT DISULFID 45 110 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12768 MW; AD1DF3A40AF1A9B CRC64;

Query Match 82.0%; Score 428; DB 1; Length 117;
Best Local Similarity 86.2%; Pred. No. 8.8e-37;
Matches 81; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRGKAPKSLIYAASLSQGVPS 61
Db 23 DIQMTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRGKAPKSLIYDASSILESGVPS 82

Qy 62 KFGSGSGTDFTLTISSLPQDEPATYCCQVNSY 95
Db 83 RFSGSGSGTDFTLTISSLPQDEPATYCCQVNSY 116

RESULT 13
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain
DE variable region (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin
antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S1977; S1977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSP; P01607; LEWV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON TER 1 1
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 81.9%; Score 427.5; DB 2; Length 107;
Best Local Similarity 87.0%; Pred. No. 8.9e-37;
Matches 87; Conservative 4; Mismatches 6; Indels 3; Gaps 2;
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QY 2 DIOLTPSSLSASVGDVRVTITCRASODISYILAWFOORPKAPKSLIYAASSLSQGVPS 61
Db 1 DIQMTQSPSSLSASVGDVRVTITCRASODISYILAWFOORPKAPKSLIYAASSLSQGVPS 60
QY 62 KFGSGSGTDTFTLTISLQPEDFATYYCQVNSY-PFTFG 100
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 RFSGSGSGTDTFTLTISLQPEDFATYYCQVNSY-PFTFG 98
[2]

RESULT 14
KV10 HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA EDP O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rei refined at 2.0-A resolution."
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; 1AR2; X-ray; @=1-107.
DR PDB; 1BWW; X-ray; A/B=1-107.
DR PDB; 1REI; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; Ig_v; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW 3D-structure, Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 33 38
FT STRAND 40 41
FT STRAND 45 49
FT STRAND 50 52
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FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 81.8%; Score 427; DB 1; Length 108;
Best Local Similarity 81.8%; Pred. No. 1e-36;
Matches 81; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 DIOLTPSSLSASVGDVRVTITCRASODISYILAWFOORPKAPKSLIYAASSLSQGVPS 61
Db 1 DIQMTQSPSSLSASVGDVRVTITCRASODISYILAWFOORPKAPKSLIYAASSLSQGVPS 60
QY 62 KFGSGSGTDTFTLTISLQPEDFATYYCQVNSY-PFTFG 100
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 RFSGSGSGTDTFTLTISLQPEDFATYYCQVNSY-PFTFG 99

RESULT 15
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC O6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
```

DR Pfam; PF07654; Cl-set; 1.  
DR Pfam; PF00047; ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25751 MW; 5BF6GA087AFAC437 CRC64;

Query Match 81.8%; Score 427; DB 2; Length 236;  
Best Local Similarity 85.7%; Pred. No. 2.4e-36;  
Matches 84; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 3 IQLTQSPSSLSASVGDRVTITCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQSGVPSK 62  
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 24 IQLTQSPSSLSASVGDRVTITCRASQGISNDLGLWYQKPGKAPKLLIYAASSLSQSGVPSR 83  
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 63 FSGSGSGTDFTLTISSLPQEDFATYYCQYNSYPFTFG 100  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 84 FSGSGSGTDFTLTISSLPQEDFATYYCLQDYNYPWTFG 121  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: March 8, 2005, 06:35:56  
Job time : 38.7184 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 46.8263 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-38  
Perfect score: 522  
Sequence: 1.LDQLTQSPSLASVGDV.....EDFATYYCQQNSVPTFGP 101

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_16Dec04.\*  
1: Geneseq\_1980s.\*  
2: Geneseq\_1990s.\*  
3: Geneseq\_2000s.\*  
4: Geneseq\_2001s.\*  
5: Geneseq\_2002s.\*  
6: Geneseq\_2003as.\*  
7: Geneseq\_2003bs.\*  
8: Geneseq\_2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	522	100.0	101	2	AAY34316 Igg antib
2	515	98.7	164	2	AAY34317 Igg antib
3	482	92.3	127	6	AEE37206 Human AB-
4	479	91.8	127	6	AEE37204 Human AB-
5	476	91.2	224	4	AAB75040 TRO005 Hu
6	474	90.8	107	4	AAB82890 Anti-huma
7	473	90.6	241	5	AAB90948 Insulin/i
8	471	90.2	107	4	AAB72880 Human ant
9	471	90.2	107	8	ADO36490 Human ant
10	471	90.2	107	8	ADO36502 Human ant
11	471	90.2	107	8	ADO36494 Human ant
12	471	90.2	108	1	AAP81246 Anti-pneu
13	471	90.2	111	1	AAP81870 Anti-pneu
14	468	89.7	109	2	AAR40956 Human ger
15	466	89.3	95	6	ABO27128 Human ger
16	466	89.3	95	7	ADF10068 VEGF anti
17	466	89.3	95	7	ADF10170 Antibody
18	466	89.3	95	7	ADF09963 Antibody
19	466	89.3	95	7	ADJ80248 V kappa ge
20	466	89.3	95	8	ADO07317 Human ant
21	466	89.3	107	4	AAB72882 Human ant
22	466	89.3	107	6	ABR54919 Light cha
23	466	89.3	109	2	AAR47041 Sequence
24	465	89.1	107	4	AAB62087 Human V1
25	465	89.1	107	4	AAB60400 Consensus

26	465	89.1	107	4	AAB61585 Human var
27	465	89.1	107	8	ADE71454 Human ant
28	465	89.1	107	8	ADJ88008 Human var
29	465	89.1	107	8	ADN12054 Variable
30	465	89.1	107	8	ADP43328 Human mon
31	465	89.1	108	2	AAW70622 Human con
32	465	89.1	108	3	AAW82345 Human con
33	465	89.1	108	5	AAU76522 Anti-Inte
34	465	89.1	108	5	ABP61191 Human ant
35	465	89.1	108	7	ADF11407 18B2 ant
36	465	89.1	108	8	ADG38991 Human con
37	465	89.1	108	8	ADR03366 Human sub
38	465	89.1	108	8	ADP79572 Human kap
39	465	89.1	109	5	AAU74544 Human sub
40	465	89.1	110	5	AAE28149 Human con
41	465	89.1	214	7	ADF11431 18B2 ant
42	464	88.9	107	4	AAB67511 Light cha
43	464	88.9	109	2	AAR30764 Consensus
44	464	88.9	236	3	AAV96297 Human IGP
45	464	88.9	299	4	AAG63637 Amino aci

ALIGNMENTS

RESULT 1  
AAY34316  
ID AAY34316 standard; protein; 101 AA.  
XX AC AAY34316;  
XX DT 19-NOV-1999 (first entry)  
XX DB Igg antibody 2.1.1 kappa chain sequence.  
XX KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX OS Homo sapiens.  
XX PN WO9945031-A2.  
XX FD 10-SEP-1999.  
XX PF 03-MAR-1999; 99WO-US004583.  
XX PR 03-MAR-1998; 98US-00034607.  
XX PR 03-FEB-1999; 99US-00244253.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX DR WPI; 1999-540816/45.  
XX N-PSDB; AAZ20417.  
XX PT New monoclonal antibody, used for treating e.g. graft versus host  
XX disease, cancer, autoimmune diseases and inflammatory diseases.  
XX FS Claim 61; Fig 31; 245pp; English.  
XX CC This sequence represents the kappa chain of an antibody of the invention.  
XX CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
XX CC complement and a variable region that binds to the epitope on CD147 bound  
XX CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
XX CC can selectively kill activated T-cells, activated B-cells or resting or  
XX CC activated monocytes. The products and methods can be used for treating  
XX CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
XX CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
XX CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
SQ Sequence 101 AA;  
Query Match 100.0%; Score 522; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDIQLTQSPSSLSASVGDRTVITICRASQDISIYLAWFQORPGKAPKSLIYAASSLSQSGVP 60  
DB 1 LDIQLTQSPSSLSASVGDRTVITICRASQDISIYLAWFQORPGKAPKSLIYAASSLSQSGVP 60  
QY 61 SKFSGSGSGTDFLTITISLQPEDFATYCCQYNSYPFTFGP 101  
DB 61 SKFSGSGSGTDFLTITISLQPEDFATYCCQYNSYPFTFGP 101  
RESULT 2  
ID AAY34317  
XX AAY34317 standard; protein; 164 AA.  
AC AAY34317;  
XX  
XX 19-NOV-1999 (first entry)  
XX  
XX Igg antibody 2.6.1 kappa chain sequence.  
XX  
XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;  
XX activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
XX organ transplant rejection disease; lymphoma; pancreatic disease;  
XX autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
XX Homo sapiens.  
XX  
XX WO9945031-A2.  
XX  
XX 10-SEP-1999.  
XX  
XX 03-MAR-1999; 99WO-US004583.  
XX  
XX 03-MAR-1998; 98US-00034607.  
XX 03-FEB-1999; 99US-00244253.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
XX Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX WPI; 1999-540816/45.  
XX N-PSDB; AAZ20418.  
XX  
XX New monoclonal antibody, used for treating e.g. graft versus host  
XX disease, cancer, autoimmune diseases and inflammatory diseases.  
XX  
XX Claim 61; Fig 33; 245pp; English.  
XX  
XX This sequence represents the kappa chain of an antibody of the invention.  
XX The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
XX complement and a variable region that binds to the epitope on CD147 bound  
XX by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
XX can selectively kill activated T-cells, activated B-cells or resting or  
XX activated monocytes. The products and methods can be used for treating  
XX diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
XX versus host disease (GVHD), organ transplant rejection diseases (e.g.  
XX renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
XX (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
XX (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
XX  
XX Sequence 164 AA;  
Query Match 98.7%; Score 515; DB 2; Length 164;  
Best Local Similarity 99.0%; Pred. No. 8.3e-32;  
XX

Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 LDIQLTQSPSSLSASVGDRTVITICRASQDISIYLAWFQORPGKAPKSLIYAASSLSQSGVP 60  
DB 4 LDIQLTQSPSSLSASVGDRTVITICRASQDISIYLAWFQORPGKAPKSLIYAASSLSQSGVP 63  
QY 61 SKFSGSGSGTDFLTITISLQPEDFATYCCQYNSYPFTFGP 101  
DB 64 SKFSGSGSGTDFLTITISLQPEDFATYCCQYNSYPFTFGP 104  
RESULT 3  
ID AAE37206  
XX AAE37206 standard; protein; 127 AA.  
AC AAE37206;  
XX  
XX 07-AUG-2003 (first entry)  
XX  
XX Human AB-PGI-XGI-051 PSMA antibody light chain variable region (VH).  
XX  
XX Human; Prostate specific membrane antigen; carcinoma; sarcoma; cancer;  
XX PSMA; melanoma; therapy; N-acetylated alpha-linked acidic dipeptidase;  
XX folate hydrolase; dipeptidyl dipeptidase IV; gamma-glutamyl hydrolase;  
XX NAALADase; antibody; light chain variable region; VH.  
XX  
XX Homo sapiens.  
XX  
XX WO2003034903-A2.  
XX  
XX 01-MAY-2003.  
XX  
XX 23-OCT-2002; 2002WO-US033944.  
XX  
XX 23-OCT-2001; 2001US-0335215P.  
XX 07-MAR-2002; 2002US-0362747P.  
XX 20-SEP-2002; 2002US-0412618P.  
XX  
XX (PSMA-) PSMA DEV CO LLC.  
XX  
XX Maddon PJ, Donovan GP, Olson WC, Schuelke N, Gardner J, Ma D;  
XX WPI; 2003-403281/38.  
XX N-PSDB; AAD56221.  
XX  
XX Novel isolated antibody which binds to epitope on prostate specific  
XX membrane antigen, and competitively inhibits binding of second antibody  
XX to its target epitope on the antigen, useful for treating prostate  
XX cancer.  
XX  
XX Claim 26; Page 233; 238pp; English.  
XX  
XX The invention relates to an antibody or its antigen-binding fragment  
XX which specifically binds to epitope on prostate specific membrane antigen  
XX (PSMA), and competitively inhibits the specific binding of a second  
XX antibody to its target epitope on PSMA. The invention is useful for  
XX diagnosing, treating or preventing PSMA-mediated disease such as prostate  
XX cancer or non-prostate cancer bladder chosen from cancer including  
XX transitional cell carcinoma, pancreatic cancer including pancreatic duct  
XX carcinoma, lung cancer including non-small cell lung carcinoma, kidney  
XX cancer including conventional renal cell carcinoma, sarcoma including  
XX soft tissue sarcoma, breast cancer including breast carcinoma, brain  
XX cancer including glioblastoma multiforme, neuroendocrine carcinoma, colon  
XX cancer including colonic carcinoma, testicular cancer including  
XX testicular embryonal carcinoma, or melanoma including malignant melanoma.  
XX The invention is useful also for inhibiting or enhancing folate hydrolase  
XX activity of a folate hydrolase polypeptide, N-acetylated alpha-linked  
XX acidic dipeptidase (NAALADase) activity of a NAALADase polypeptide,  
XX dipeptidyl dipeptidase IV activity of a dipeptidyl dipeptidase IV  
XX polypeptide, gamma-glutamyl hydrolase activity of a gamma-glutamyl  
XX hydrolase polypeptide. The present sequence is human PSMA antibody light  
XX chain variable region (VH)  
XX

CC polypeptide, gamma-glutamyl hydrolase activity of a gamma-glutamyl  
CC hydrolase polypeptide. The present sequence is human PSMA antibody light  
CC chain variable region (VH)  
XX  
XX  
SQ Sequence 127 AA;  
  
Query Match 91.8%; Score 479; DB 6; Length 127;  
Best Local Similarity 92.9%; Pred. No. 3.6e-29;  
Matches 92; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 DIQLTQSPSSLASVGDVRVITCRASQDISIYLAWFOORCKAPKSLIYRASSLSQSGVPS 61  
DB 21 DIQWTSPLSLSASVGDVRVITCRASQGITNYLAWFOOKPKAPKSLIYAASSLQSGVPS 80  
QY 62 KFGSGSGDTFTLITISLSQLEDFATYYCQQYNSTPFTFG 100  
DB 81 KFGSGSGDTFTLITISLSQLEDFATYYCQQYNSTPFTFG 119  
  
RESULT 5  
AAB75040  
ID AAB75040 standard; protein; 224 AA.  
XX  
AC AAB75040;  
XX  
DT 19-JUL-2001 (first entry)  
XX  
XX TRO005 HuMab kappa chain protein sequence 3E2K.  
DE  
XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;  
XX human antibody phage display library; immunisation; transgenic animal.  
XX Homo sapiens.  
OS Synthetic.  
QS  
XX WC200125492-A1.  
PN  
XX  
PD 12-APR-2001.  
XX  
XX 02-OCT-2000; 2000WO-US027237.  
PF  
XX 02-OCT-1999; 99US-0157415P.  
PR  
XX 01-DEC-1999; 99US-00453234.  
PR  
XX  
XX (BIOS-) BIOSITE DIAGNOSTICS INC.  
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.  
PA  
XX  
XX Buechler J, Valkirs G, Gray J, Lonberg N;  
PI  
XX  
XX WPI; 2001-335567/35.  
DR  
XX  
XX Producing a human antibody phage display library comprises providing a  
PT transgenic animal whose genome comprises human immunoglobulin genes and  
PT isolating nucleic acids encoding antibody chains from lymphatic cells.  
PT  
XX  
XX Example 37; Page 121-122; 16ipp; English.  
PS  
XX  
XX The present invention describes a method (M1) for producing a human  
CC antibody phage display library (I), comprising: (1) providing a nonhuman  
CC transgenic animal (II) whose genome comprises human immunoglobulin genes;  
CC (2) isolating nucleic acids encoding human antibody chains (III) from  
CC lymphatic cells; and (3) forming a library of display packages whose  
CC members comprise a nucleic acid encoding (III) which is displayed from  
CC the package. The method is used for producing a human antibody display  
CC library, e.g., a Fab phage display library. The display method may be  
CC used to screen nucleic acids encoding antibody chains obtained from  
CC immunised nonhuman transgenic animals, and from this a population of  
CC antibodies may be prepared. Production of a human monoclonal antibodies  
CC display library using this method means there is no need to immunise  
CC humans with antigens, and the difficulties faced with immortalising B  
CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056  
XX represent sequences used in the exemplification of the present invention  
XX



PR 29-MAR-2000; 2000WO-US008528.  
XX (DGIB-) DGI BIOTECHNOLOGIES LLC.  
FA (NOVO) NOVO NORDISK AS.  
XX  
XX Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;  
PI Briesette R, Spetzler J, Cheng W, Ostergaard S, Mandrecki WS;  
PI Hansen PH, Ravera M, Hsiao K;  
XX  
XX WPI; 2002-025774/03.  
DR  
XX  
XX Modulating insulin activity in mammalian cells, for treating e.g.  
PT diabetes and tumors, comprises using peptides that bind to insulin or  
PT insulin-like growth factor receptors.  
XX  
XX Disclosure; Fig 58; 390pp; English.  
XX  
XX The invention relates to a method of modulating insulin activity in  
CC mammalian cells by administering a peptide that binds the insulin  
CC receptor (IR). A composition containing a peptide, optionally expressed  
CC from gene therapy vectors, that binds to Site 1 of IR and an insulin  
CC agonist are useful for treating diabetes. Also, peptides that are  
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are  
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours  
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1  
CC receptor agonists are useful for treating neurological diseases,  
CC including stroke and diabetic neuropathy. The peptides are also useful in  
CC screening for compounds that bind to IR or IGF-1 receptor, potential  
CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or  
CC IGF-1 receptor-binding peptides and related amino acid sequences of the  
CC invention  
XX  
XX SQ Sequence 241 AA;  
Query Match 90.6%; Score 473; DB 5; Length 241;  
Best Local Similarity 91.0%; Pred. No. 1.9e-28;  
Matches 91; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 DIQQTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQRPCKAPKSLIYAASSLSQGVPS 61  
Db 135 DIQQTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQRPCKAPKSLIYAASSLSQGVPS 194  
Qy 62 KFGSGSGTDTLTITSLQPEDFATYCCQYNSTPFTFGP 101  
Db 195 RFGSGSGTDTLTITSLQPEDFATYCCQYNSTPFTFGP 234  
RESULT 8  
AAB72880  
ID AAB72880 standard; protein; 107 AA.  
XX  
XX AAB72880;  
XX  
XX 10-MAY-2001 (first entry)  
XX  
XX Human anti-HER2/neu antibody 3-F2 light chain.  
XX  
XX Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;  
XX 1-D2; 2-E8; growth factor receptor.  
XX  
XX Homo sapiens.  
XX  
XX WO200109187-A2.  
XX  
XX 08-FEB-2001.  
XX  
XX 25-JUL-2000; 2000WO-US020272.  
XX  
XX 29-JUL-1999; 99US-0146313P.  
XX  
XX 10-MAR-2000; 2000US-0188539P.  
XX  
XX (MEDA-) MEDAREX INC.  
XX

PI Keler T, Deo Y;  
XX  
XX WPI; 2001-168698/17.  
DR  
XX N-PSDB; AAF75586.  
XX  
XX New human monoclonal antibody that specifically binds to growth factor  
PT receptor HER2/neu, for treating, preventing or diagnosing diseases  
PT characterized by aberrant HER2/neu expression e.g. cancers.  
XX  
XX Disclosure; Page 104-105; 113pp; English.  
XX  
XX The present invention provides the protein and coding sequences for human  
CC monoclonal antibodies which bind specifically to the HER2/neu growth  
CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2  
CC and 2-E8. They can be used in the immunotherapy-based treatment and  
CC prognosis of cancers, particularly adenocarcinomas such as salivary  
CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,  
CC and ovarian cancer. The present sequence is part of an antibody of the  
CC invention  
XX  
XX SQ Sequence 107 AA;  
Query Match 90.2%; Score 471; DB 4; Length 107;  
Best Local Similarity 90.9%; Pred. No. 1.2e-28;  
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 DIQQTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQRPCKAPKSLIYAASSLSQGVPS 61  
Db 1 DIQQTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQRPCKAPKSLIYAASSLSQGVPS 60  
Qy 62 KFGSGSGTDTLTITSLQPEDFATYCCQYNSTPFTFG 100  
Db 61 RFGSGSGTDTLTITSLQPEDFATYCCQYNSTPFTFG 99  
RESULT 9  
ADO36490  
ID ADO36490 standard; protein; 107 AA.  
XX  
XX ADO36490;  
XX  
XX 12-AUG-2004 (first entry)  
XX  
XX Human anti-heparanase 2H8 Vh amino acid sequence SEQ ID NO:4.  
XX  
XX human; monoclonal antibody; heparanase; heparanase inhibitor;  
XX anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;  
XX antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;  
XX neuroprotective; nontropic; heparanase antagonist; cancer; tumour;  
XX melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;  
XX bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;  
XX mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;  
XX autoimmune disease; arthritis; asthma; lupus erythematosus;  
XX allograft rejection; vascular restenosis; atherosclerosis;  
XX Alzheimer's disease.  
XX  
XX Homo sapiens.  
XX  
XX WO2004043989-A2.  
XX  
XX 27-MAY-2004.  
XX  
XX 05-NOV-2003; 2003WO-US035464.  
XX  
XX 07-NOV-2002; 2002US-0424803P.  
XX  
XX (MEDA-) MEDAREX INC.  
XX (CELL-) CELLTech R & D.  
XX  
XX Huang H, Holmes S, Mason S;  
XX  
XX WPI; 2004-411694/38.  
XX N-PSDB; ADO36489.  
XX

```

XX PT New human monoclonal antibody to heparanase, for use in treating or
PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
PT erythematous, allograft rejection, atherosclerosis, and Alzheimer's
PT disease.
XX PT
PS Claim 47; SEQ ID NO 4; 108pp; English.
XX CC The present invention describes an isolated human monoclonal antibody
CC which binds to and inhibits activity of human heparanase. Human anti-
CC heparanase antibodies of the present invention have cytostatic,
CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
CC dermatological, antiarteriosclerotic, neuroprotective and neurotropic
CC activities, and can be used as heparanase antagonists. The antibody,
CC methods and compositions of the present invention are useful in treating
CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
CC erythematous, allograft rejection, vascular restenosis, atherosclerosis,
CC and Alzheimer's disease. The present sequence represents a human anti-
CC heparanase 2H8 Vk amino acid sequence, which is used in the
CC exemplification of the present invention.
XX CC
SQ Sequence 107 AA;
Query Match 90.2%; Score 471; DB 8; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.2e-28;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGISLWAWYQQKPEKAPKSLIYAASSLSQSGVPS 60
Qy 62 KFSGSGSGTDTLTITISLQPEDFATYYCQYNVPYTFG 100
Db 61 RFSGSGSGTDTLTITISLQPEDFATYYCQYNVPYTFG 99
RESULT 10
ADO36502
ID ADO36502 standard; protein; 107 AA.
AC ADO36502;
XX AC
XX DT 12-AUG-2004 (first entry)
XX DE Human anti-heparanase 5G10 Vk amino acid sequence SEQ ID NO:16.
XX KW human; monoclonal antibody; heparanase; heparanase inhibitor;
XX anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
XX antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
XX neuroprotective; neurotropic; heparanase antagonist; cancer; tumour;
XX melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
XX bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
XX mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
XX autoimmune disease; arthritis; asthma; lupus erythematous;
XX allograft rejection; vascular restenosis; atherosclerosis;
XX Alzheimer's disease.
XX OS Homo sapiens.
XX OS
XX PN WO2004043989-A2.
XX PD 27-MAY-2004.
XX PF 05-NOV-2003; 2003WO-US035464.
XX PR 07-NOV-2002; 2002US-0424803P.
XX PA (MEDA-) MEDAREX INC.
XX PA (CELL-) CELLTECH R & D.
XX

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PI Huang H, Holmes S, Mason S;
XX WPI; 2004-411694/38.
DR N-PSDB; ADO36501.
XX PT New human monoclonal antibody to heparanase, for use in treating or
PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
PT erythematous, allograft rejection, atherosclerosis, and Alzheimer's
PT disease.
XX PT
PS Claim 47; SEQ ID NO 16; 108pp; English.
XX CC The present invention describes an isolated human monoclonal antibody
CC which binds to and inhibits activity of human heparanase. Human anti-
CC heparanase antibodies of the present invention have cytostatic,
CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
CC dermatological, antiarteriosclerotic, neuroprotective and neurotropic
CC activities, and can be used as heparanase antagonists. The antibody,
CC methods and compositions of the present invention are useful in treating
CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
CC erythematous, allograft rejection, vascular restenosis, atherosclerosis,
CC and Alzheimer's disease. The present sequence represents a human anti-
CC heparanase 5G10 Vk amino acid sequence, which is used in the
CC exemplification of the present invention.
XX CC
SQ Sequence 107 AA;
Query Match 90.2%; Score 471; DB 8; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.2e-28;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGISLWAWYQQKPEKAPKSLIYAASSLSQSGVPS 60
Qy 62 KFSGSGSGTDTLTITISLQPEDFATYYCQYNVPYTFG 100
Db 61 RFSGSGSGTDTLTITISLQPEDFATYYCQYNVPYTFG 99
RESULT 11
ADO36494
ID ADO36494 standard; protein; 107 AA.
XX AC ADO36494;
XX AC
XX DT 12-AUG-2004 (first entry)
XX DE Human anti-heparanase 2D9 Vk amino acid sequence SEQ ID NO:8.
XX KW human; monoclonal antibody; heparanase; heparanase inhibitor;
XX anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
XX antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
XX neuroprotective; neurotropic; heparanase antagonist; cancer; tumour;
XX melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
XX bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
XX mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
XX autoimmune disease; arthritis; asthma; lupus erythematous;
XX allograft rejection; vascular restenosis; atherosclerosis;
XX Alzheimer's disease.
XX OS Homo sapiens.
XX OS
XX PN WO2004043989-A2.
XX PD 27-MAY-2004.
XX PF 05-NOV-2003; 2003WO-US035464.
XX PR 07-NOV-2002; 2002US-0424803P.
XX

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XX PA (MEDA-) MEDAREX INC.  
 XX PA (CELL-) CELTECH R & D.  
 XX PI Huang H, Holmes S, Mason S;  
 XX DR WPI; 2004-411694/38.  
 XX DR N-PSDB; ADO36493.  
 XX  
 PT New human monoclonal antibody to heparanase, for use in treating or  
 PT preventing cancer, autoimmune disease, arthritis, asthma, lupus  
 PT erythematous, allograft rejection, atherosclerosis, and Alzheimer's  
 PT disease.  
 XX PS Claim 11; SEQ ID NO 8; 108pp; English.  
 XX  
 CC The present invention describes an isolated human monoclonal antibody  
 CC which binds to and inhibits activity of human heparanase. Human anti-  
 CC heparanase antibodies of the present invention have cytostatic,  
 CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,  
 CC dermatological, antiarteriosclerotic, neuroprotective and nootropic  
 CC activities, and can be used as heparanase antagonists. The antibody,  
 CC methods and compositions of the present invention are useful in treating  
 CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate  
 CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,  
 CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a  
 CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus  
 CC erythematous, allograft rejection, vascular restenosis, atherosclerosis,  
 CC and Alzheimer's disease. The present sequence represents a human anti-  
 CC heparanase 2D9 V<sub>k</sub> amino acid sequence, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 107 AA;  
 Query Match 90.2%; Score 471; DB 8; Length 107;  
 Best Local Similarity 90.9%; Pred. No. 1.2e-28;  
 Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 DIQTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOQRPKAPKSLIYAASSLSQSGVPS 61  
 Db 1 DIQTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOQRPKAPKSLIYAASSLSQSGVPS 60  
 Qy 62 KFSGSGGTDTLTITISSLOPEDFATYTCQQVNSYPFTFG 100  
 Db 61 KFSGSGGTDTLTITISSLOPEDFATYTCQQVNSYPFTFG 99  
 RESULT 12  
 AAP81246  
 ID AAP81246 standard; protein; 108 AA.  
 XX  
 AC AAP81246;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-JAN-1991 (first entry)  
 XX  
 DE Anti-pseudomonas aeruginosa human type antibody L-chain contg. constant  
 DE region of kappa and lambda types.  
 XX  
 KW Pseudomonas aeruginosa P4; Pseudomonas aeruginosa HI; immunotherapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FN JP63152984-A.  
 XX  
 PD 25-JUN-1988.  
 XX  
 PF 20-MAR-1986; 86JP-00064183.  
 XX  
 PR 18-AUG-1986; 86JP-00191687.  
 PR 20-MAR-1987; 87JP-00064183.  
 XX  
 PA (WAKT ) WAKUNAGA SEIYAKU KK.

XX WPI; 1988-216877/31.  
 DR N-PSDB; AAN81636.  
 XX  
 PT Anti-Pseudomonas aeruginosa type antibody L-chain coding DNA - contains  
 PT constant kappa and lambda type regions, and versatile region recognising  
 PT psaeuruginosa F4 and HI types.  
 XX  
 PS Claim 8; Page 602; 12pp; Japanese.  
 XX  
 CC It also contains a variable region recognising Ps.aeruginosa F4 and HI  
 CC types. The Ab can be used for immunologic control of infection caused by  
 CC Ps.aeruginosa. The antibody is made effective against various classes or  
 CC subclasses of resistant Ps.aeruginosa by recombining corresp. DNA L-chain  
 CC contg. versatile coding region. (Updated on 25-MAR-2003 to correct PF  
 CC field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-  
 CC 2003 to correct PA field.)  
 XX  
 SQ Sequence 108 AA;  
 Query Match 90.2%; Score 471; DB 1; Length 108;  
 Best Local Similarity 92.9%; Pred. No. 1.3e-28;  
 Matches 92; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 2 DIQTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOQRPKAPKSLIYAASSLSQSGVPS 61  
 Db 1 DIQTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOQRPKAPKSLIYAASSLSQSGVPS 60  
 Qy 62 KFSGSGGTDTLTITISSLOPEDFATYTCQQVNSYPFTFG 100  
 Db 61 KFSGSGGTDTLTITISSLOPEDFATYTCQQVNSYPFTFG 99  
 RESULT 13  
 AAP81870  
 ID AAP81870 standard; protein; 111 AA.  
 XX  
 AC AAP81870;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 05-JAN-1991 (first entry)  
 XX  
 DE Anti-pseudomonas aeruginosa human type antibody L-chain contg. constant  
 DE region of kappa and lambda types.  
 XX  
 KW Pseudomonas aeruginosa F4; Pseudomonas aeruginosa HI; immunotherapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FN JP63152984-A.  
 XX  
 PD 25-JUN-1988.  
 XX  
 PF 20-MAR-1986; 86JP-00064183.  
 XX  
 PR 18-AUG-1986; 86JP-00191687.  
 PR 20-MAR-1987; 87JP-00064183.  
 XX  
 PA (WAKT ) WAKUNAGA SEIYAKU KK.  
 XX  
 DR WPI; 1988-216877/31.  
 DR N-PSDB; AAN81636.  
 XX  
 PT Anti-Pseudomonas aeruginosa type antibody L-chain coding DNA - contains  
 PT constant kappa and lambda type regions, and versatile region recognising  
 PT psaeuruginosa F4 and HI types.  
 XX  
 PS Disclosure; Fig 6 Page 612; 12pp; Japanese.  
 XX  
 CC The Ab can also be used for immunologic control of infection caused by  
 CC Ps.aeruginosa. The antibody is made effective against various classes or  
 CC subclasses of resistant Ps.aeruginosa by recombining corresp. DNA L-chain  
 CC contg. versatile coding region. (Updated on 25-MAR-2003 to correct PF

```
CC field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
SQ Sequence 111 AA;

Query Match      90.2%; Score 471; DB 1; Length 111;
Best Local Similarity 92.9%; Pred. No. 1.3e-28;
Matches 92; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQGVPS 61
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Db 4 DIQWTQSPSSLSASVGDRTVITCRASQDISNYLAWFOQPGKAPKSLIQAASSLSQGVPS 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 62 KFSGSGSGTDFTLTISLSQPEDFATYCCQYNSYPFTFG 100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 KFSGSGSGTDFTLTISLSQPEDFATYCCQYNYPRTFG 102
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
AAR40956
ID AAR40956 standard; protein; 109 AA.
XX
AC AAR40956;
XX
DT 25-MAR-2003 (revised)
DT 25-FEB-1994 (first entry)
XX
DE Human germ-line gene HK137 antibody light (kappa) chain.
XX
KW humanised antibody; human germ-line; light chain; variable region;
KW framework region; reshaped antibody; CDR-grafted antibody;
KW complementarity determining region; immuno silent.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..23
   /label= FR1
FT FT /note= "framework region"
FT Region 24..34
   /label= CDR1
FT Region 35..49
   /label= FR2
FT FT /note= "framework region"
FT Region 50..56
   /label= CDR2
FT Region 57..88
   /label= FR3
FT FT /note= "framework region"
FT Region 89..97
   /label= CDR3
FT Region 98..109
   /label= FR4
FT FT /note= "framework region"
XX
FN WO9317105-A1.
XX
PD 02-SEP-1993.
XX
PF 19-FEB-1993; 93WO-GB000363.
XX
PR 19-FEB-1992; 92GB-00003459.
XX
PA (SCOT-) SCOTGEN LTD.
XX
PI Winter GP, Carr FJ, Harris WJ;
XX
DR WPI; 1993-288411/36.
XX
PT New altered antibodies with reduced immune responses - have germ-line
PT aminoacid residues replacing somatically mutated residues.
XX
PS Example 3; Fig 4b; 53pp; English.
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XX A humanised antibody comprised CDRs originally from a mouse MAb RSV19
CC specific for Respiratory Syncytial Virus transplanted onto heavy and
CC light chain V region domains derived from NEM and RE1 myeloma proteins,
CC respectively. The framework regions of this CDR-grafted antibody were
CC converted to the germ-line equivalent. For conversion of the K-chain, the
CC germ-line light chain VK137 (AAR40956) was used. Germ-line framework
CC regions are those present in immature B cells, i.e. prior to any somatic
CC mutation which takes place during maturation. Unlike mutations in the
CC CDRs, any mutation in framework regions does not affect affinity for an
CC antigen and is therefore essentially random. The mutation may, however,
CC cause the "self" antibody to be recognised as "foreign" and conversion to
CC the unmutated germ-line sequence renders the framework regions "immuno
CC silent". (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 109 AA;

Query Match      89.7%; Score 468; DB 2; Length 109;
Best Local Similarity 91.9%; Pred. No. 2.1e-28;
Matches 91; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQGVPS 61
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Db 1 DIQWTQSPSSLSASVGDRTVITCRASQGISNYLAWFOQPGKAPKLLIYAASSLSQGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 62 KFSGSGSGTDFTLTISLSQPEDFATYCCQYNSYPFTFG 100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGTDFTLTISLSQPEDFATYCCQYNSYRLTFG 99
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
ABO27128
ID ABO27128 standard; protein; 95 AA.
XX
AC ABO27128;
XX
DT 10-SEP-2003 (first entry)
DE Human germline light chain variable region gene segment #8.
XX
KW Human; light chain variable region; VK; humanised antibody;
KW chimeric antibody; complementarity determining region; CDR;
KW canonical CDR structure type.
XX
OS Homo sapiens.
XX
FN US2003039649-A1.
XX
PD 27-FEB-2003.
XX
PF 12-JUL-2002; 2002US-00194975.
XX
PR 12-JUL-2001; 2001US-0305111P.
XX
PA (FOOT/) FOOTE J.
XX
PI Foote J;
XX
DR WPI; 2003-492151/46.
XX
PT Making humanized antibody for converting antibody, by making chimeric
PT antibodies containing complementarity determining region from non-human
PT antibody and appropriate framework sequences of human antibodies.
XX
PS Example 1; Fig 2; 31pp; English.
XX
CC The invention describes a method of making a humanised antibody,
CC comprising making chimeric antibodies containing a complementarity
CC determining region (CDR) from a non-human antibody and appropriate
CC framework sequences (I) of human antibodies. (I) is selected by using
CC canonical CDR structure types of non-human antibody in comparison to
CC germline canonical CDR structure types of human antibodies as the basis
CC for selection, for humanisation. The method is useful for making a
```



CC humanised antibody or a converted antibody. The method is applicable for  
CC converting a subject antibody sequence of any subject species to a less  
CC immunogenic form suitable for use in an object species. The method is  
CC reliable for identifying suitable human framework sequences to support  
CC non-human CDR regions and to provide humanised antibodies that retain  
CC high antigen binding with low immunogenicity in humans, without the need  
CC for direct comparison of framework sequences, without the need for  
CC determining critically important amino acid residues in the framework,  
CC and without the need for multiple iteration and construction to obtain  
CC humanised antibodies with suitable therapeutic properties. The antibody  
CC has high affinity and low immunogenicity without need for comparing  
CC framework sequences between non-human and human antibodies. This sequence  
CC represents a human light chain variable region gene segment used in the  
CC creation of humanised antibodies  
XX  
SQ Sequence 95 AA;

Query Match 89.3%; Score 466; DB 6; Length 95;  
Best Local Similarity 94.7%; Pred. No. 2.7e-28;  
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 DIQLTQSPSSLASVGDRTTITCRASQDISIYLAWFQQRPGKAPKSLIYAASSLQSGVPS 61  
Db 1 DIQMTQSPSSLASVGDRTTITCRASQGISNYLAWFQQRPGKAPKSLIYAASSLQSGVPS 60  
Qy 62 KFGSGSGTDFTLTISSLPEDFATYYCQYNYP 96  
Db 61 RFGSGSGTDFTLTISSLPEDFATYYCQYNYP 95

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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Maximum Match 100%

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#### SUMMARIES

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4	479	91.8	127	16	US-10-395-894-21
5	474	90.8	127	15	US-10-221-529-4
6	471	90.2	107	16	US-10-703-714-4
7	471	90.2	107	16	US-10-703-714-8
8	471	90.2	107	16	US-10-703-714-16
9	467	89.5	108	17	US-10-783-311-126
10	466	89.3	95	14	US-10-194-975-61
11	466	89.3	95	15	US-10-308-817-8
12	466	89.3	95	15	US-10-453-698-8
13	466	89.3	95	16	US-10-379-392-68
					Sequence 25, Appl
					Sequence 25, Appl
					Sequence 21, Appl
					Sequence 21, Appl
					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 8, Appl
					Sequence 16, Appl
					Sequence 126, Appl
					Sequence 61, Appl
					Sequence 8, Appl
					Sequence 8, Appl

14	466	89.3	107	15	US-10-351-085B-145	Sequence 145, App
15	466	89.3	107	16	US-10-737-252-145	Sequence 145, App
16	465	89.1	107	14	US-10-268-501-5	Sequence 5, Appl
17	465	89.1	107	15	US-10-608-626-5	Sequence 5, Appl
18	465	89.1	107	15	US-10-600-152-14	Sequence 14, Appl
19	465	89.1	107	16	US-10-619-754-5	Sequence 5, Appl
20	465	89.1	108	9	US-09-056-160B-12	Sequence 12, Appl
21	465	89.1	108	10	US-09-520-262A-8	Sequence 8, Appl
22	465	89.1	108	10	US-09-795-798-3	Sequence 3, Appl
23	465	89.1	108	14	US-10-234-671-12	Sequence 12, Appl
24	465	89.1	108	15	US-10-408-901-20	Sequence 20, Appl
25	465	89.1	108	16	US-10-912-994-8	Sequence 8, Appl
26	465	89.1	109	9	US-09-811-123-6	Sequence 6, Appl
27	465	89.1	110	14	US-10-044-896-4	Sequence 4, Appl
28	465	89.1	214	15	US-10-408-901-44	Sequence 44, Appl
29	464	88.9	107	9	US-09-948-939-13	Sequence 13, Appl
30	463	88.7	214	14	US-10-153-382-19	Sequence 19, Appl
31	461	88.3	107	15	US-10-309-762-62	Sequence 62, Appl
32	461	88.3	107	15	US-10-309-762-164	Sequence 164, App
33	461	88.3	107	17	US-10-638-265-76	Sequence 76, Appl
34	460	88.1	107	10	US-09-851-614-2	Sequence 2, Appl
35	460	88.1	107	14	US-10-035-637-2	Sequence 4, Appl
36	460	88.1	107	14	US-10-073-644C-4	Sequence 4, Appl
37	460	88.1	108	17	US-10-725-962-40	Sequence 40, Appl
38	460	88.1	111	14	US-10-203-754A-18	Sequence 18, Appl
39	459	87.9	291	15	US-10-406-830-10	Sequence 10, Appl
40	458	87.7	116	17	US-10-783-311-174	Sequence 174, App
41	458	87.7	128	15	US-10-389-221-12	Sequence 12, Appl
42	457	87.5	107	15	US-10-309-762-61	Sequence 61, Appl
43	457	87.5	107	15	US-10-309-762-64	Sequence 64, Appl
44	457	87.5	107	15	US-10-309-762-88	Sequence 88, Appl
45	457	87.5	126	16	US-10-469-125-8	Sequence 8, Appl

#### ALIGNMENTS

RESULT 1  
US-10-395-894-25  
; Sequence 25, Application US/10395894  
; Publication No. US20040033229A1  
; GENERAL INFORMATION:  
; APPLICANT: MADON, Paul J.  
; APPLICANT: DONOVAN, Gerald P.  
; APPLICANT: OLSON, William C.  
; APPLICANT: SCHLKE, No. US20040033229Albert  
; APPLICANT: GARDNER, Jason  
; APPLICANT: MA Dangehe  
; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS  
; FILE REFERENCE: P00741.70005.US  
; CURRENT APPLICATION NUMBER: US/10/395,894  
; CURRENT FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: PCT/US02/33944  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/335,215  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/362,747  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/412,618  
; PRIOR FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 25  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-395-894-25

Query Match 92.3%; Score 482; DB 15; Length 127;  
Best Local Similarity 93.9%; Pred. No. 1,4e-34;  
Matches 93; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQQTSPSSLSASVGRVTTCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQGVPS 61

Db 21 DIQMTQSPSSLSASVGRVTITCRASQGISHYLAWFQKPKAPKSLIYAASSLSQSGVPS 80  
Qy 62 KFSGSGSGTDTLTITSLQPEDFATYYCQQNSYPFTFG 100  
Db 81 KFSGSGSGTDTLTITSLQPEDFATYYCQQNSYPFTFG 119

## RESULT 2

US-10-695-667-25  
; Sequence 25, Application US/10695667  
; Publication No. US20040161776A1  
; GENERAL INFORMATION:  
; APPLICANT: MADDON, Paul J.  
; APPLICANT: DONOVAN, Gerald P.  
; APPLICANT: OLSON, William C.  
; APPLICANT: SCHSLKE, Norbert  
; APPLICANT: GARDNER, Jason  
; APPLICANT: MA, Dangshe  
; TITLE OF INVENTION: PSMA FORMULATIONS AND USES THEREOF  
; FILE REFERENCE: P0741.70006US00  
; CURRENT APPLICATION NUMBER: US/10/695,667  
; PRIOR FILING DATE: 2003-10-27  
; PRIOR APPLICATION NUMBER: US 10/395,894  
; PRIOR FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: PCT/US02/33944  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/335,215  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/362,747  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/412,618  
; PRIOR FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-695-667-25

Query Match 92.3%; Score 482; DB 16; Length 127;  
Best Local Similarity 93.9%; Pred. No. 1.4e-34;  
Matches 93; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQMTQSPSSLSASVGRVTITCRASQGISHYLAWFQKPKAPKSLIYAASSLSQSGVPS 61  
Db 21 DIQMTQSPSSLSASVGRVTITCRASQGISHYLAWFQKPKAPKSLIYAASSLSQSGVPS 80

Qy 62 KFSGSGSGTDTLTITSLQPEDFATYYCQQNSYPFTFG 100  
Db 81 KFSGSGSGTDTLTITSLQPEDFATYYCQQNSYPFTFG 119

## RESULT 3

US-10-395-894-21  
; Sequence 21, Application US/10395894  
; Publication No. US20040033229A1  
; GENERAL INFORMATION:  
; APPLICANT: MADDON, Paul J.  
; APPLICANT: DONOVAN, Gerald P.  
; APPLICANT: OLSON, William C.  
; APPLICANT: SCHSLKE, Norbert  
; APPLICANT: GARDNER, Jason  
; APPLICANT: MA, Dangshe  
; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS  
; FILE REFERENCE: P0741.70005US  
; CURRENT APPLICATION NUMBER: US/10/395,894  
; CURRENT FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: PCT/US02/33944  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/335,215  
; PRIOR FILING DATE: 2001-10-23

; PRIOR APPLICATION NUMBER: US 60/362,747  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/412,618  
; PRIOR FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-395-894-21

Query Match 91.8%; Score 479; DB 15; Length 127;  
Best Local Similarity 92.9%; Pred. No. 2.5e-34;  
Matches 92; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQMTQSPSSLSASVGRVTITCRASQGISHYLAWFQKPKAPKSLIYAASSLSQSGVPS 61  
Db 21 DIQMTQSPSSLSASVGRVTITCRASQGISHYLAWFQKPKAPKSLIYAASSLSQSGVPS 80

Qy 62 KFSGSGSGTDTLTITSLQPEDFATYYCQQNSYPFTFG 100  
Db 81 KFSGSGSGTDTLTITSLQPEDFATYYCQQNSYPFTFG 119

## RESULT 4

US-10-695-667-21  
; Sequence 21, Application US/10695667  
; Publication No. US20040161776A1  
; GENERAL INFORMATION:  
; APPLICANT: MADDON, Paul J.  
; APPLICANT: DONOVAN, Gerald P.  
; APPLICANT: OLSON, William C.  
; APPLICANT: SCHSLKE, Norbert  
; APPLICANT: GARDNER, Jason  
; APPLICANT: MA, Dangshe  
; TITLE OF INVENTION: PSMA FORMULATIONS AND USES THEREOF  
; FILE REFERENCE: P0741.70006US00  
; CURRENT APPLICATION NUMBER: US/10/695,667  
; CURRENT FILING DATE: 2003-10-27  
; PRIOR APPLICATION NUMBER: US 10/395,894  
; PRIOR FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: PCT/US02/33944  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/335,215  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/362,747  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/412,618  
; PRIOR FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-695-667-21

Query Match 91.8%; Score 479; DB 16; Length 127;  
Best Local Similarity 92.9%; Pred. No. 2.5e-34;  
Matches 92; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQMTQSPSSLSASVGRVTITCRASQGISHYLAWFQKPKAPKSLIYAASSLSQSGVPS 61  
Db 21 DIQMTQSPSSLSASVGRVTITCRASQGISHYLAWFQKPKAPKSLIYAASSLSQSGVPS 80

Qy 62 KFSGSGSGTDTLTITSLQPEDFATYYCQQNSYPFTFG 100  
Db 81 KFSGSGSGTDTLTITSLQPEDFATYYCQQNSYPFTFG 119

## RESULT 5

US-10-221-529-4

```
; Sequence 4, Application US/10221529
; Publication No. US20040038293A1
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS AG
; TITLE OF INVENTION: ANTIBODIES TO HUMAN CD154
; FILE REFERENCE: 4-31266A
; CURRENT APPLICATION NUMBER: US/10/221,529
; CURRENT FILING DATE: 2003-05-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-221-529-4

Query Match      90.8%; Score 474; DB 15; Length 107;
Best Local Similarity 91.9%; Pred. No. 5.8e-34;
Matches 91; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 99
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
US-10-703-714-4
; Sequence 4, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Haichun
; APPLICANT: Holmes, Steven
; APPLICANT: Mason, Sean
; APPLICANT: Mason, Sean
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
; FILE REFERENCE: MXI-294
; CURRENT APPLICATION NUMBER: US/10/703,714
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/424803
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-703-714-4

Query Match      90.2%; Score 471; DB 16; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.1e-33;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 99
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
US-10-703-714-8
; Sequence 8, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Haichun
; APPLICANT: Holmes, Steven
; APPLICANT: Mason, Sean
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
; FILE REFERENCE: MXI-294
; CURRENT APPLICATION NUMBER: US/10/703,714
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/424803
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-703-714-8

Query Match      90.2%; Score 471; DB 16; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.1e-33;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 99
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-10-703-714-16
; Sequence 16, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Haichun
; APPLICANT: Holmes, Steven
; APPLICANT: Mason, Sean
; APPLICANT: Mason, Sean
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
; FILE REFERENCE: MXI-294
; CURRENT APPLICATION NUMBER: US/10/703,714
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/424803
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-703-714-16

Query Match      90.2%; Score 471; DB 16; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.1e-33;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 99
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-10-783-311-126
; Sequence 126, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/449,515
```

```
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
; US-10-783-311-126

Query Match      89.5%; Score 467; DB 17; Length 108;
Best Local Similarity 89.9%; Pred. No. 2.4e-33;
Matches 89; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy  2 DIQLTQSPSSLASVGDVRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASLSQGVPS 61
Db  2 DIQMTQSPSSFSASTGDRVITTCRASQGISYLLAWYQQKPGKAPKLLIYAASLTQGVPS 61

Qy  62 KFGSGSGTDFTLTISSLPQEDFATYYCQQYNSYPFTFG 100
Db  62 KFGSGSGTDFTLTISSLPQEDFATYYCQQYNSYPFTFG 100

RESULT 10
US-10-194-975-61
; Sequence 61, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-194-975-61

Query Match      89.3%; Score 466; DB 14; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.5e-33;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy  2 DIQLTQSPSSLASVGDVRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASLSQGVPS 61
Db  1 DIQMTQSPSSLASVGDVRVITTCRASQGISNYLAWFOQKPGKAPKSLIYAASLSQGVPS 60

Qy  62 KFGSGSGTDFTLTISSLPQEDFATYYCQQYNSYP 96
Db  61 RFSGSGSGTDFTLTISSLPQEDFATYYCQQYNSYP 95

RESULT 11
US-10-308-817-8
; Sequence 8, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
```

```
; LENGTH: 95
; TYPE: PRT
; ORGANISM: human
; US-10-308-817-8

Query Match      89.3%; Score 466; DB 15; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.5e-33;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy  2 DIQLTQSPSSLASVGDVRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASLSQGVPS 61
Db  1 DIQMTQSPSSLASVGDVRVITTCRASQGISNYLAWFOQKPGKAPKSLIYAASLSQGVPS 60

Qy  62 KFGSGSGTDFTLTISSLPQEDFATYYCQQYNSYP 96
Db  61 RFSGSGSGTDFTLTISSLPQEDFATYYCQQYNSYP 95

RESULT 12
US-10-453-698-8
; Sequence 8, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 95
; TYPE: PRT
; ORGANISM: human
; US-10-453-698-8

Query Match      89.3%; Score 466; DB 15; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.5e-33;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy  2 DIQLTQSPSSLASVGDVRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASLSQGVPS 61
Db  1 DIQMTQSPSSLASVGDVRVITTCRASQGISNYLAWFOQKPGKAPKSLIYAASLSQGVPS 60

Qy  62 KFGSGSGTDFTLTISSLPQEDFATYYCQQYNSYP 96
Db  61 RFSGSGSGTDFTLTISSLPQEDFATYYCQQYNSYP 95

RESULT 13
US-10-379-392-68
; Sequence 68, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Mahiyat, Basil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-379-392-68
```

```
Query Match      89.3%; Score 466; DB 16; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.5e-33;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVITTCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFSGSGSGTDFTLTISSSLQPEDFATYYCQYNSYP 96
Db 61 RFSGSGSGTDFTLTISSSLQPEDFATYYCQYNSYP 95

RESULT 14
US-10-251-085B-145
; Sequence 145, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 145
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-145

Query Match      89.3%; Score 466; DB 15; Length 107;
Best Local Similarity 89.9%; Pred. No. 2.9e-33;
Matches 89; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVITTCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFSGSGSGTDFTLTISSSLQPEDFATYYCQYNSYP 100
Db 61 RFSGSGSGTDFTLTISSSLQPEDFATYYCQYNYPLTFG 99

RESULT 15
US-10-737-252-145
; Sequence 145, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 145
; LENGTH: 107
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; TYPE: PRT
; ORGANISM: human
US-10-737-252-145

Query Match      89.3%; Score 466; DB 16; Length 107;
Best Local Similarity 89.9%; Pred. No. 2.9e-33;
Matches 89; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVITTCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFSGSGSGTDFTLTISSSLQPEDFATYYCQYNSYP 100
Db 61 RFSGSGSGTDFTLTISSSLQPEDFATYYCQYNYPLTFG 99

Search completed: March 8, 2005, 07:05:57
Job time : 53.5981 secs
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**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 11.1056 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-38

Perfect score: 522

Sequence: 1 LDQLTQSPSLSASVGRV.....EDFATYYCQQNSVPTFTGP 101

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	90.6	109	2	US-07-934-373C-3
2	473	90.6	109	3	US-08-437-642B-3
3	473	90.6	109	4	US-08-146-206C-3
4	473	90.6	109	4	US-09-705-686-3
5	473	90.6	109	4	US-09-705-392A-3
6	473	90.6	109	4	US-09-705-398-3
7	473	90.6	109	5	PCT-US93-07832-3
8	465	89.1	107	2	US-07-934-373C-18
9	465	89.1	107	3	US-08-437-642B-18
10	465	89.1	107	4	US-08-146-206C-18
11	465	89.1	107	4	US-09-648-067A-14
12	465	89.1	107	4	US-09-705-686-18
13	465	89.1	107	4	US-09-705-392A-18
14	465	89.1	107	4	US-09-705-398-18
15	465	89.1	107	5	PCT-US93-07832-18
16	465	89.1	108	3	US-08-974-899-3
17	465	89.1	108	4	US-09-795-798-3
18	463	88.7	214	4	US-09-472-087-71
19	452	86.6	108	3	US-09-025-769B-14
20	452	86.6	108	4	US-09-490-070A-14
21	452	86.6	108	4	US-09-490-153-14
22	452	86.6	108	4	US-09-490-324-14
23	451	86.4	108	2	US-08-378-939-32
24	451	86.4	108	2	US-08-378-939-34
25	451	86.4	108	3	US-08-974-899-2
26	451	86.4	108	4	US-08-795-798-2
27	451	86.4	109	3	US-09-157-370-3

28	451	86.4	111	2	US-08-887-352B-7	Sequence 7, Appli
29	451	86.4	111	3	US-09-109-207C-7	Sequence 7, Appli
30	451	86.4	111	3	US-09-296-005-7	Sequence 7, Appli
31	451	86.4	111	4	US-09-920-171-7	Sequence 7, Appli
32	451	86.4	111	4	US-09-716-028-7	Sequence 7, Appli
33	451	86.4	111	4	US-10-113-996-7	Sequence 7, Appli
34	451	86.4	117	3	US-09-042-353-48	Sequence 48, Appli
35	451	86.4	117	3	US-08-758-417A-313	Sequence 313, App
36	446	85.6	236	4	US-09-859-053-30	Sequence 30, Appl
37	446	85.4	107	3	US-09-240-274-40	Sequence 40, Appl
38	446	85.4	109	3	US-09-025-769B-28	Sequence 28, Appl
39	446	85.4	109	3	US-09-025-769B-43	Sequence 43, Appl
40	446	85.4	109	4	US-09-490-070A-28	Sequence 28, Appl
41	446	85.4	109	4	US-09-490-153-28	Sequence 28, Appl
42	446	85.4	109	4	US-09-490-153-43	Sequence 43, Appl
43	446	85.4	109	4	US-09-490-324-28	Sequence 28, Appl
44	446	85.4	109	4	US-09-490-324-43	Sequence 43, Appl
45	446	85.4	109	4	US-09-490-324-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1  
US-07-934-373C-3  
; Sequence 3, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-07-934-373C-3

Query Match 90.6%; Score 473; DB 2; Length 109;  
Best Local Similarity 89.9%; Pred. No. 1.7e-35;  
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 DIQLTQSPSLSASVGRVITTCRASODISIYLANFQORFGKAPKSLIYAASSLQSGVPS 61

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Db 1 DIQWTSPLSASVGRVITTCRASQDVSSYLAWYQOKPKAPKLLIYAASSLSGVPS 60
Qy 62 KFSGSGSGTDTLTITISSLPQEDFATYYCQOYNSYPFTFG 100
Db 61 RFSGSGSGTDTLTITISSLPQEDFATYYCQOYNSLPYTFG 99

RESULT 2
US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-3

Query Match 90.6%; Score 473; DB 3; Length 109;
Best Local Similarity 89.9%; Pred. No. 1.7e-35;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQWTSPLSASVGRVITTCRASQDISIYLAWFOORPKAPKSLIYAASSLSGVPS 61
Db 1 DIQWTSPLSASVGRVITTCRASQDVSSYLAWYQOKPKAPKLLIYAASSLSGVPS 60
Qy 62 KFSGSGSGTDTLTITISSLPQEDFATYYCQOYNSYPFTFG 100
Db 61 RFSGSGSGTDTLTITISSLPQEDFATYYCQOYNSLPYTFG 99

RESULT 3
US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-3

Query Match 90.6%; Score 473; DB 3; Length 109;
Best Local Similarity 89.9%; Pred. No. 1.7e-35;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQWTSPLSASVGRVITTCRASQDISIYLAWFOORPKAPKSLIYAASSLSGVPS 61
Db 1 DIQWTSPLSASVGRVITTCRASQDVSSYLAWYQOKPKAPKLLIYAASSLSGVPS 60
Qy 62 KFSGSGSGTDTLTITISSLPQEDFATYYCQOYNSYPFTFG 100
Db 61 RFSGSGSGTDTLTITISSLPQEDFATYYCQOYNSLPYTFG 99

RESULT 4
US-09-705-686-3
; Sequence 3, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
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US-08-146-206C-3
; Sequence 3, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-3

Query Match 90.6%; Score 473; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1.7e-35;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQWTSPLSASVGRVITTCRASQDISIYLAWFOORPKAPKSLIYAASSLSGVPS 61
Db 1 DIQWTSPLSASVGRVITTCRASQDVSSYLAWYQOKPKAPKLLIYAASSLSGVPS 60
Qy 62 KFSGSGSGTDTLTITISSLPQEDFATYYCQOYNSYPFTFG 100
Db 61 RFSGSGSGTDTLTITISSLPQEDFATYYCQOYNSLPYTFG 99

RESULT 5
US-09-705-686-3
; Sequence 3, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/705,686  
FILING DATE: 02-NOV-1993  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P1D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-705-686-3

Query Match 90.6%; Score 473; DB 4; Length 109;  
Best Local Similarity 89.9%; Pred. No. 1.7e-35;  
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQQTSPSSLSASVGRVVTITCRASQDISIYLAWFOORPGKAPKSIYAAASSLSQSGVPS 61  
Db 1 DIQMTQSPSSLSASVGRVVTITCRASQDVSSYLAWYQOKPGKAPKLLIYAASSLSQSGVPS 60

Qy 62 KFGSGSGTDFTLTISSLPQEDFATYYCQYNSTPFTFG 100  
Db 61 RFGSGSGTDFTLTISSLPQEDFATYYCQYNSTPFTFG 99

RESULT 5

US-09-705-392A-3  
Sequence 3, Application US/09705392A  
Patent No. 6719971  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
Presta, Leonard G.  
TITLE OF INVENTION: Method for Making Humanized Antibodies  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/705,392A  
FILING DATE: 02-NOV-1993  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-705-392A-3

Query Match 90.6%; Score 473; DB 4; Length 109;  
Best Local Similarity 89.9%; Pred. No. 1.7e-35;  
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQQTSPSSLSASVGRVVTITCRASQDISIYLAWFOORPGKAPKSIYAAASSLSQSGVPS 61  
Db 1 DIQMTQSPSSLSASVGRVVTITCRASQDVSSYLAWYQOKPGKAPKLLIYAASSLSQSGVPS 60

Qy 62 KFGSGSGTDFTLTISSLPQEDFATYYCQYNSTPFTFG 100  
Db 61 RFGSGSGTDFTLTISSLPQEDFATYYCQYNSTPFTFG 99

RESULT 6

US-09-705-398-3  
Sequence 3, Application US/09705398  
Patent No. 6800738  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
Presta, Leonard G.  
TITLE OF INVENTION: Method for Making Humanized Antibodies  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/705,398  
FILING DATE: 02-NOV-1993  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/146206  
FILING DATE: 17-NOV-1993  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P1D2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-705-398-3

Query Match 90.6%; Score 473; DB 4; Length 109;  
Best Local Similarity 89.9%; Pred. No. 1.7e-35;  
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORFGKAPKSLIYAASSLSQGVPS 61  
Db 1 DIQMTQSPSSLSASVGRVITTCRASQDVSSYLAWYQQKFGKAPKLLIYAASSLSQGVPS 60  
Qy 62 KFSGSGSGTDTLTITSSLPQEDFATYYCQYNSVPFTFG 100  
Db 61 RFSGSGSGTDTLTITSSLPQEDFATYYCQYNSLPFTFG 99

## RESULT 7

PCT-US93-07832-3  
; Sequence 3, Application PC/TUS9307832  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07832  
; FILING DATE: 19930820  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/934373  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 709P2PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
PCT-US93-07832-3

Query Match 90.6%; Score 473; DB 5; Length 109;  
Best Local Similarity 89.9%; Pred. No. 1.7e-35;  
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORFGKAPKSLIYAASSLSQGVPS 61  
Db 1 DIQMTQSPSSLSASVGRVITTCRASQDVSSYLAWYQQKFGKAPKLLIYAASSLSQGVPS 60  
Qy 62 KFSGSGSGTDTLTITSSLPQEDFATYYCQYNSVPFTFG 100  
Db 61 RFSGSGSGTDTLTITSSLPQEDFATYYCQYNSLPFTFG 99

## RESULT 8

US-07-934-373C-18  
; Sequence 18, Application US/07934373C  
; Patent No. 5821337

; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-07-934-373C-18

Query Match 89.1%; Score 465; DB 2; Length 107;  
Best Local Similarity 89.9%; Pred. No. 8.5e-35;  
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORFGKAPKSLIYAASSLSQGVPS 61  
Db 1 DIQMTQSPSSLSASVGRVITTCRASQISNLYAWYQQKFGKAPKLLIYAASSLSQGVPS 60  
Qy 62 KFSGSGSGTDTLTITSSLPQEDFATYYCQYNSVPFTFG 100  
Db 61 RFSGSGSGTDTLTITSSLPQEDFATYYCQYNSLPFTFG 99

## RESULT 9

US-08-437-642B-18  
; Sequence 18, Application US/08437642B  
; Patent No. 6054297  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-18

Query Match      89.1%; Score 465; DB 3; Length 107;
Best Local Similarity 89.9%; Pred. No. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy  2 DIQLTQSPSSLSASVGRVTTTCRASQDISIYLAWFOORPKGKAPKSLIYAASSLSQSGVPS 61
Db  1 DIQMTQSPSSLSASVGRVTTTCRASQDISIYLAWFOORPKGKAPKSLIYAASSLSQSGVPS 60

Qy  62 KFGSGSGTDTFTLTISLQPEDFATYYCQVNSYPPTFG 100
Db  61 RFSGSGSGTDTFTLTISLQPEDFATYYCQVNSLPWTFG 99

RESULT 10
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-18

Query Match      89.1%; Score 465; DB 4; Length 107;
Best Local Similarity 89.9%; Pred. No. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy  2 DIQLTQSPSSLSASVGRVTTTCRASQDISIYLAWFOORPKGKAPKSLIYAASSLSQSGVPS 61
Db  1 DIQMTQSPSSLSASVGRVTTTCRASQDISIYLAWFOORPKGKAPKSLIYAASSLSQSGVPS 60

Qy  62 KFGSGSGTDTFTLTISLQPEDFATYYCQVNSYPPTFG 100
Db  61 RFSGSGSGTDTFTLTISLQPEDFATYYCQVNSLPWTFG 99

RESULT 11
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1775R1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
; US-09-648-067A-14

Query Match      89.1%; Score 465; DB 4; Length 107;
Best Local Similarity 89.9%; Pred. No. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy  2 DIQLTQSPSSLSASVGRVTTTCRASQDISIYLAWFOORPKGKAPKSLIYAASSLSQSGVPS 61
Db  1 DIQMTQSPSSLSASVGRVTTTCRASQDISIYLAWFOORPKGKAPKSLIYAASSLSQSGVPS 60

Qy  62 KFGSGSGTDTFTLTISLQPEDFATYYCQVNSYPPTFG 100
Db  61 RFSGSGSGTDTFTLTISLQPEDFATYYCQVNSLPWTFG 99

RESULT 12
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
```



;  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-705-398-18

Query Match 89.1%; Score 465; DB 4; Length 107;  
Best Local Similarity 89.9%; Pred. No. 8.5e-35;  
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAAASSLSQSGVPS 61  
Db 1 DIQMTQSPSSLSASVGRVITTCRASQDISIYNLAWYQQKPKAPKLLIYAAASSLESQVPS 60  
Qy 62 KFGSGSGTDFTLTISSLPQEDFATYYCQQYNSLPWTFG 100  
Db 61 RFGSGSGTDFTLTISSLPQEDFATYYCQQYNSLPWTFG 99

## RESULT 15

PCT-US93-07832-18  
; Sequence 18, Application PC/TUS9307832  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07832  
; FILING DATE: 19930820  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/934373  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 709P2PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
PCT-US93-07832-18

Query Match 89.1%; Score 465; DB 5; Length 107;  
Best Local Similarity 89.9%; Pred. No. 8.5e-35;  
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAAASSLSQSGVPS 61  
Db 1 DIQMTQSPSSLSASVGRVITTCRASQDISIYNLAWYQQKPKAPKLLIYAAASSLESQVPS 60

Qy 62 KFGSGSGTDFTLTISSLPQEDFATYYCQQYNSLPWTFG 100  
Db 61 RFGSGSGTDFTLTISSLPQEDFATYYCQQYNSLPWTFG 99

Search completed: March 8, 2005, 05:54:14  
Job time : 12.1056 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 11.3 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-39

Perfect score: 856

Sequence: 1 LTCTFSGFSLITRGVGVDMW.....PVTVMNSGALTSQVHTFQL 159

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.\*

2: PIR1.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488.5	57.1	124	2 A49002	Ig heavy chain v r
2	480.5	56.1	472	2 S31459	Ig gamma-1 chain -
3	474	55.4	220	2 A49444	Ig gamma-1 heavy c
4	450.5	52.6	241	2 S69131	Ig heavy chain (DO
5	449.5	52.5	374	2 S69339	Ig heavy chain v r
6	447.5	52.3	470	2 S22080	Ig heavy chain pre
7	442	51.6	231	2 PC4155	Ig gamma-2b chain
8	433	50.6	138	2 S31513	Ig heavy chain - h
9	411	48.0	119	2 S18555	Ig heavy chain v r
10	410.5	48.0	220	2 S68211	Ig heavy chain (Ma
11	410.5	48.0	444	2 PC4436	monoclonal antibod
12	393	45.9	121	1 GIHUHE	Ig heavy chain v-I
13	392	45.8	121	2 A36005	Ig heavy chain v r
14	389	45.4	213	2 S68213	Ig heavy chain (Ma
15	388	45.3	125	1 MEHUMC	Ig heavy chain v-I
16	383.5	44.8	548	2 S38864	Ig epsilon chain C
17	377	44.0	221	2 S49220	Ig gamma-1 chain -
18	371.5	43.4	118	2 S18556	Ig heavy chain v r
19	371	43.3	246	2 S38950	Ig gamma chain - m
20	371	43.3	446	2 S40295	Ig gamma-2a chain
21	362.5	42.3	469	2 S37483	Ig gamma-2a chain
22	357.5	41.8	122	2 S11740	Ig heavy chain pre
23	356.5	41.6	254	2 B31790	Ig heavy chain v r
24	355.5	41.5	231	2 B23746	Ig Fab region IV-J
25	351.5	41.1	474	1 G2MS11	Ig gamma-2b chain
26	350.5	40.9	475	2 S01321	Ig gamma-2b chain
27	348.5	40.7	143	2 PT0174	Ig heavy chain pre
28	348.5	40.7	214	2 PC4202	monoclonal antibod
29	347.5	40.6	113	2 S26465	Ig heavy chain v r

30 345.5 40.4 147 1 G2HUCS  
31 342 40.0 96 2 S26923  
32 340 39.7 549 2 S04845  
33 339.5 39.7 568 2 A34891  
34 338 39.5 143 2 S23624  
35 337 39.4 107 2 A49442  
36 336 39.3 96 2 S26924  
37 332.5 38.8 120 1 GIHUCO  
38 330 38.6 592 2 S25705  
39 323.5 37.8 116 2 S26328  
40 318 37.1 119 1 GIHUDW  
41 316 36.9 96 2 S26922  
42 316 36.9 509 2 S17597  
43 314 36.7 121 2 S09959  
44 313.5 36.6 380 2 S12839  
45 313 36.6 149 2 S30752

Ig heavy chain pre  
Ig heavy chain v r  
Ig heavy chain pre  
Ig heavy chain pre  
Ig heavy chain v r  
Ig heavy chain v r  
Ig heavy chain v r  
Ig heavy chain v-I  
Ig mu chain - shee  
Ig heavy chain v r  
Ig heavy chain v-I  
Ig heavy chain v r  
Ig delta chain (WI  
Ig heavy chain v r  
Ig heavy chain pre  
Ig heavy chain pre

#### ALIGNMENTS

##### RESULT 1

A49002

Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999

C/Accession: A49002

R/Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.;

Arthritis Rheum. 35, 900-904, 1992

A/Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene

A/Reference number: A49002; MUID:92352481; PMID:1322670

A/Accession: A49002

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-124 <STU>

A/Cross-references: GB:M0808; NID:G185515; PIDN:AA52989.1; PID:G567176

A/Experimental source: EBV-transformed lymphoblastoid cell line SSH23

A/Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBIP:110262)

C/Superfamily: immunoglobulin v region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 57.1%; Score 488.5; DB 2; Length 124;

Best Local Similarity 88.6%; Pred. No. 2.9e-34;

Matches 93; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

Qy 1 LTCTFSGFSLITRGVGVDMWIRQPPGKALWLIYWNDDKRYSPSLKSLRLTITKDTSKNQ 60

Db 20 LTCTFSGFSLTSGVGWIRQPPGKALEWLIYWNDDRRYSPSLKSLRLTITKDTSKNQ 79

Qy 61 VLTLTMTNMDPVDATYTCARHFFDSSGYV-PFDSWGQGLVSVSS 104

Db 80 VLTLTMTNMDPVDATYTCARHFFDSSGYVLPFDYWGQGLVTVSS 124

##### RESULT 2

S31459

Ig gamma-1 chain - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999

C/Accession: S31459

R/Patri, S.; Nau, F.

submitted to the EMBL Data Library, December 1992

A/Reference number: S31459

A/Accession: S31459

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-472 <PAT>

A/Cross-references: EMBL:X69797

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin

F;277-346/Domain: immunoglobulin homology <IMM>

```
Query Match          56.1%; Score 480.5; DB 2; Length 472;
Best Local Similarity 59.4%; Pred. No. 5.9e-33;
Matches 95; Conservative 17; Mismatches 43; Indels 5; Gaps 2;

QY 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 37 VTCTISGFSL--NNYGVDMVRQAPGKALEWLGSGYDEDIDYFVLKSLRLSIYKDTSKSQ 94
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 VVLTMTNMDPVDATATYCAHHFFDSS--GYPPDSWGQGTLYSVSSASTKGPSVFLAP 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 95 VSLTSLVTMTEDTAVYICARVDVSSHAFAIYASDFWFGGLLSVLASASTTPPKRVPLTS 154
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 CSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSQVHTF 157
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 155 CCGDTSSIVTLGCLVSSYMPPEPVTVWNSGALTSQVHTF 194
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
A49444
Ig gamma-1 heavy chain (New) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999
C;Accession: A49444
R;Saul, F.A.; Poljak, R.J.
Proteins 14, 363-371, 1992
A;Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A res
A;Reference number: A49444; MUID:93066153; PMID:1438175
A;Accession: A49444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-220 <SAU>
A;Note: this sequence modified after extraction from NCBI backbone
A;Note: this sequence report includes corrections based on crystal structure refinement
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;137-202/Domain: immunoglobulin homology <IMM>

Query Match          55.4%; Score 474; DB 2; Length 220;
Best Local Similarity 57.4%; Pred. No. 9e-33;
Matches 93; Conservative 19; Mismatches 34; Indels 16; Gaps 3;

QY 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 55
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 LTCTVSGTSF-----DDVYTWVVRQPPGKLEWIGVFTGTTLLDPSLRGRVTMLVN 72
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 56 TSKNQVLTMTNMDPVDATATYCAHHFFDSSGYPPFDSWGQGTLYSVSSASTKGPSVFL 115
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 TSKNQFSLRLSSVTAADTAVYICARNLIAGG-----IDVWGQGLVTVSSASTKGPSVFL 128
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 APCRSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSQVHTF 157
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 APSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSQVHTF 170
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
S69131
Ig heavy chain (DOT) - human (fragment)
N;Alternate names: anti-riboflavin IGG Fd fragment
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C;Accession: S69131
R;Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A;Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins
A;Reference number: S69130; MUID:95255298; PMID:7737190
A;Accession: S69131
A;Molecule type: protein
A;Residues: 1-241 <STO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: blocked amino end; heterotrimer; immunoglobulin; pyroglutamic acid
F;1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAR>
F;140-205/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
```

```
Query Match          52.6%; Score 450.5; DB 2; Length 241;
Best Local Similarity 57.3%; Pred. No. 9.4e-31;
Matches 90; Conservative 17; Mismatches 47; Indels 3; Gaps 2;

QY 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 ISCKASGYAF--ENYIHWVRQAPGLGLEWMGIFNPVAGAVSEKFRDRLVMSDTSANT 77
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 VVLTMTNMDPVDATATYCAHHFFDSSGYPPFDSWGQGTLYSVSSASTKGPSVFLAPCSR 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 VSMQLNRLNSDDTGRYFCARVSYDFS--QYGMVWGQGTIVIVSSASTKGPSVFLAPCSR 136
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 STSESTAALGCLVKDYFPEPVTVSNWNGALTSQVHTF 157
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 STSESTAALGCLVKDYFPEPVTVSNWNGALTSQVHTF 173
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140, 'C', 142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match          52.5%; Score 449.5; DB 2; Length 374;
Best Local Similarity 56.5%; Pred. No. 1.8e-30;
Matches 95; Conservative 13; Mismatches 35; Indels 25; Gaps 4;

QY 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 39 LTCTFGSFLSKSGVGVDMIRQPPGQALEWLALIFWDDDKRYSPSLRLTIYKDTSKNQ 98
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 VVLTMTNMDPVDATATYCAHHFFDSSGY---YPPDSWGQGTLYSVSSASTK----- 108
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 99 VVLTMTNMDPADTATATTCG---YSVEGYGGYGRFHSWGQGTLYSVSSSEPKSCKDTHTCPP 155
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 109 -----GPSVFLAPCSRST--SESTAALGCLVKDYFPEPVTVSNW 146
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 156 CPABELLGSGSVFLFPKPKDTLMISETPEVTCVVVDVSHEDPEVKEN 203
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
S22080
Ig heavy chain precursor (B/MT. 4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
```

```
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:g440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.3%; Score 447.5; DB 2; Length 470;
Best Local Similarity 56.3%; Pred. No. 3.5e-30;
Matches 89; Conservative 20; Mismatches 46; Indels 3; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGVWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 39 LTCTVSGFSL--SSYALTWVRQAPKALEWGGITSGGTTYNPALKSRSLTITKENSQ 96
Qy 61 VVLTMTNMDPVDATYTYCAHHFPDSSGYYPF--DSWGQGTLLVSVSSASTKGPSVFPAPCS 119
Db 97 VLSVSSVTPEDATYTYCARSTYGEVGDGATADAGQGLLVTVSSASTAPKVPYPLSQC 156
Qy 120 RSTSESTAALGCLVKDYRPPPTVTSWNSGALTSVHTF 157
Db 157 GDKSSSTVTLGCLVSSYMPPEPTVTWNSGALKSGVHTF 194

RESULT 7
PC4155
Ig gamma-2b chain V-C region Mabb23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C;Accession: PC4155
R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 169, 237-239, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
A;Reference number: PC4155; MUID:96194809; PMID:8647454
A;Accession: PC4155
A;Molecule type: mRNA
A;Residues: 1-231 <KWA>
A;Cross-references: GB:U28970; NID:g1262180; PIDN:AAC52489.1; PID:g1262181
A;Note: This protein has unusual amino acid compared with the conserved sequences of mou
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;1-231/Product: heavy chain #status predicted <MAT>
F;98-102/Region: unique D sequence
F;103-119/Region: V region
F;139-203/Domain: immunoglobulin homology <IMM>

Query Match 51.6%; Score 442; DB 2; Length 231;
Best Local Similarity 57.3%; Pred. No. 4.6e-30;
Matches 90; Conservative 18; Mismatches 45; Indels 4; Gaps 3;

Qy 1 LTCTFSGFSLITRGVGVWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 ITCTVSGFSL--TDYGVSWIRQPGKLEWLVWAGGSTFYNSGALKSRSLINKDNSKQ 77
Qy 61 VVLTMTNMDPVDATYTYCAHHFPDSSGYYPFDSWGQGTLLVSVSSASTKGPSVFPAPCSR 120
Db 78 VFLKQNSLHTDDTAMYYCVKH--EDRYDWY--FDVWAGTFTVTVSSAKTTPPSVYFLAPRCG 135
Qy 121 STSESTAALGCLVKDYRPPPTVTSWNSGALTSVHTF 157
Db 136 DTTGSSVTGLGCLVKGYFPPEPTVTWNSGSLSSVHTF 172
```

```
RESULT 8
S31513
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31513
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-138 <CHA>
A;Cross-references: EMBL:X69861; NID:g33084; PIDN:CAA49495.1; PID:g33085
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-114/Domain: immunoglobulin homology <IMM>

Query Match 50.6%; Score 433; DB 2; Length 138;
Best Local Similarity 80.6%; Pred. No. 1.5e-29;
Matches 83; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 1 LTCTFSGFSLITRGVGVWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 35 LTCTFSGFSLSTSGVGVWIRQPGKLTLEWLIYWNDDKRYSPSLKSLRLTITKDTSQN 94
Qy 61 VVLTMTNMDPVDATYTYCAHHFPDSSGYYPFDSWGQGTLLVSVS 103
Db 95 VVLTMTNMDPVDATYTYCAHPRGIATVGGNFDYWGQGTLLVTVS 137

RESULT 9
S18555
Ig heavy chain V region precursor (VII-5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 21-Jul-2000
C;Accession: S18555
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Hc
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18555
A;Molecule type: DNA
A;Residues: 1-119 <SHI>
A;Cross-references: EMBL:X62111; NID:g37839; PIDN:CAA44021.1; PID:g3980125
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-119/Product: Ig heavy chain V region (VII-5) #status predicted <MAT>
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 48.0%; Score 411; DB 2; Length 119;
Best Local Similarity 95.0%; Pred. No. 9.1e-28;
Matches 76; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LTCTFSGFSLITRGVGVWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 39 LTCTFSGFSLSTSGVGVWIRQPGKALEWLIYWNDDKRYSPSLKSLRLTITKDTSKNQ 98
Qy 61 VVLTMTNMDPVDATYTYCAH 80
Db 99 VVLTMTNMDPVDATYTYCAH 118

RESULT 10
S68211
Ig heavy chain (Mab13-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000
```

C;Accession: S68211  
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
FEBS Lett. 375, 273-276, 1995  
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
A;Reference number: S68211; MUID:96085223; PMID:7498516  
A;Accession: S68211  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-220 <TAK>  
A;Cross-references: EMBL:D29669; NID:g473958; PIDN:BA06140.1; PID:g473959  
A;Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequence  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;136-200/Domain: immunoglobulin homology <IMM>

Query Match 48.0%; Score 410.5; DB 2; Length 220;  
Best Local Similarity 51.2%; Pred. No. 2e-27;  
Matches 82; Conservative 22; Mismatches 47; Indels 9; Gaps 3;

Qy 1 LTCFSGFLITRGVGDWIRQPGKALQWLALYWNDDK---RYSPSLKSLRLTIKDTKS 57  
Db 16 LSLTSGFTF--SNYRMHLRQPPGKLEIAVITVKSNDYGAKYAESVGRFTISRDDS 73

Qy 58 KNQVLTWNTMNDPVDATYYCAHHFFDSSGGYPPDPSWGQGLTVSVSSASTKGPSVFPLAP 117  
Db 74 KSSVYLQMNRLREEDTATYYCCR-----TPWVYAMDCWGQGLTVSVSSAKTTPPSVYPLAP 129

Qy 118 CSRSTSSSTAALGCLVKDYPPPEVTVSWNSGALTSGVHTF 157  
Db 130 GSAAQTNSMTLGLCLVKGYFPEPVTVWNSGSLSSGVHTF 169

RESULT 11  
PC4436  
monoclonal antibody 13-1 heavy chain - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
C;Accession: PC4436  
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin  
A;Reference number: JC5810; MUID:980632277; PMID:9398605  
A;Accession: PC4436  
A;Molecule type: protein  
A;Residues: 1-444 <AKA>  
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;251-320/Domain: immunoglobulin homology <IMM>  
F;99/Disulfide bonds: interchain (to 98) #status predicted  
F;99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 48.0%; Score 410.5; DB 2; Length 444;  
Best Local Similarity 51.2%; Pred. No. 4.2e-27;  
Matches 82; Conservative 22; Mismatches 47; Indels 9; Gaps 3;

Qy 1 LTCFSGFLITRGVGDWIRQPGKALQWLALYWNDDK---RYSPSLKSLRLTIKDTKS 57  
Db 20 LSLTSGFTF--SNYRMHLRQPPGKLEIAVITVKSNDYGAKYAESVGRFTISRDDS 77

Qy 58 KNQVLTWNTMNDPVDATYYCAHHFFDSSGGYPPDPSWGQGLTVSVSSASTKGPSVFPLAP 117  
Db 78 KSSVYLQMNRLREEDTATYYCCR-----TPWVYAMDCWGQGLTVSVSSAKTTPPSVYPLAP 133

Qy 118 CSRSTSSSTAALGCLVKDYPPPEVTVSWNSGALTSGVHTF 157  
Db 134 GSAAQTNSMTLGLCLVKGYFPEPVTVWNSGSLSSGVHTF 173

RESULT 12  
GIHUHE  
Ig heavy chain V-II region (He) - human  
C;Species: Homo sapiens (man)  
C;Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 09-Jul-2004  
C;Accession: A02093

R;Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 64, 997-1003, 1969  
A;Title: Subgroups of amino acid sequences in the variable regions of immunoglobulin heavy  
A;Reference number: A02093; MUID:70114712; PMID:5264153  
A;Accession: A02093  
A;Molecule type: protein  
A;Residues: 1-121 <GUN>  
A;Cross-references: UNIPROT:P01818  
C;Comment: This gamma-1 chain was isolated from a myeloma protein.  
C;Genetics:  
A;Gene: GDB:IGHV@  
A;Cross-references: GDB:128528; OMIM:147070  
A;Map position: 14q32.33-14q32.33  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: blocked amino end; heterotetramer; immunoglobulin  
F;15-100/Domain: immunoglobulin homology <IMM>  
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status

Query Match 45.9%; Score 393; DB 1; Length 121;  
Best Local Similarity 70.6%; Pred. No. 3e-26;  
Matches 77; Conservative 9; Mismatches 11; Indels 12; Gaps 3;

Qy 1 LTCFSGFLITRGVGDWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTIKDTSKN 59  
Db 20 LTCFSGFLITRGVGDWIRQPGKALEWLAIDWDDDKRFSPSLKSLRLTIKDTSKN 79

Qy 60 QVLTWNTMNDPVDATYYCAHHFFDSSGGYVP---FDSWGQGLTVSVSS 104  
Db 80 QVLTWNTMNDPVDATYYCVHR-----HPRTLAFDVGQGLTKVAVSS 121

RESULT 13  
A36005  
Ig heavy chain V region (M60) - human  
C;Species: Homo sapiens (man)  
C;Date: 21-Dec-1990 #sequence\_revision 13-Sep-1991 #text\_change 16-Dec-1998  
C;Accession: A36005  
R;Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A;Reference number: A36005; MUID:90349571; PMID:2117273  
A;Accession: A36005  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-121 <SCH>  
A;Cross-references: GB:M34027  
C;Genetics:  
A;Gene: GDB:IGH@; IGHDX1  
A;Cross-references: GDB:118731; OMIM:146910  
A;Map position: 14q32.33-14q32.33  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 45.8%; Score 392; DB 2; Length 121;  
Best Local Similarity 75.0%; Pred. No. 3.7e-26;  
Matches 78; Conservative 7; Mismatches 17; Indels 2; Gaps 1;

Qy 1 LTCFSGFLITRGVGDWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTIKDTSKN 60  
Db 20 LTCFSGFLITSGMCMVSWIRQPGKALEWLAIDWDDDKYYSTSLKRLTIKDTSKN 79

Qy 61 VLVTWNTMNDPVDATYYCAHHFFDSSGGYPPDPSWGQGLTVSVSS 104  
Db 80 VLVTWNTMNDPVDATYYCARINNWGGY--FDLWGRGLTVTVSS 121

RESULT 14  
S68213  
Ig heavy chain (Mab03-1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 29-Jul-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: S68213



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 59.3785 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-39  
Perfect score: 856  
Sequence: 1 LTCFSGFSLITRGVGDWI.....PVTVMNSGALTSQVHTFQL 159

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	60.5	476	2 Q6GMX1	Q6gm1 homo sapien
2	516	60.3	476	2 Q6MZK7	Q6mzx7 homo sapien
3	513.5	60.0	465	2 Q6GMX6	Q6gm6 homo sapien
4	506.5	59.2	473	2 Q8TC63	Q8tc63 homo sapien
5	496	57.9	493	2 Q68CN4	Q68cn4 homo sapien
6	494.5	57.8	473	2 Q6P055	Q6p055 homo sapien
7	493.5	57.7	544	2 Q6PJ95	Q6pj95 homo sapien
8	493	57.6	417	2 Q6N093	Q6n093 homo sapien
9	489	57.1	472	2 Q6N089	Q6n089 homo sapien
10	484	56.5	470	2 Q6PJ44	Q6pja4 homo sapien
11	482	56.3	464	2 Q6MZU6	Q6mzu6 homo sapien
12	476	55.6	482	2 Q7Z351	Q7z351 homo sapien
13	474	55.4	480	2 Q6N094	Q6n094 homo sapien
14	471.5	55.1	465	2 Q6P6C4	Q6p6c4 homo sapien
15	471	55.0	466	2 Q6IN78	Q6in78 homo sapien
16	470	54.9	478	2 Q6PI81	Q6pi81 homo sapien
17	466	54.4	521	2 Q8N4Y9	Q8n4y9 homo sapien
18	465.5	54.4	473	2 Q6MZV7	Q6mzv7 homo sapien
19	463.5	54.1	475	2 Q6MZQ6	Q6mq6 homo sapien
20	458.5	53.6	518	2 Q6N030	Q6n030 homo sapien
21	454.5	53.1	475	2 Q6N095	Q6n095 homo sapien
22	452	52.8	466	2 Q6N096	Q6n096 homo sapien
23	452	52.8	470	2 Q7Z5W1	Q7z5w1 homo sapien
24	450.5	52.6	481	2 Q6N097	Q6n097 homo sapien
25	440.5	51.5	469	2 Q7Z7P5	Q7z7p5 homo sapien
26	436.5	51.0	208	2 Q6ZP87	Q6zpb87 homo sapien
27	434	50.7	121	2 Q9UL96	Q9ul96 homo sapien
28	433.5	50.6	475	2 Q6GMW7	Q6gmw7 homo sapien
29	431	50.4	480	2 Q6PJ21	Q6pj21 homo sapien
30	409.5	47.8	471	2 Q66K04	Q66k04 mus musculus
31	393	45.9	121	1 HV2E_HUMAN	P01818 homo sapien

32	388.5	45.4	465	2	Q6PJB2	Q6pjb2 mus musculus
33	388	45.3	125	1	HV2D_HUMAN	P01817 homo sapien
34	385	45.0	458	2	Q65ZQ1	Q65zq1 homo sapien
35	383	44.7	464	2	Q6PIP8	Q6pip8 mus musculus
36	379.5	44.3	463	2	Q99LC4	Q99lc4 mus musculus
37	376	43.9	492	2	Q7Z374	Q7z374 homo sapien
38	375.5	43.9	473	2	Q91Z05	Q91z05 mus musculus
39	370	43.2	470	2	Q7TMK1	Q7tmk1 mus musculus
40	370	43.2	605	2	Q6GN83	Q6gn83 xenopus lae
41	368	43.0	472	2	Q6PJA7	Q6pja7 mus musculus
42	364.5	42.6	496	2	Q96KX8	Q96kx8 homo sapien
43	356	41.6	473	2	Q9D8L4	Q9d8l4 mus musculus
44	355	41.5	585	2	Q6GPX4	Q6gpx4 xenopus lae
45	351	41.0	484	2	Q6PF95	Q6pf95 mus musculus

ALIGNMENTS

RESULT 1  
Q6GMX1 PRELIMINARY; PRT; 476 AA.  
AC Q6GMX1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (human).  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MDLLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M.J., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Srausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073773; AAH73773.1; -;  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig ci.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR PROSITE; PSS00290; IG\_MHC; UNKNOWN\_2.





## RESULT 4

Q8TC63 ID Q8TC63 PRELIMINARY; PRT; 473 AA.  
AC Q8TC63  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGHG4 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,  
RA Krzywinski M.I., Skalski A., Smalusz D.B., Schnerch A., Schein J.B.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Strausberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC025985; AA025985.1; -.  
DR HSP; P01861; IADQ.  
DR InterPro; IPR000923; BlueCu\_1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00196; COPPER\_BLUE; UNKNOWN\_1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 59.2%; Score 506.5; DB 2; Length 473;  
Best Local Similarity 63.3%; Pred. No. 5.6e-41;  
Matches 100; Conservative 17; Mismatches 36; Indels 5; Gaps 2;  
Qy 1 LTCTFSGSLITRGVGVWIRQPGKALOWLALYVNDKKR-YSPSLKSLRTITKDTSKN 60  
Db 46 LTCTVSGDSVASSSYNGWVRQPPGKLEWIGTINFGNMYSPSLRSRVMTSDMSNS 105  
Qy 61 VLTMTNMDPVDATYTC-AHHPDSSGYVFPDSSGQGLVSVSSASTKGPSVFPLAPS 119  
Db 106 FYLKLDVTAADTAVYCAAGHVMGFAH---WGQKLVSVSPASTKGPSVFPLAPS 161  
Qy 120 RSTSESTAALGCLVKDYFPPEPTVSMNSGALTSVGHFT 157  
Db 162 RSTSESTAALGCLVKDYFPPEPTVSMNSGALTSVGHFT 199

## RESULT 5

Q68CN4 ID Q68CN4 PRELIMINARY; PRT; 493 AA.  
AC Q68CN4  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein DKFZp686E23209 (Fragment).  
GN Name=DKFZp686E23209;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Rectum tumor;  
RG The German cDNA Consortium;  
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,  
RA Osanger A., Pobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR749861; CAH18705.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 493 AA; 54117 MW; A1E4F5ED3FABAB40 CRC64;

Query Match 57.9%; Score 496; DB 2; Length 493;  
Best Local Similarity 60.9%; Pred. No. 6.3e-40;  
Matches 98; Conservative 17; Mismatches 40; Indels 6; Gaps 3;  
Qy 1 LTCTFSGSLITRGVGVWIRQPGKALOWLALYVNDKKR-YSPSLKSLRTITKDTSKN 59  
Db 62 LSCAAGDFDST--YAHHWVRQSPRLWVAVISYEGGKHQVADSVKGRATISRDNSNK 119  
Qy 60 QVVLTMTNMDPVDATYTC-AHHPDSSGY---YFPDSSGQGLVSVSSASTKGPSVFPLA 116  
Db 120 TVSLQLSLSTEDTGVVYCYCARDPLPLSSWHTNVALDVWGQGTAVIVSSASTKGPSVFPLA 179  
Qy 117 PCSRSTSESTAALGCLVKDYFPPEPTVSMNSGALTSVGHFT 157  
Db 180 PCSRSTSESTAALGCLVKDYFPPEPTVSMNSGALTSVGHFT 220

## RESULT 6

Q6P055 ID Q6P055 PRELIMINARY; PRT; 473 AA.  
AC Q6P055  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 03-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral Nervous System;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,



RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fodo G., Han M., Wiemann S.,  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640623; CAB45777.1; -.  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig.cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;

Query Match 57.6%; Score 493; DB 2; Length 417;  
 Best Local Similarity 67.9%; Pred. No. 1e-39;  
 Matches 95; Conservative 15; Mismatches 26; Indels 4; Gaps 2;

QY 19 WIRPPGKALQWALI-YWDDKRYSPSLKSLRLTITKDTSKNOVLTNNMDPVDVDTATYY 77  
 Db 8 WVRQAPGKLEWAVIAIYDGTQYADSVRGRTFLENNLSRPEDTAVY 67  
 QY 78 CAHFFDSSGGYYPFDSWGQGLVSVSSASTKPSVFPPLAPCSRSTSESTAALGCLVKDYF 137  
 Db 68 CAK---AHSGTSKDPWQGGTLVTVSSASTKPSVFPPLAPCSRSTSESTAALGCLVKDYF 124

QY 138 PEPVTVSNNGALTSQGVHTF 157  
 Db 125 PEPVTVSNNGALTSQGVHTF 144

## RESULT 9

Q6N089 PRELIMINARY; PRT; 472 AA.  
 ID Q6N089  
 AC Q6N089  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686P15220.  
 GN Name=DKFZp686P15220;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RG The German Human cDNA Consortium;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fodo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640627; CAB45781.1; -.  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig.cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 57.1%; Score 489; DB 2; Length 472;  
 Best Local Similarity 59.5%; Pred. No. 2.9e-39;  
 Matches 97; Conservative 18; Mismatches 36; Indels 12; Gaps 4;  
 QY 1 LCTCFSGSLITRGVGVWDIROPKQKALQWALILYWNDDK-RYSPSLKSLRLTITKDTSKN 59  
 Db 39 LSCAASGFTF--DDYAHWHVROAPKGLGWVSGISWNSGSYAYADSVKGRFTISRDCKN 96  
 QY 60 QVLTMTNMDPVDVDTATYYC-----AHFFDSSGGYYPFDSWGQGLVSVSSASTKPSVFP 114  
 Db 97 SLYLQMSLRAEDTALYYCAKEIGHNFFY----YGMVDVWQGGTLVTVSSASTKPSVFP 152  
 QY 115 LAPCSRSTSESTAALGCLVKDYFPPEPVTVSNNGALTSQGVHTF 157  
 Db 153 LAPSSKSTSGTAAALGCLVKDYFPPEPVTVSNNGALTSQGVHTF 195

## RESULT 10

Q6PJM4 PRELIMINARY; PRT; 470 AA.  
 ID Q6PJM4  
 AC Q6PJM4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Colling P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018747; AAH18747.1; -.  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig.cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS0835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;



[illegible]

```
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0CDEB81076E CRC64;

Query Match 55.0%; Score 471; DB 2; Length 466;
Best Local Similarity 59.1%; Pred. No. 1.6e-37;
Matches 94; Conservative 20; Mismatches 35; Indels 10; Gaps 3;

Qy 1 LTCFTSGFSLITRGVGVNDIRQPPGKALQWLALIYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
39 LSCAASGLTVSSN--YMHVVRQAPGKGLEWVSVLYIGGATYYADSVKGRFTISRDNKNT 96

Qy 61 VVLTMTNMDPVDATATYYCAHHFFDSSGVY--PFDSWGOGTLVSVSSASTKGPSVFPLAPC 118
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
97 LYLQMNLSRAEDTAVYYCAR-----GNYVVPAPWGOGTLVTVSSASTKGPSVFPLAPS 150

Qy 119 SRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTF 157
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
151 SKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTF 189
```

Search completed: March 8, 2005, 06:35:57  
Job time : 60.3785 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 73.7167 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-39  
Perfect score: 856  
Sequence: 1 LTCTFSGLITRGVGDWI.....PVTVWNSGALTSGVHTFQL 159

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	856	100.0	159	2 AAY34307	Aay34307 Igg antib
2	766	89.5	149	2 AAY34305	Aay34305 Igg antib
3	700.5	81.8	517	6 ABU08019	Abu08019 Monoclonal
4	700.5	81.8	518	7 ADF65782	Adf65782 Human ant
5	700.5	81.8	518	8 ADJ92518	Adj92518 Human SOJ
6	678.5	79.3	448	8 ADF71916	Adf71916 Hu3G8VH-2
7	670	78.3	453	6 ABP58287	Abp58287 Humanised
8	670	78.3	472	6 ABP58289	Abp58289 Humanised
9	664.5	77.6	448	8 ADF71908	Adf71908 Hu3G8VH-1
10	664.5	77.6	448	8 ADF71912	Adf71912 Hu3G8VH-5
11	664	77.6	228	7 ADJ32130	Adj32130 Human int
12	644.5	75.3	450	5 ABP66596	Abp66596 Human RSV
13	644.5	75.3	450	5 ABP66594	Abp66594 Human RSV
14	644.5	75.3	450	5 ABP66598	Abp66598 Human RSV
15	644.5	75.3	450	5 ABP66564	Abp66564 Human RSV
16	644.5	75.3	450	5 ABP66592	Abp66592 Human RSV
17	644.5	75.3	450	5 ABP66600	Abp66600 Human RSV
18	644.5	75.3	450	6 ABU69427	Abu69427 Respirato
19	644.5	75.3	450	6 ABU69455	Abu69455 Respirato
20	644.5	75.3	450	6 ABU69459	Abu69459 Respirato
21	644.5	75.3	450	6 ABU69457	Abu69457 Respirato
22	644.5	75.3	450	6 ABU69463	Abu69463 Respirato
23	644.5	75.3	450	6 ABU69461	Abu69461 Respirato
24	644.5	75.3	450	7 ADE35952	Ade35952 SYNAGIS a
25	644.5	75.3	450	7 ADE35956	Ade35956 SYNAGIS a

26	644.5	75.3	450	7 ADE35958	Ade35958 SYNAGIS a
27	644.5	75.3	450	7 ADE35954	Ade35954 SYNAGIS a
28	644.5	75.3	450	7 ADE35922	Ade35922 SYNAGIS a
29	644.5	75.3	450	7 ADE35950	Ade35950 SYNAGIS a
30	643.5	75.2	450	5 ABP66562	Abp66562 Human RSV
31	643.5	75.2	450	6 ABU69425	Abu69425 Respirato
32	643.5	75.2	450	7 ADE35920	Ade35920 SYNAGIS a
33	641.5	74.9	434	7 ADE35960	Ade35960 SYNAGIS a
34	641.5	74.9	450	5 ABP66590	Abp66590 Human RSV
35	641.5	74.9	450	5 ABP66588	Abp66588 Human RSV
36	641.5	74.9	450	5 ABP66602	Abp66602 Human RSV
37	641.5	74.9	450	5 ABP66586	Abp66586 Human RSV
38	641.5	74.9	450	6 ABU69451	Abu69451 Respirato
39	641.5	74.9	450	6 ABU69453	Abu69453 Respirato
40	641.5	74.9	450	6 ABU69465	Abu69465 Respirato
41	641.5	74.9	450	6 ABU69449	Abu69449 Respirato
42	641.5	74.9	450	7 ADE35948	Ade35948 SYNAGIS a
43	641.5	74.9	450	7 ADE35946	Ade35946 SYNAGIS a
44	641.5	74.9	450	7 ADE35944	Ade35944 SYNAGIS a
45	640.5	74.8	450	4 AAE10517	Aae10517 Humanised

## ALIGNMENTS

RESULT 1  
AAY34307  
ID AAY34307 standard; protein; 159 AA.

XX AC AAY34307;  
XX DT 19-NOV-1999 (first entry)  
XX DE Igg antibody 2.3.2 heavy chain sequence.  
XX KW Antibody: CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX OS Homo sapiens.  
XX PN WO9945031-A2.  
XX PD 10-SEP-1999.  
XX PF 03-MAR-1999; 99WO-US004583.  
XX PR 03-MAR-1998; 98US-00034607.  
XX PR 03-FEB-1999; 99US-00244253.  
XX PA (ABGE-) ABGENIX INC.  
XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;  
XX DR WPI; 1999-540816/45.  
XX DR N-PSDB; AAZ20408.  
XX FT New monoclonal antibody, used for treating e.g. graft versus host  
XX PT disease, cancer, autoimmune diseases and inflammatory diseases.  
XX PS Claim 60; Fig 32; 245pp; English.  
XX CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the Igm Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
XX (e.g. lupus), and inflammatory diseases (e.g. arthritis)  
SQ Sequence 159 AA;  
Query Match 100.0%; Score 856; DB 2; Length 159;  
Best Local Similarity 100.0%; Pred. No. 5.1e-70;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LTCTFSGFSLITRGVGVDMIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITKDTSKNQ 60  
Db 1 LTCTFSGFSLITRGVGVDMIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITKDTSKNQ 60  
Qy 61 VVLTMTNMDPVDATYTYCAHHFFDSSGYPPFDSGQGTLSVSSASTKGPSVFLAPCSR 120  
Db 61 VVLTMTNMDPVDATYTYCAHHFFDSSGYPPFDSGQGTLSVSSASTKGPSVFLAPCSR 120  
Qy 121 STSESTAALGCLVKDYFPEPVTWNSGALTSGVHTFQL 159  
Db 121 STSESTAALGCLVKDYFPEPVTWNSGALTSGVHTFQL 159  
RESULT 2  
AAV34305  
ID AAY34305 standard; protein; 149 AA.  
XX  
AC AAY34305;  
XX  
DT 19-NOV-1999 (first entry)  
XX  
DE Igg antibody 2.4.4 heavy chain sequence.  
XX  
KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.  
XX  
OS Homo sapiens.  
XX  
PN WO9945031-A2.  
XX  
PD 10-SEP-1999.  
XX  
PF 03-MAR-1999; 99WO-US004583.  
XX  
PR 03-MAR-1998; 98US-00034607.  
PR 03-FEB-1999; 99US-00244253.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;  
XX  
DR WPI; 1999-540816/45.  
DR N-PSDB; AAZ20406.  
XX  
PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.  
XX  
PS Claim 60; Fig 30; 245pp; English.  
XX  
CC This sequence represents the heavy chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the Igm Mab ABX-CBL, providing that the antibody is not CBL1. The Mab  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood  
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases  
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)

SQ Sequence 149 AA;  
Query Match 89.5%; Score 766; DB 2; Length 149;  
Best Local Similarity 100.0%; Pred. No. 7.6e-62;  
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LTCTFSGFSLITRGVGVDMIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITKDTSKNQ 60  
Db 8 LTCTFSGFSLITRGVGVDMIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITKDTSKNQ 67  
Qy 61 VVLTMTNMDPVDATYTYCAHHFFDSSGYPPFDSGQGTLSVSSASTKGPSVFLAPCSR 120  
Db 68 VVLTMTNMDPVDATYTYCAHHFFDSSGYPPFDSGQGTLSVSSASTKGPSVFLAPCSR 127  
Qy 121 STSESTAALGCLVKDYFPEPVT 142  
Db 128 STSESTAALGCLVKDYFPEPVT 149  
RESULT 3  
ABU08019  
ID ABU08019 standard; protein; 517 AA.  
XX  
AC ABU08019;  
XX  
DT 10-MAY-2003 (first entry)  
XX  
DE Monoclonal rabies virus antibody heavy chain, clone JB.1.  
XX  
KW Human; antibody; constant region; monoclonal antibody 57; Mab 57;  
KW variable region; Rabies; neurological disease; infection;  
KW central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;  
KW pathogen; vaccine; virucide; heavy chain.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016501-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 21-AUG-2002; 2002WO-US026584.  
XX  
PR 21-AUG-2001; 2001US-0314023P.  
XX  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
PI Hooper DC, Dietzschold B;  
XX  
DR WPI; 2003-278566/27.  
DR N-PSDB; ABX12861.  
XX  
PT New recombinant antibody comprising a constant region of Mab 57 linked to  
PT a non-Mab 57 variable region, useful for treating an individual exposed  
PT to a pathogen, e.g. rabies infection.  
XX  
PS Claim 1; Page 35; 38pp; English.  
XX  
CC The invention discloses a recombinant antibody comprising a constant  
CC region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable  
CC region. Rabies is an acute, neurological disease caused by infection of  
CC the central nervous system with the rabies virus, a member of the  
CC Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods  
CC for producing an isolated recombinant antibody by culturing a host cell,  
CC containing a recombinant expression vector comprising the nucleic acid  
CC molecule encoding the antibody, and isolating the recombinant antibody  
CC expressed and treating an individual exposed to a pathogen by  
CC administering to the individual the recombinant antibody. The recombinant  
CC antibodies are useful for preventing (vaccine) and treating an individual  
CC exposed to a pathogen, e.g. rabies infection. They are also useful for  
CC the qualitative and quantitative determination of the rabies virus. The  
CC sequences presented are the antibody protein fragments, the nucleic acids  
CC encoding them or the PCR primers used to construct the recombinant  
CC expression vector



XX SQ Sequence 517 AA;  
Query Match 81.8%; Score 700.5; DB 6; Length 517;  
Best Local Similarity 84.2%; Pred. No. 3e-55;  
Matches 133; Conservative 9; Mismatches 13; Indels 3; Gaps 2;  
Qy 1 LTCFSGSLTRGVGVWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 39 LTCFSGSLSTSGVGWIRQPGKALEWVTLIYWDKRYSPSLENRVIRKDTSKNQ 98  
Qy 61 VLTMTNMDPVDATYYCAHFFDSSGYYP-FDSWGQGLTVSVSSASTKGPSVFLAPCS 119  
Db 99 VALTMTNMDPLDTGTYTCAHROHISS--FPWFDWGQGLTVSVSSASTKGPSVFLAPCS 156  
Qy 120 RSTSESTAALGCLVKDYPPPTVTVSNWNSGALTSGVHTF 157  
Db 157 RSTSGTAAALGCLVKDYPPPTVTVSNWNSGALTSGVHTF 194  
RESULT 4  
ADP65782  
ID ADP65782 standard; protein; 518 AA.  
XX AC ADP65782;  
XX DT 12-FEB-2004 (first entry)  
XX DE Human anti-rabies MAb JB.1 antibody heavy chain.  
XX KW Immunoglobulin; Ig; heavy chain; light chain; human;  
XX KW monoclonal rabies virus neutralising antibody; rabies virus protein;  
XX KW neuronal tissue; antirabies; MAb JB.1.  
XX OS Homo sapiens.  
XX PN US2003157112-A1.  
XX PD 21-AUG-2003.  
XX PF 21-AUG-2002; 2002US-00225108.  
XX PR 16-MAY-2000; 2000US-0204518P.  
XX PR 04-MAY-2001; 2001US-00848832.  
XX PR 21-AUG-2001; 2001US-0314023P.  
XX PA (HOOP/) HOOPER D C.  
XX PA (DIET/) DIETZSCHOLD B.  
XX PI Hooper DC, Dietzschold B;  
XX DR WPI; 2003-777974/73.  
XX DR N-PSDB; ADP65781.  
XX PT New isolated nucleic acid molecule encoding a sequence that neutralizes  
XX PT an antibody that binds to rabies virus protein, useful for diagnosing,  
XX PT preventing or treating infection of pathogens that target neuronal  
XX PT tissues, e.g. rabies.  
XX PS Claim 2; SEQ ID NO 10; 22pp; English.  
XX CC The present invention relates to the isolation of immunoglobulin (Ig)  
XX CC heavy and light chains of human monoclonal rabies virus neutralising  
XX CC antibody, and the polynucleotide sequences encoding them. The antibody  
XX CC specifically binds to a rabies virus protein. Also disclosed is a fused  
XX CC gene encoding a chimeric immunoglobulin light or heavy chain comprising a  
XX CC first DNA sequence encoding an immunoglobulin light or heavy chain  
XX CC variable region of a monoclonal rabies virus neutralising antibody  
XX CC produced by a heterohybridoma cell line and a second DNA sequence  
XX CC encoding a human light or heavy chain constant region, and methods of  
XX CC producing a recombinant antibody. The polynucleotide sequences,  
XX CC antibodies and methods are useful for diagnosing, preventing or treating  
XX CC an infection of pathogens that target neuronal tissues, particularly

CC rabies. The present sequence represents human anti-rabies MAb JB.1  
CC antibody heavy chain.  
XX SQ Sequence 518 AA;  
Query Match 81.8%; Score 700.5; DB 7; Length 518;  
Best Local Similarity 84.2%; Pred. No. 3e-55;  
Matches 133; Conservative 9; Mismatches 13; Indels 3; Gaps 2;  
Qy 1 LTCFSGSLTRGVGVWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 39 LTCFSGSLSTSGVGWIRQPGKALEWVTLIYWDKRYSPSLENRVIRKDTSKNQ 98  
Qy 61 VLTMTNMDPVDATYYCAHFFDSSGYYP-FDSWGQGLTVSVSSASTKGPSVFLAPCS 119  
Db 99 VALTMTNMDPLDTGTYTCAHROHISS--FPWFDWGQGLTVSVSSASTKGPSVFLAPCS 156  
Qy 120 RSTSESTAALGCLVKDYPPPTVTVSNWNSGALTSGVHTF 157  
Db 157 RSTSGTAAALGCLVKDYPPPTVTVSNWNSGALTSGVHTF 194  
RESULT 5  
ADJ92518  
ID ADJ92518 standard; protein; 518 AA.  
XX AC ADJ92518;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human SOJB monoclonal antibody heavy chain protein.  
XX KW Rabies virus infection; pharmaceutical; vaccine; gene therapy; virucide;  
XX KW human; SOJB monoclonal antibody.  
XX OS Homo sapiens.  
XX PN US2004013672-A1.  
XX PD 22-JAN-2004.  
XX PF 13-JUN-2003; 2003US-00461148.  
XX PR 16-MAY-2000; 2000US-0204518P.  
XX PR 04-MAY-2001; 2001US-00848832.  
XX PR 21-AUG-2001; 2001US-0314023P.  
XX PR 21-AUG-2002; 2002US-00225108.  
XX PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX PI Hooper DC, Dietzschold B;  
XX DR WPI; 2004-108190/11.  
XX DR N-PSDB; ADJ92517.  
XX PT New pharmaceutical composition comprising at least two recombinant rabies  
XX PT virus-neutralizing human antibodies, useful for treating or preventing  
XX PT rabies virus infection.  
XX PS Claim 1; SEQ ID NO 4; 28pp; English.  
XX CC The present invention relates to a method of treating or preventing a  
XX CC rabies virus infection in a subject. The invention also relates to novel  
XX CC pharmaceutical composition comprising a carrier and at least two  
XX CC recombinant rabies virus-neutralising human antibodies, where the  
XX CC antibody comprises an antibody comprising an antibody light chain or its  
XX CC homologue and an antibody heavy chain or its homologue. The  
XX CC pharmaceutical composition is useful for treating or preventing rabies  
XX CC virus infection. The invention is also useful as vaccine and in gene  
XX CC therapy. The pharmaceutical composition is useful for treating or  
XX CC preventing rabies virus infection. The present sequence is rabies virus-  
XX CC neutralising human SOJB monoclonal antibody heavy chain protein used in  
XX CC the invention.

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XX SQ Sequence 518 AA;
Query Match      81.8%; Score 700.5; DB 8; Length 518;
Best Local Similarity 84.2%; Pred. No. 3e-55;
Matches 133; Conservative 9; Mismatches 13; Indels 3; Gaps 2;

Qy 1 LCTFSGSLITRGVGVDMIRQPGKALQWLALYWNDDKRYSPSLKSLRTITKDTSKNQ 60
Db 39 LCTFSGSLSTSGVGVDMIRQPGKALEWTLIYWNDDKRYSPSLKSLRTITKDTSKNQ 98
Qy 61 VVLTMTNMDPVDATYYCAHHFFDSSGYYP-FDSWGQGTLYVSSASTKGPSVFPPLAPCS 119
Db 99 VALTMTNMDPLDTGYTCAHRRHSS--FPWFDSWGQGTLYVSSASTKGPSVFPPLAPCS 156
Qy 120 RSTSESTAALGCLVKDYFPEPTVSWNSGALTSVGHVF 157
Db 157 RSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVF 194

RESULT 6
ADF71916
ID ADF71916 standard; protein; 448 AA.
XX AC
XX ADF71916;
XX AC
XX 26-FEB-2004 (first entry)
XX DT
XX DE HuJG8VH-22GIa9 amino acid sequence SEQ ID NO:115.
XX KW anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
XX KW immune response; haemostatic; antirheumatic; antiarthritic;
XX KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
XX KW vasotrophic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
XX KW ophthalmological; antiasthmatic; inflammatory response;
XX KW autoimmune disease; idiopathic thrombocytopenic purpura;
XX KW rheumatoid arthritis; systemic lupus erythematosus;
XX KW autoimmune haemolytic anaemia; scleroderma;
XX KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
XX KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
XX KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
XX KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
XX KW allergic asthma.
XX KW
XX OS Synthetic.
XX OS Mus sp.
XX OS Homo sapiens.
XX XX
XX WO2003101485-A1.
XX PN
XX 11-DEC-2003.
XX PD
XX 29-MAY-2003; 2003WO-US017111.
XX PF
XX 30-MAY-2002; 2002US-0384689P.
XX PR
XX 10-JAN-2003; 2003US-0439320P.
XX XX
XX (MACR-) MACROGENICS INC.
XX PA
XX Johnson LS, Huang L, Li H, Tuailon N;
XX PI
XX WPI; 2004-042985/04.
XX DR
XX Novel anti-CD16A antibody comprising complementarity determining regions
XX PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
XX PT lacks effector function, useful for treating deleterious immune response.
XX XX
XX Disclosure; SEQ ID NO 115; 103pp; English.
XX PS
XX The present invention describes an anti-CD16A antibody (I) comprising a
XX CC VH domain comprising complementarity determining regions (CDRs) derived
XX CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
XX CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A

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CC antibody (II) that lacks effector function and comprises all six CDRs of
CC mouse antibody 3G8. Also described is a method (M1) for reducing a
CC deleterious immune response in a mammal in need of such reduction, which
CC involves administering to the mammal a CD16A binding protein comprising
CC an Fc region derived from a human IgG heavy chain, where the Fc region
CC lacks effector function or is modified to reduce binding to an Fc
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
CC antianaemic, vasotrophic, nephrotropic, neuroprotective, antipsoriatic,
CC utropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
CC useful for reducing a deleterious immune response in a mammal which
CC involves administering to the mammal (I) or (II). The deleterious immune
CC response is an inflammatory response caused by autoimmune disease such as
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
CC and also for treating diseases susceptible to treatment with intravenous
CC immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence
CC is used in the exemplification of the present invention.
XX CC
XX SQ Sequence 448 AA;
Query Match      79.3%; Score 678.5; DB 8; Length 448;
Best Local Similarity 83.4%; Pred. No. 2.6e-53;
Matches 131; Conservative 9; Mismatches 12; Indels 5; Gaps 2;

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Qy 1 LCTFSGSLITRGVGVDMIRQPGKALQWLALYWNDDKRYSPSLKSLRTITKDTSKNQ 60
Db 20 LCTFSGSLSTSGVGVDMIRQPGKALEWTLIYWNDDKRYSPSLKSLRTITKDTSKNQ 79
Qy 61 VVLTMTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGTLYVSSASTKGPSVFPPLAPCSR 120
Db 80 VVLTMTNMDPVDATYYCAR---INPAYFAY--WGQGTLYVSSASTKGPSVFPPLAPSK 134
Qy 121 STSESTAALGCLVKDYFPEPTVSWNSGALTSVGHVF 157
Db 135 STSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVF 171

RESULT 7
ABP58287
ID ABP58287 standard; protein; 453 AA.
XX AC
XX ABP58287;
XX AC
XX 23-OCT-2003 (revised)
XX DT 31-MAR-2003 (first entry)
XX DE Humanised 10D5 antibody heavy chain.
XX XX
XX Monoclonal antibody; 10D5; complementarity determining region; CDR;
XX KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
XX KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX XX
XX Mus sp.
XX OS Homo sapiens.
XX OS Chimeric.
XX XX
XX Key Location/Qualifiers
XX FT Region 1..123
XX FT /note= "light chain variable region"
XX FT Region 31..135
XX FT /note= "CDR1"
XX FT Region 52..167
XX FT /note= "CDR2"
XX FT Region 100..112
XX FT /note= "CDR3"
XX XX
XX WO200288307-A2.
XX XX

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PD 07-NOV-2002.
XX
PF 26-APR-2002; 2002WO-US011854.
XX
PR 30-APR-2001; 2001US-0287653P.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Hinton PR, Vasquez M;
XX
XX WPI; 2003-183836/18.
XX
XX New humanized 10D5 antibody, useful for the manufacture of a medicament
PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
PT disease or cerebral amyloid angiopathy.
XX
XX Claim 5; Page 10-12; 52pp; English.
XX
XX The present sequence is the protein sequence of the heavy chain of a
CC humanised antibody of the present invention. In the variable portion, the
CC complementarity determining regions (CDRs) originate from murine
CC monoclonal antibody 10D5 and the framework region originates from human
CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
CC of the invention have CDRs from 10D5 and human framework sequences. These
CC humanised antibodies have binding affinities (affinity and epitope
CC location) approximately the same as those of the mouse 10D5 antibody. The
CC invention includes antibodies, single chain antibodies, and their
CC fragments, as well as nucleotide sequences, vectors, transformed host
CC cells, and methods of using the humanised antibody to treat, prevent,
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC OS field)
XX
XX Sequence 453 AA;
XX
XX Query Match 78.3%; Score 670; DB 6; Length 453;
XX Best Local Similarity 81.5%; Pred. No. 1.6e-52;
XX Matches 128; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
XX
QY 1 LTCTFGSFLITRGVGDWIRQPGKALQWLALYIWNDDKRYSPSLKSLRLTITKDTSKNQ 60
DB 20 LTCTFGSFLSTSGMGVSWIRQPPGKALEWLAHIYWNDDKRYNPSLSKSLRLTISKDTSKSQ 79
QY 61 VLTLTNTNMDPVDATYTCVRRPITPVLVDANDYWGQGLTVTVSSASTKGSVPFLAPCSR 120
DB 80 VLTLTNTNMDPVDATYTCVRRPITPVLVDANDYWGQGLTVTVSSASTKGSVPFLAPSSK 139
QY 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
DB 140 STSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 176
XX
RESULT 8
ABP58289
ID ABP58289 standard; protein; 472 AA.
XX
XX ABP58289;
AC
XX
XX 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX
XX Humanised 10D5 antibody heavy chain.
XX
XX Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
XX Mus sp.
OS
OS Homo sapiens.
OS Chimeric.
XX
```

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FH Key Location/Qualifiers
FT 1..19 /label= Signal_peptide
FT 20..472 /label= Mature_protein
FT /note= "the mature light chain is claimed in Claim 5"
FT 20..142 /note= "light chain variable region, claimed in Claim 4"
FT 50..56 /note= "CDR1"
FT 71..86 /note= "CDR2"
FT 119..131 /note= "CDR3"
XX
XX WO200288307-A2.
XX
XX 07-NOV-2002.
XX
XX 26-APR-2002; 2002WO-US011854.
XX
XX 30-APR-2001; 2001US-0287653P.
XX
XX (ELIL ) LILLY & CO ELI.
XX
XX Hinton PR, Vasquez M;
XX
XX WPI; 2003-183836/18.
XX
XX N-PSDB; ABZ24639, ABZ24641.
XX
XX New humanized 10D5 antibody, useful for the manufacture of a medicament
PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
PT disease or cerebral amyloid angiopathy.
XX
XX Disclosure; Page 13-15; 52pp; English.
XX
XX The present sequence is the protein sequence of the heavy chain of a
CC humanised antibody of the present invention. In the variable portion, the
CC complementarity determining regions (CDRs) originate from murine
CC monoclonal antibody 10D5 and the framework region originates from human
CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
CC of the invention have CDRs from 10D5 and human framework sequences. These
CC humanised antibodies have binding affinities (affinity and epitope
CC location) approximately the same as those of the mouse 10D5 antibody. The
CC invention includes antibodies, single chain antibodies, and their
CC fragments, as well as nucleotide sequences, vectors, transformed host
CC cells, and methods of using the humanised antibody to treat, prevent,
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC OS field)
XX
XX Sequence 472 AA;
XX
XX Query Match 78.3%; Score 670; DB 6; Length 472;
XX Best Local Similarity 81.5%; Pred. No. 1.6e-52;
XX Matches 128; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
XX
QY 1 LTCTFGSFLITRGVGDWIRQPGKALQWLALYIWNDDKRYSPSLKSLRLTITKDTSKNQ 60
DB 39 LTCTFGSFLSTSGMGVSWIRQPPGKALEWLAHIYWNDDKRYNPSLSKSLRLTISKDTSKSQ 98
QY 61 VLTLTNTNMDPVDATYTCVRRPITPVLVDANDYWGQGLTVTVSSASTKGSVPFLAPCSR 120
DB 99 VLTLTNTNMDPVDATYTCVRRPITPVLVDANDYWGQGLTVTVSSASTKGSVPFLAPSSK 158
QY 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
DB 159 STSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 195
XX
XX RESULT 9
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AD71908  
ID ADF71908 standard; protein; 448 AA.  
XX  
AC ADF71908;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Hu3G8VH-1G1 amino acid sequence SEQ ID NO:107.  
XX  
KW anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;  
KW immune response; haemostatic; antirheumatic; antiarthritic;  
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;  
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;  
KW ophthalmological; antiasthmatic; inflammatory response;  
KW autoimmune disease; idiopathic thrombocytopenic purpura;  
KW rheumatoid arthritis; systemic lupus erythematosus;  
KW autoimmune haemolytic anaemia; scleroderma;  
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;  
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;  
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;  
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;  
KW allergic asthma.  
XX  
OS Synthetic.  
OS Mus sp.  
OS Homo sapiens.  
XX  
PN W02003101485-A1.  
XX  
PD 11-DEC-2003.  
XX  
XX 29-MAY-2003; 2003WO-US017111.  
XX  
XX 30-MAY-2002; 2002US-0384689P.  
PR  
PR 10-JAN-2003; 2003US-0439320P.  
XX  
XX (MACR-) MACROGENICS INC.  
XX  
XX Johnson LS, Huang L, Li H, Tuailon N;  
XX  
XX WPI; 2004-042985/04.  
XX  
XX Novel anti-CD16A antibody comprising complementarity determining regions  
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that  
PT lacks effector function, useful for treating deleterious immune response.  
XX  
XX Disclosure; SEQ ID NO 107; 103pp; English.  
XX  
XX The present invention describes an anti-CD16A antibody (I) comprising a  
CC VH domain comprising complementarity determining regions (CDRs) derived  
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs  
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A  
CC antibody (II) that lacks effector function and comprises all six CDRs of  
CC mouse antibody 3G8. Also described is a method (M1) for reducing a  
CC deleterious immune response in a mammal in need of such reduction, which  
CC involves administering to the mammal a CD16A binding protein comprising  
CC an FC region derived from a human IgG heavy chain, where the FC region  
CC lacks effector function or is modified to reduce binding to an FC  
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,  
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,  
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,  
CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is  
CC useful for reducing a deleterious immune response in a mammal which  
CC involves administering to the mammal (I) or (II). The deleterious immune  
CC response is an inflammatory response caused by autoimmune disease such as  
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),  
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),  
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis  
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis  
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,  
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis.  
CC and also for treating diseases susceptible to treatment with intravenous  
CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence

CC is used in the exemplification of the present invention.  
XX  
SQ Sequence 448 AA;  
XX  
Query Match 77.6%; Score 664.5; DB 8; Length 448;  
Best Local Similarity 81.1%; Pred. No. 4.9e-52;  
Matches 129; Conservative 9; Mismatches 12; Indels 9; Gaps 2;  
XX  
QY 1 LCTFSGFSLITRGVGVDMIRQPPGKALQWLALYNNDDKRYSPSLKSLRTITKDTSKNQ 60  
DB 20 LCTFSGFSLUSTSGMGVIRQPPGKALELHWMDDDKRYNPALKSLRUTISKTSKQ 79  
QY 61 VLVTMTNMDPVDATYTCYCAHFFDSSGYTP--FDSMGQGTLLVSSASTKGPSVFFLAPC 118  
DB 80 VLVTMTNMDPVDATYTCAR-----INPAWYMGQGTLLVSSASTKGPSVFFLAPS 132  
QY 119 SRSTSSSTAALGCLVXDYPPPEPVTVSNWNSGALTSGVHTF 157  
DB 133 SKSTSGTAAALGCLVXDYPPPEPVTVSNWNSGALTSGVHTF 171  
XX  
RESULT 10  
AD71912  
ID ADF71912 standard; protein; 448 AA.  
XX  
AC ADF71912;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Hu3G8VH-5G1Ag amino acid sequence SEQ ID NO:111.  
XX  
KW anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;  
KW immune response; haemostatic; antirheumatic; antiarthritic;  
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;  
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;  
KW ophthalmological; antiasthmatic; inflammatory response;  
KW autoimmune disease; idiopathic thrombocytopenic purpura;  
KW rheumatoid arthritis; systemic lupus erythematosus;  
KW autoimmune haemolytic anaemia; scleroderma;  
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;  
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;  
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;  
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;  
KW allergic asthma.  
XX  
OS Synthetic.  
OS Mus sp.  
OS Homo sapiens.  
XX  
PN W02003101485-A1.  
XX  
PD 11-DEC-2003.  
XX  
XX 29-MAY-2003; 2003WO-US017111.  
XX  
XX 30-MAY-2002; 2002US-0384689P.  
PR  
PR 10-JAN-2003; 2003US-0439320P.  
XX  
XX (MACR-) MACROGENICS INC.  
XX  
XX Johnson LS, Huang L, Li H, Tuailon N;  
XX  
XX WPI; 2004-042985/04.  
XX  
XX Novel anti-CD16A antibody comprising complementarity determining regions  
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that  
PT lacks effector function, useful for treating deleterious immune response.  
XX  
XX Disclosure; SEQ ID NO 111; 103pp; English.  
XX  
XX The present invention describes an anti-CD16A antibody (I) comprising a  
CC VH domain comprising complementarity determining regions (CDRs) derived  
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs  
CC derived from the mouse 3G8 antibody light chain and a humanised anti-CD16A  
CC antibody (II) that lacks effector function and comprises all six CDRs of  
CC mouse antibody 3G8. Also described is a method (M1) for reducing a  
CC deleterious immune response in a mammal in need of such reduction, which  
CC involves administering to the mammal a CD16A binding protein comprising  
CC an FC region derived from a human IgG heavy chain, where the FC region  
CC lacks effector function or is modified to reduce binding to an FC  
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,  
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,  
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,  
CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is  
CC useful for reducing a deleterious immune response in a mammal which  
CC involves administering to the mammal (I) or (II). The deleterious immune  
CC response is an inflammatory response caused by autoimmune disease such as  
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),  
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),  
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis  
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis  
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,  
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis.  
CC and also for treating diseases susceptible to treatment with intravenous  
CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence

CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A  
 CC mouse antibody (II) that lacks effector function and comprises all six CDRs of  
 CC mouse antibody 3G8. Also described is a method (MI) for reducing a  
 CC deleterious immune response in a mammal in need of such reduction, which  
 CC involves administering to the mammal a CD16A binding protein comprising  
 CC an FC region derived from a human IGG heavy chain, where the FC region  
 CC lacks effector function or is modified to reduce binding to an FC  
 CC effector ligand. (I) and (II) have haemostatic, antithrombotic,  
 CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,  
 CC antianemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,  
 CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is  
 CC useful for reducing a deleterious immune response in a mammal which  
 CC involves administering to the mammal (I) or (II). The deleterious immune  
 CC response is an inflammatory response caused by autoimmune disease such as  
 CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),  
 CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),  
 CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis  
 CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis  
 CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,  
 CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis,  
 CC and also for treating diseases susceptible to treatment with intravenous  
 CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence  
 CC is used in the exemplification of the present invention.

XX Sequence 448 AA;

Query Match 77.6%; Score 664.5; DB 8; Length 448;  
 Best Local Similarity 81.1%; Pred. No. 4.9e-52;  
 Matches 129; Conservative 9; Mismatches 12; Indels 9; Gaps 2;

Qy 1 LTCFSGSLITRGVGDWIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
 Db 20 LTCFSGSLITRGVGDWIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTITKDTSKNQ 79  
 Qy 61 VLTMTNMDPVDATYYCAHFFDSSGYYP--FDSWGGTILVSVSSASTKGPSVFPPLAPC 118  
 Db 80 VLTMTNMDPVDATYYCAQ-----INPAFYWGQGLTVTVSSASTKGPSVFPPLAPS 132

Qy 119 SRSTSESTAALGCLVKDYFPEPTVTVSNWGALTSGVHTF 157  
 Db 133 SKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTF 171

RESULT 11  
 ADJ32130  
 ID ADJ32130 standard; protein; 228 AA.

AC ADJ32130;  
 XX 22-APR-2004 (first entry)  
 DT Human interferon-gamma antibody heavy chain amino acid sequence SeqIDB4.  
 DE antibody; antigen binding domain; interferon-gamma; INF-gamma;  
 KW antagonist antibody; antiinflammatory; immunosuppressive;  
 KW autoimmune disease; inflammatory condition; human; heavy chain.  
 XX Homo sapiens.

XX US2003099647-A1.  
 XX 29-MAY-2003.  
 XX 05-OCT-2001; 2001US-00972656.  
 XX 05-OCT-2001; 2001US-00972656.  
 XX (DESH/) DESHPANDE R V.  
 XX (TSAI/) TSAI M.

XX Deshpande RV, Tsai M;  
 XX WPI; 2003-696068/66.

DR N-PSDB; ADJ32129.

XX New antibody or antigen binding domain, or its fragment, variant or  
 PT derivative, which binds to an interferon-gamma protein, useful for  
 PT preparing a composition for preventing or treating inflammatory or  
 PT autoimmune disorders.

XX Claim 10; SEQ ID NO 84; 113pp; English.

XX This invention relates to a novel antibody or antigen binding domain, or  
 CC its fragment, variant or derivative, which binds to an interferon-gamma  
 CC (INF-gamma) protein, and is an antagonist antibody. The invention may be  
 CC useful for the development of compounds with an antiinflammatory or  
 CC immunosuppressive activity through action as interferon-gamma agonists. A  
 CC composition containing the antibody is useful for preventing or treating  
 CC an autoimmune disease and an inflammatory condition. The present sequence  
 CC is that of an antibody heavy chain of a human IFN-gamma antibody which  
 CC may be part of the invention.

XX Sequence 228 AA;

Query Match 77.6%; Score 664; DB 7; Length 228;  
 Best Local Similarity 78.6%; Pred. No. 2.5e-52;  
 Matches 125; Conservative 11; Mismatches 21; Indels 2; Gaps 1;

Qy 1 LTCFSGSLITRGVGDWIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
 Db 20 LTCFSGSLITRGVGDWIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTITKDTSKNQ 79  
 Qy 61 VLTMTNMDPVDATYYCAHFFDSSGYYP--FDSWGGTILVSVSSASTKGPSVFPPLAPC 118  
 Db 80 VLTMTNMDPVDATYYCAHRLVRYGGYSTGGFDVWGQGLTVTVSSASTKGPSVFPPLAPS 139  
 Qy 119 SRSTSESTAALGCLVKDYFPEPTVTVSNWGALTSGVHTF 157  
 Db 140 SKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTF 178

RESULT 12  
 ABP66596  
 ID ABP66596 standard; protein; 450 AA.

XX AC ABP66596;  
 XX 04-DEC-2002 (first entry)  
 DT Human RSV antibody variable heavy chain.

XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;  
 KW complementarity determining region; respiratory syncytial virus;  
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;  
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;  
 KW bronchopulmonary dysplasia; congenital heart disease;  
 KW congenital immunodeficiency; acquired immunodeficiency.

XX OS Homo sapiens.  
 XX WO200243660-A2.  
 XX 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044807.  
 XX 28-NOV-2000; 2000US-00724396.  
 XX 28-NOV-2000; 2000US-00724531.  
 XX (MEDI-) MEDIUMMUNE INC.

XX Young JF, Koenig S, Johnson LS;  
 XX WPI; 2002-706803/76.

XX Antibody for treating respiratory syncytial virus (RSV) infection,  
 PT

PT comprises a variable heavy/light domain or complementarity determining  
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically  
 XX binds to RSV antigen.

PS Disclosure; Page 279-281; 298pp; English.

XX The invention relates to a novel antibody comprising a variable heavy  
 CC (VH) domain, variable light (VL) domain, VH complementarity determining  
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the  
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)  
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the  
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,  
 CC and immunostimulant activity. The polynucleotides of the invention may  
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for  
 CC treating or ameliorating a RSV infection in a human. The antibody is also  
 CC useful for preventing, treating or ameliorating one or more symptoms  
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,  
 CC bronchopulmonary dysplasia, congenital heart disease, congenital  
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow  
 CC transplant. The sequence represents a variable domain of a human RSV  
 CC antibody of the invention

XX Sequence 450 AA;

Query Match 75.3%; Score 644.5; DB 5; Length 450;  
 Best Local Similarity 79.0%; Pred. No. 3.3e-50;  
 Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;

Qy 1 LTCTFSGSLITRGVGVNTRQPGKALQWLALYWNDDKRYSPSLKSLRTITKDTSKNQ 60  
 Db 20 LTCTFSGSLSTAGMSVGMIRQPPGKALEWLADIWDDKDYNPSSLKSLRTISKDTSKNQ 79

Qy 61 VLTMTNMDPVDATYTCYCAHHFFDSSGYPFDSWGQGTLSVSSASTKGSVPFLAPCSR 120  
 Db 80 VLVKVTNMDPADTATYTCARDMI--TNFY-FDVMGQGTITVTVSSASTKGSVPFLAPSSK 136

Qy 121 STSESTAALGCLVKDYPPPEPTVTVSWNSGALTSGVHTF 157

Db 137 STSGTAAALGCLVKDYPPPEPTVTVSWNSGALTSGVHTF 173

RESULT 13

ID ABP66594 standard; protein; 450 AA.

AC ABP66594;

DT 04-DEC-2002 (first entry)

DE Human RSV antibody variable heavy chain.

XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;  
 KW complementarity determining region; respiratory syncytial virus;  
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;  
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;  
 KW bronchopulmonary dysplasia; congenital heart disease;  
 KW congenital immunodeficiency; acquired immunodeficiency.

OS Homo sapiens.

XX WO200243660-A2.

XX 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044807.

XX 28-NOV-2000; 2000US-00724396.

XX 28-NOV-2000; 2000US-00724531.

XX (MEDI-) MEDIUMMUNE INC.

XX Young JF, Koenig S, Johnson LS;

XX

DR WPI; 2002-706803/76.

XX Antibody for treating respiratory syncytial virus (RSV) infection,  
 PT comprises a variable heavy/light domain or complementarity determining  
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically  
 PT binds to RSV antigen.

XX Disclosure; Page 277-278; 298pp; English.

XX The invention relates to a novel antibody comprising a variable heavy  
 CC (VH) domain, variable light (VL) domain, VH complementarity determining  
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the  
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)  
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the  
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,  
 CC and immunostimulant activity. The polynucleotides of the invention may  
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for  
 CC treating or ameliorating a RSV infection in a human. The antibody is also  
 CC useful for preventing, treating or ameliorating one or more symptoms  
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,  
 CC bronchopulmonary dysplasia, congenital heart disease, congenital  
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow  
 CC transplant. The sequence represents a variable domain of a human RSV  
 CC antibody of the invention

XX Sequence 450 AA;

Query Match 75.3%; Score 644.5; DB 5; Length 450;  
 Best Local Similarity 79.0%; Pred. No. 3.3e-50;  
 Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;

Qy 1 LTCTFSGSLITRGVGVNTRQPGKALQWLALYWNDDKRYSPSLKSLRTITKDTSKNQ 60  
 Db 20 LTCTFSGSLSTAGMSVGMIRQPPGKALEWLADIWDDKDYNPSSLKSLRTISKDTSKNQ 79

Qy 61 VLTMTNMDPVDATYTCYCAHHFFDSSGYPFDSWGQGTLSVSSASTKGSVPFLAPCSR 120  
 Db 80 VLVKVTNMDPADTATYTCARDMI--TNFY-FDVMGQGTITVTVSSASTKGSVPFLAPSSK 136

Qy 121 STSESTAALGCLVKDYPPPEPTVTVSWNSGALTSGVHTF 157

Db 137 STSGTAAALGCLVKDYPPPEPTVTVSWNSGALTSGVHTF 173

RESULT 14

ABP66598

ID ABP66598 standard; protein; 450 AA.

AC ABP66598;

DT 04-DEC-2002 (first entry)

DE Human RSV antibody variable heavy chain.

XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;  
 KW complementarity determining region; respiratory syncytial virus;  
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;  
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;  
 KW bronchopulmonary dysplasia; congenital heart disease;  
 KW congenital immunodeficiency; acquired immunodeficiency.

OS Homo sapiens.

XX WO200243660-A2.

XX 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044807.

XX 28-NOV-2000; 2000US-00724396.

XX 28-NOV-2000; 2000US-00724531.

XX (MEDI-) MEDIUMMUNE INC.

XX Young JF, Koenig S, Johnson LS;  
 PI WPI; 2002-706803/76.  
 XX Antibody for treating respiratory syncytial virus (RSV) infection,  
 PT comprises a variable heavy/light domain or complementarity determining  
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically  
 binds to RSV antigen.  
 XX Disclosure; Page 282-283; 298pp; English.  
 XX The invention relates to a novel antibody comprising a variable heavy  
 CC (VH) domain, variable light (VL) domain, VH complementarity determining  
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the  
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)  
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the  
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,  
 CC and immunostimulant activity. The polynucleotides of the invention may  
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for  
 CC treating or ameliorating a RSV infection in a human. The antibody is also  
 CC useful for preventing, treating or ameliorating one or more symptoms  
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,  
 CC bronchopulmonary dysplasia, congenital heart disease, congenital  
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow  
 CC transplant. The sequence represents a variable domain of a human RSV  
 CC antibody of the invention  
 XX Sequence 450 AA;  
 SQ Query Match 75.3%; Score 644.5; DB 5; Length 450;  
 Best Local Similarity 79.0%; Pred. No. 3.3e-50;  
 Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;  
 Qy 1 LTCTFGSFLITRGVGVNDIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
 Db 20 LTCTFGSFLITAGMSVGIWIRQPPGKALEWLADIWDDKDYNSLSKSLRLTISKDTSKNQ 79  
 Qy 61 VVLTMTNMDPVDATYTCYCAHHFFDSSGYYPPDSGQGTLSVSSASTKGPSVFPPLACSR 120  
 Db 80 VVLTMTNMDPADTATYTCARSMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFPPLAPSSK 136  
 Qy 121 STSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTF 157  
 Db 137 STSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTF 173  
 RESULT 15  
 ABP66564  
 ID ABP66564 standard; protein; 450 AA.  
 XX AC ABP66564;  
 XX 04-DEC-2002 (first entry)  
 DT Human RSV antibody variable heavy chain.  
 DE Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;  
 KW complementarity determining region; respiratory syncytial virus;  
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;  
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;  
 KW bronchopulmonary dysplasia; congenital heart disease;  
 KW congenital immunodeficiency; acquired immunodeficiency.  
 XX Homo sapiens.  
 OS WO200243660-A2.  
 FN 06-JUN-2002.  
 PD 28-NOV-2001; 2001WO-US044807.  
 PP 28-NOV-2000; 2000US-00724396.  
 PR

PR 28-NOV-2000; 2000US-00724531.  
 XX (MEDI-) MEDIUMMUNE INC.  
 XX Young JF, Koenig S, Johnson LS;  
 PI WPI; 2002-706803/76.  
 XX Antibody for treating respiratory syncytial virus (RSV) infection,  
 PT comprises a variable heavy/light domain or complementarity determining  
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically  
 binds to RSV antigen.  
 XX Disclosure; Page 243-245; 298pp; English.  
 XX The invention relates to a novel antibody comprising a variable heavy  
 CC (VH) domain, variable light (VL) domain, VH complementarity determining  
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the  
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)  
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the  
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,  
 CC and immunostimulant activity. The polynucleotides of the invention may  
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for  
 CC treating or ameliorating a RSV infection in a human. The antibody is also  
 CC useful for preventing, treating or ameliorating one or more symptoms  
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,  
 CC bronchopulmonary dysplasia, congenital heart disease, congenital  
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow  
 CC transplant. The sequence represents a variable domain of a human RSV  
 CC antibody of the invention  
 XX Sequence 450 AA;  
 SQ Query Match 75.3%; Score 644.5; DB 5; Length 450;  
 Best Local Similarity 79.0%; Pred. No. 3.3e-50;  
 Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;  
 Qy 1 LTCTFGSFLITRGVGVNDIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
 Db 20 LTCTFGSFLITAGMSVGIWIRQPPGKALEWLADIWDDKDYNSLSKSLRLTISKDTSKNQ 79  
 Qy 61 VVLTMTNMDPVDATYTCYCAHHFFDSSGYYPPDSGQGTLSVSSASTKGPSVFPPLACSR 120  
 Db 80 VVLTMTNMDPADTATYTCARSMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFPPLAPSSK 136  
 Qy 121 STSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTF 157  
 Db 137 STSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTF 173  
 Search completed: March 8, 2005, 06:17:23  
 Job time : 73.7167 secs

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Db 99 VALTMTNMDPLDTGTYTCAHQHSS--FPWFDSWGQGLTVTVSSASTKGPSVFPPLAPCS 156
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-449-566-115

RESULT 2
US-10-461-148-4
; Sequence 4, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
; APPLICANT: Dietzschold, Bernhard
; APPLICANT: Hooper, Douglas C.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 8321-110C11-185685
; CURRENT APPLICATION NUMBER: US/10/461,148
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 10/225,108
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human
US-10-461-148-4

Query Match 81.8%; Score 700.5; DB 15; Length 518;
Best Local Similarity 84.2%; Pred. No. 3.8e-47;
Matches 133; Conservative 9; Mismatches 13; Indels 3; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGVDMIRQPPGKALQWLALIIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 60
Db 39 LTCTFSGFSLITRGVGVDMIRQPPGKALQWLALIIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 98
Qy 61 VLVTMTNMDPVDATYYCAHHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSVFPPLAPCS 119
Db 99 VALTMTNMDPLDTGTYTCAHQHSS--FPWFDSWGQGLTVTVSSASTKGPSVFPPLAPCS 156
Qy 120 RSTSESTAALGCLVKDYFPEPVTVMNSGALTSGVHTF 157
Db 157 RSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTF 194

RESULT 3
US-10-449-566-115
; Sequence 115, Application US/10449566
; Publication No. US20040010124A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Leslie S.
; APPLICANT: HUANG, Ling
; APPLICANT: LI, Hua
; APPLICANT: TUAILLON, Nadine
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 529392000100
; CURRENT APPLICATION NUMBER: US/10/449,566
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,689
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/439,320
; PRIOR FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
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; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-449-566-115

Query Match 79.3%; Score 678.5; DB 15; Length 448;
Best Local Similarity 83.4%; Pred. No. 1.8e-45;
Matches 131; Conservative 9; Mismatches 12; Indels 5; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGVDMIRQPPGKALQWLALIIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 60
Db 20 LTCTFSGFSLITRGVGVDMIRQPPGKALQWLALIIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 79
Qy 61 VLVTMTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLTVSVSSASTKGPSVFPPLAPCS 120
Db 80 VLVTMTNMDPVDATYYCAR---INPAYFAY--WGQGLTVTVSSASTKGPSVFPPLAPSK 134
Qy 121 STSESTAALGCLVKDYFPEPVTVMNSGALTSGVHTF 157
Db 135 STSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTF 171

RESULT 4
US-10-449-566-107
; Sequence 107, Application US/10449566
; Publication No. US20040010124A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Leslie S.
; APPLICANT: HUANG, Ling
; APPLICANT: LI, Hua
; APPLICANT: TUAILLON, Nadine
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 529392000100
; CURRENT APPLICATION NUMBER: US/10/449,566
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,689
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/439,320
; PRIOR FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-449-566-107

Query Match 77.6%; Score 664.5; DB 15; Length 448;
Best Local Similarity 81.1%; Pred. No. 2.2e-44;
Matches 129; Conservative 9; Mismatches 12; Indels 9; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGVDMIRQPPGKALQWLALIIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 60
Db 20 LTCTFSGFSLITRGVGVDMIRQPPGKALQWLALIIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 79
Qy 61 VLVTMTNMDPVDATYYCAHHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSVFPPLAPC 118
Db 80 VLVTMTNMDPVDATYYCAR-----INPAWYWGQGLTVTVSSASTKGPSVFPPLAPS 132
Qy 119 SRSTSSTAALGCLVKDYFPEPVTVMNSGALTSGVHTF 157
Db 133 SKSTSGTAALGCLVKDYFPEPVTVMNSGALTSGVHTF 171

RESULT 5
US-10-449-566-111
; Sequence 111, Application US/10449566
; Publication No. US20040010124A1
```

GENERAL INFORMATION:  
APPLICANT: JOHNSON, Leslie S.  
APPLICANT: HUANG, Ling  
APPLICANT: LI, Hua  
APPLICANT: TUAILLON, Nadine  
TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE  
TREATMENT OF IMMUNE DISORDERS  
FILE REFERENCE: 59392000100  
CURRENT APPLICATION NUMBER: US/10/449,566  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: 60/384,689  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: 60/439,320  
PRIOR FILING DATE: 2003-01-10  
NUMBER OF SEQ ID NOS: 119  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 111  
LENGTH: 448  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-449-566-111

Query Match 77.6%; Score 664.5; DB 15; Length 448;  
Best Local Similarity 81.1%; Pred. No. 2.2e-44;  
Matches 129; Conservative 9; Mismatches 12; Indels 9; Gaps 2;  
Qy 1 LTCTFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 20 LTCTFSGFSLTSGVGWIRQPPGKALEWLALHWWDDKRYNPAKLSRLTISKDTSKNQ 79  
Qy 61 VLWTMTNMDPVDATYYCAHHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSVFPPLAPC 118  
Db 80 VLWTMTNMDPVDATYYCAQ-----INPAFWYWGQGLTVTVSSASTKGPSVFPPLAPS 132  
Qy 119 SRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157  
Db 133 SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 171

RESULT 6  
US-09-972-656-84  
Sequence 84, Application US/09972656  
Publication No. US20030099647A1  
GENERAL INFORMATION:  
APPLICANT: Deshpande, Rajendra  
APPLICANT: Tsai, Mei-Mei  
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
Neutralizing Activity  
FILE REFERENCE: A-799  
CURRENT APPLICATION NUMBER: US/09/972,656  
CURRENT FILING DATE: 2001-10-05  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 84  
LENGTH: 228  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-972-656-84

Query Match 77.6%; Score 664; DB 10; Length 228;  
Best Local Similarity 78.6%; Pred. No. 1.2e-44;  
Matches 125; Conservative 11; Mismatches 21; Indels 2; Gaps 1;  
Qy 1 LTCTFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 20 LTCSYSGFSLSSNAGWIRQPPGKAPWALYWNDDKRYSPSLKSLRLTVNKTSKSQ 79  
Qy 61 VLWTMTNMDPVDATYYCAHHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSVFPPLAPC 118  
Db 80 VLWTMTNMDPVDATYYCAHRLVRYGGYSTGDFWVGQGLTVTVSSASTKGPSVFPPLAPS 139

Qy 119 SRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157  
Db 140 SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 178  
RESULT 7  
US-09-996-288-210  
Sequence 210, Application US/09996288  
Patent No. US20020177126A1  
GENERAL INFORMATION:  
APPLICANT: Young, James  
APPLICANT: Scott, Koenig  
APPLICANT: Leslie, Johnson  
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
and Treatment  
FILE REFERENCE: 10271-047-999  
CURRENT APPLICATION NUMBER: US/09/996,288  
CURRENT FILING DATE: 2001-11-28  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 210  
LENGTH: 450  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-996-288-210

Query Match 75.3%; Score 644.5; DB 9; Length 450;  
Best Local Similarity 79.0%; Pred. No. 8.5e-43;  
Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;  
Qy 1 LTCTFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 20 LTCTFSGFSLTAGMSVGWIRQPPGKALEWLADLWDDKDYNSFLKSLRLTISKDTSKNQ 79  
Qy 61 VLWTMTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLTVSVSSASTKGPSVFPPLAPCSR 120  
Db 80 VLKVTNMDPADATYYCARSMI--TNFY-FDVGQGLTVTVSSASTKGPSVFPPLAPSSK 136  
Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157  
Db 137 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

RESULT 8  
US-09-996-288-238  
Sequence 238, Application US/09996288  
Patent No. US20020177126A1  
GENERAL INFORMATION:  
APPLICANT: Young, James  
APPLICANT: Scott, Koenig  
APPLICANT: Leslie, Johnson  
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
and Treatment  
FILE REFERENCE: 10271-047-999  
CURRENT APPLICATION NUMBER: US/09/996,288  
CURRENT FILING DATE: 2001-11-28  
NUMBER OF SEQ ID NOS: 259  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 238  
LENGTH: 450  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-996-288-238

Query Match 75.3%; Score 644.5; DB 9; Length 450;  
Best Local Similarity 79.0%; Pred. No. 8.5e-43;  
Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;  
Qy 1 LTCTFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 20 LTCTFSGFSLTAGMSVGWIRQPPGKALEWLADLWDDKDYNSFLKSLRLTISKDTSKNQ 79  
Qy 61 VLWTMTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLTVSVSSASTKGPSVFPPLAPCSR 120

Db	80	VVLKVTNDPADTATYCARDMI--TNPY-EDVNGQGTVTVSSASTKGPSPFLAPSSK	136
Qy	121	STSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHP	157
Db	137	STSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTF	173

```

RESULT 9
US-09-996-288-240
; Sequence 240, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 240
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-240

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	Query Match	75.3%; Score 644.5; DB 9;	Length 450;
	Best Local Similarity	79.0%; Pred.No. 8.5e-43;	
	Matches 124;	Conservative 11;	Mismatches 19; Indels 3; Gaps 2
Qy	1	LCTCGSGFLITRGGVGDWIRPPGKALQLWLAIYWNDDKRYSPSLKSRLTITKTDSKNQ	60
		:           :           :           :	
Ddb	20	LCTCTSGFSLTAGMSVGWIHQPKGALEWLAIDIWDDKKDYNPSLKSRLTISKDTSKNQ	79
		:           :           :           :	
Qy	61	VVLVTNTNDPVDATATYYCAHHFFDSSGYYPFDMSGQGTLVSVSSASTKGSPVFPLAPCSR	120
		:           :           :           :	
Ddb	80	VVLKVNTNMDPADTATYYCARSMI--TNFY-FDVWGQGTTVTVSSASTKGSPVFPLAPSSK	136
		:           :           :           :	
Qy	121	STSESTAALGCILVKDYFPPEPVTVSWNSGALTSGVHTPF	157
		:           :           :           :	
Ddb	137	STISGGTAALGCILVKDYFPPEPVTVSWNSGALTSGVHTF	173
		:           :           :           :	

Db	20	LTCITSGFSLSTAGNSVCGWIRQPECKALEMLADIWDDKKDYNPSLKSRLTISKDTSKNQ	79
Qy	61	VVLWTNNMDPVDTATYYCAHHFFDSGGYPPDSHGQGTLSVSVSASTKGSVPFLAPCSR	120
Db	80	VVLKVTNNMDPADTATYYCARDMI--TNFY-FDVMGQGTITVTVSSASTKGSVPFLAPSSK	136
Qy	121	STSESTAALGCLVKDYFPPEPVTVSWNSGALTSGVHTF	157
Db	137	STSGGTAALGCLVKDYFPPEPVTVSWNSGALTSGVHTF	173

```

RESULT 11
US-09-996-288-244
; Sequence 244, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 244
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-244

```

```

RESULT 12
US-09-996-288-246
; Sequence 246, Application US/09996288
; Patent NO. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 246
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-246

```

Query Match 75.3%; Score 644.5; DB 9; Length 450;  
Best Local Similarity 79.0%; Pred. NO. 8.5e-43;  
Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2

Qy 1 LKCTSGFSLITRGVGVDMIRPPGKALQWLAIALYWNDDKRYSPLSKRLTITTKDTSKNQ 60  
||||||| : ||||| : ||||| : ||||| : ||||| :  
||||||| : ||||| : ||||| : ||||| : ||||| :

```

RESULT 14
US-09-996-265-238
; Sequence 238, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-238

```

Query Match	75.3%	Score 644.5	DB 10	Length 450
Best Local Similarity	79.0%	Pred. No. 8.5e-43		
Matches 124	Conservative 11	Mismatches 19	Indels 3	Gaps 2
Qy 1	LTCTFSGFSLITRGVGDWIRQPPGKALQWLALVWDDKEYSPSLKSLRLTITKDTSKNQ 60			
Db				
Qy 20	LTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIWDDKDYNSPSLKRLLTISKDTSKNQ 79			
Db				
Qy 61	VLLTMTNMDDPVDATYYCAHHFDFSSGYPYPPDSWGQGTLVSVSSASTKSPSVFPLAPCSR 120			
Db				
Qy 80	VLLKVTNMDDPADTATYYCARSMI--TFYF-FDVWGQGTTVTVSSASTKSPSVFPLAPSSK 136			
Db				
Qy 121	STSESTAAALGCLVKDYPPEPVTYVSWNSGALTSGVHVF 157			
Db				
Qy 137	STSGGTAAALGCLVKDYPPEPVTYVSWNSGALTSGVHVF 173			
Db				

Search completed: March 8, 2005, 07:05:58  
Job time : 85.3771 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 17.4831 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-39

Perfect score: 856

Sequence: 1 LTCTFSGFSLITRGVGDWI.....PVTVWSNGALTSVGHVFQL 159

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
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5: /cgn2\_6/ptodata/1/iaa/PCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644.5	75.3	450	4	US-09-996-288-210
2	644.5	75.3	450	4	US-09-996-288-238
3	644.5	75.3	450	4	US-09-996-288-240
4	644.5	75.3	450	4	US-09-996-288-242
5	644.5	75.3	450	4	US-09-996-288-244
6	644.5	75.3	450	4	US-09-996-288-246
7	643.5	75.2	450	4	US-09-996-288-208
8	641.5	74.9	450	4	US-09-996-288-232
9	641.5	74.9	450	4	US-09-996-288-234
10	641.5	74.9	450	4	US-09-996-288-236
11	641.5	74.9	450	4	US-09-996-288-248
12	640.5	74.8	450	4	US-09-996-288-226
13	640.5	74.8	450	4	US-09-996-288-252
14	640.5	74.8	450	4	US-09-996-288-254
15	640.5	74.8	450	4	US-09-996-288-256
16	640.5	74.8	475	4	US-09-740-002-27
17	639.5	74.7	450	4	US-09-996-288-212
18	639.5	74.7	450	4	US-09-996-288-214
19	638.5	74.6	450	4	US-09-996-288-228
20	633	73.9	451	4	US-09-996-288-230
21	632.5	73.9	450	4	US-09-996-288-218
22	632.5	73.9	450	4	US-09-996-288-222
23	632.5	73.9	450	4	US-09-996-288-224
24	632.5	73.9	450	4	US-09-996-288-250
25	631.5	73.8	450	4	US-09-996-288-216
26	631.5	73.8	450	4	US-09-996-288-220
27	623.5	72.8	462	4	US-09-288-942A-7

28	611.5	71.4	475	4	US-09-740-002-25	Sequence 25, Appl
29	559.5	65.4	172	4	US-09-472-087-7	Sequence 7, Appl
30	559.5	65.4	172	4	US-09-472-087-86	Sequence 86, Appl
31	532.5	62.2	473	3	US-09-049-672A-4	Sequence 4, Appl
32	532	62.1	499	3	US-09-049-672A-1	Sequence 1, Appl
33	530.5	62.0	241	4	US-09-736-219A-187	Sequence 187, App
34	530.5	62.0	832	3	US-08-630-820-7	Sequence 7, Appl
35	530.5	62.0	832	4	US-09-273-453-7	Sequence 7, Appl
36	529.5	61.9	167	4	US-09-472-087-74	Sequence 74, Appl
37	529.5	61.9	463	4	US-09-472-087-1	Sequence 1, Appl
38	529.5	61.9	463	4	US-09-472-087-63	Sequence 63, Appl
39	529.5	61.9	463	4	US-09-472-087-64	Sequence 64, Appl
40	526.5	61.5	255	3	US-09-171-945-57	Sequence 57, Appl
41	525	61.3	166	4	US-09-472-087-75	Sequence 75, Appl
42	525	61.3	464	4	US-09-472-087-2	Sequence 2, Appl
43	525	61.3	464	4	US-09-472-087-66	Sequence 66, Appl
44	523.5	61.2	463	4	US-09-472-087-4	Sequence 4, Appl
45	523.5	61.2	463	4	US-09-472-087-68	Sequence 68, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-996-288-210

; Sequence 210, Application US/09996288

; Patent No. 6818216

; GENERAL INFORMATION:

; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis

; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996.288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 210

; LENGTH: 450

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-288-210

Query Match 75.3%; Score 644.5; DB 4; Length 450;

Best Local Similarity 79.0%; Pred. No. 1.2e-54;

Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGDWIRQPGKALQWLIYWNDDKYSPLKSLRLITKDTSKNQ 60

Db 20 LTCTFSGFSLITAGMSVGIWIRQPGKALEWLIWDDKKDYNFSLKSLRLITKDTSKNQ 79

Qy 61 VLWTWMDPVDATYTCANHHFFDSSGYPPDSGGQTLVSVSSASTKGPVFPPLACSR 120

Db 80 VLKVTWMDPADTATYTCARSMI--TNFY-FDVNGQGTIVTSSASTKGPVFPPLAPSSK 136

Qy 121 STSESTAALGCLVKDYPPEPVTVSWNSGALTSVGHVTF 157

Db 137 STSGGTAALGCLVKDYPPEPVTVSWNSGALTSVGHVTF 173

Qy 121 STSESTAALGCLVKDYPPEPVTVSWNSGALTSVGHVTF 157

Db 137 STSGGTAALGCLVKDYPPEPVTVSWNSGALTSVGHVTF 173

Qy 121 STSESTAALGCLVKDYPPEPVTVSWNSGALTSVGHVTF 157

Db 137 STSGGTAALGCLVKDYPPEPVTVSWNSGALTSVGHVTF 173

##### RESULT 2

US-09-996-288-238

; Sequence 238, Application US/09996288

; Patent No. 6818216

; GENERAL INFORMATION:

; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis

; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996.288





; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 246  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-246

Query Match 75.3%; Score 644.5; DB 4; Length 450;  
Best Local Similarity 79.0%; Pred. No. 1.2e-54;  
Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGVWDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 20 LTCTFSGFSLSTAGMSVGVIRQPPGKALEWLADIWDDKKDYNPSLKSRLTISKDTSKNQ 79  
Qy 61 VLVLTMTNMDPVDATATYCAHHFFDSSGYPPFDSGQGTLSVSSASTKGPSPVFLAPCSR 120  
Db 80 VLVLTMTNMDPADTATYCARMI--TNFY-FDVWGQGTITVSSASTKGPSPVFLAPSSK 136  
Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157  
Db 137 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

## RESULT 7

US-09-996-288-208  
; Sequence 208, Application US/09996288  
; Patent No. 6818216  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 208  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-208

Query Match 75.2%; Score 643.5; DB 4; Length 450;  
Best Local Similarity 79.0%; Pred. No. 1.5e-54;  
Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGVWDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 20 LTCTFSGFSLSTAGMSVGVIRQPPGKALEWLADIWDDKKDYNPSLKSRLTISKDTSKNQ 79  
Qy 61 VLVLTMTNMDPVDATATYCAHHFFDSSGYPPFDSGQGTLSVSSASTKGPSPVFLAPCSR 120  
Db 80 VLVLTMTNMDPADTATYCARSMI--TNWY-FDVWGQGTITVSSASTKGPSPVFLAPSSK 136  
Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157  
Db 137 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

## RESULT 8

US-09-996-288-232  
; Sequence 232, Application US/09996288

; Patent No. 6818216  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 232  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-232

Query Match 74.9%; Score 641.5; DB 4; Length 450;  
Best Local Similarity 79.0%; Pred. No. 2.4e-54;  
Matches 124; Conservative 10; Mismatches 20; Indels 3; Gaps 1;  
Qy 1 LTCTFSGFSLITRGVGVWDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 20 LTCTFSGFSLSTAGMSVGVIRQPPGKALEWLADIWDDKKDYNPSLKSRLTISKDTSKNQ 79  
Qy 61 VLVLTMTNMDPVDATATYCAHHFFDSSGYPPFDSGQGTLSVSSASTKGPSPVFLAPCSR 120  
Db 80 VLVLTMTNMDPADTATYCAR--DMIFNWYFDVWGQGTITVSSASTKGPSPVFLAPSSK 136  
Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157  
Db 137 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

## RESULT 9

US-09-996-288-234  
; Sequence 234, Application US/09996288  
; Patent No. 6818216  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-047-999  
; CURRENT APPLICATION NUMBER: US/09/996,288  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 234  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-288-234

Query Match 74.9%; Score 641.5; DB 4; Length 450;  
Best Local Similarity 79.0%; Pred. No. 2.4e-54;  
Matches 124; Conservative 10; Mismatches 20; Indels 3; Gaps 1;  
Qy 1 LTCTFSGFSLITRGVGVWDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 20 LTCTFSGFSLSTAGMSVGVIRQPPGKALEWLADIWDDKKDYNPSLKSRLTISKDTSKNQ 79  
Qy 61 VLVLTMTNMDPVDATATYCAHHFFDSSGYPPFDSGQGTLSVSSASTKGPSPVFLAPCSR 120  
Db 80 VLVLTMTNMDPADTATYCAR--DMIFNWYFDVWGQGTITVSSASTKGPSPVFLAPSSK 136  
Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157  
Db 137 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173



Qy 121 STSESTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 157  
Db 137 STSGTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 173

## RESULT 14

US-09-996-288-254

; Sequence 254, Application US/09996288

; Patent No. 6818216

; GENERAL INFORMATION:

; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis

; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996,288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 254

; LENGTH: 450

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-288-254

Query Match 74.8%; Score 640.5; DB 4; Length 450;  
Best Local Similarity 78.3%; Pred. No. 3e-54;  
Matches 123; Conservative 10; Mismatches 21; Indels 3; Gaps 1;

Qy 1 LTCFSGFSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 20 LTCFSGFSLTAGMSVGVIRQPPGKALEWLAIDWDDKKHYNFSLKDLRLTISKDTSKNQ 79

Qy 61 VVLTMTNMDPVDATYCAHHFPDSSGYYPFDSWGQGLVSVSSASTKGPSVFLAPCSR 120  
Db 80 VVLTMTNMDPADTATYYCAR---DMIFNFYFDVWGQGLTVTVSSASTKGPSVFLAPSSK 136

Qy 121 STSESTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 157  
Db 137 STSGTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 173

## RESULT 15

US-09-996-288-256

; Sequence 256, Application US/09996288

; Patent No. 6818216

; GENERAL INFORMATION:

; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis

; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996,288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 256

; LENGTH: 450

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-996-288-256

Query Match 74.8%; Score 640.5; DB 4; Length 450;  
Best Local Similarity 78.3%; Pred. No. 3e-54;  
Matches 123; Conservative 10; Mismatches 21; Indels 3; Gaps 1;

Qy 1 LTCFSGFSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60  
Db 20 LTCFSGFSLTAGMSVGVIRQPPGKALEWLAIDWDDKKHYNFSLKDLRLTISKDTSKNQ 79

Qy 61 VVLTMTNMDPVDATYCAHHFPDSSGYYPFDSWGQGLVSVSSASTKGPSVFLAPCSR 120  
Db 80 VVLTMTNMDPADTATYYCAR---DMIFNFYFDVWGQGLTVTVSSASTKGPSVFLAPSSK 136  
Qy 121 STSESTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 157  
Db 137 STSGTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 173

Search completed: March 8, 2005, 05:54:14

Job time : 17.4831 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 11.8686 Seconds  
(without alignments)  
1353.842 Million cell updates/sec

Title: US-09-784-950-40

Perfect score: 867

Sequence: 1 GGLVQPGGSLRLSCAASGF.....SWNLGALTSGVHTFPAVLQS 167

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	623.5	71.9	548	2	S38864
2	590	68.1	213	2	S68213
3	582	67.1	143	2	S23624
4	576.5	66.5	254	2	S31790
5	555.5	64.1	220	2	S68211
6	555.5	64.1	444	2	PC4436
7	546	63.0	220	2	A49444
8	535.5	61.8	241	2	S69131
9	518	59.7	160	2	S05271
10	514.5	59.3	470	2	S22080
11	497.5	57.4	249	2	S69340
12	495.5	57.2	124	2	S20782
13	493.5	56.9	469	2	S37483
14	492	56.7	509	2	S17597
15	491	56.6	231	2	PC4155
16	489	56.4	246	2	S38950
17	489	56.4	446	2	S40295
18	485	55.9	119	2	S31108
19	484.5	55.9	108	2	PH1648
20	483.5	55.8	214	2	PC4202
21	481.5	55.5	147	2	I37780
22	481	55.5	138	2	S31666
23	480.5	55.4	572	2	B46529
24	480	55.4	119	2	D36005
25	479	55.2	119	2	S31107
26	478	55.1	140	2	S31686
27	477	55.0	123	2	S31114
28	477	55.0	140	2	S31588
29	476.5	55.0	120	2	S48798

30 476 54.9 119 2 C36005 Ig heavy chain V r  
31 476 54.9 221 2 S49220 Ig gamma-1 chain -  
32 471.5 54.4 112 2 PH1647 Ig heavy chain V r  
33 469 54.1 109 2 PH1649 Ig heavy chain V r  
34 468.5 54.0 135 2 I37778 Ig variable region  
35 467.5 53.9 475 2 S01321 Ig gamma-2b chain  
36 466.5 53.8 114 2 S46391 Ig heavy chain V r  
37 465.5 53.7 120 2 S49590 Ig heavy chain V r  
38 465 53.6 134 2 S31679 Ig heavy chain V r  
39 464 53.5 134 2 S31699 Ig heavy chain V r  
40 463.5 53.5 136 2 S31587 Ig heavy chain V r  
41 460.5 53.1 114 2 S46390 Ig heavy chain V r  
42 460.5 53.1 114 2 S31120 Ig heavy chain - h  
43 460 53.1 121 2 I35673 Ig heavy chain - h  
44 460 53.1 127 2 S38489 Ig heavy chain - h  
45 459 52.9 123 2 S26794 Ig heavy chain V r

## ALIGNMENTS

### RESULT 1

S38864

Ig epsilon chain C region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-May-2001

C/Accession: S38864

R/Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A/Description: Combination of a defined specificity and desired isotype by cloning of an

A/Reference number: S38864

A/Accession: S38864

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-548 <KIP>

A/Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782

C/Superfamily: immunoglobulin C region; immunoglobulin homology

F;353-421/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 623.5; DB 2; Length 548;

Best Local Similarity 70.3%; Pred. No. 2.2e-42;

Matches 121; Conservative 17; Mismatches 29; Indels 5; Gaps 1;

Qy 1 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60

Db 8 GGLVQPGGSLRLSCAASGLTFSYGMWVRQIPDKLEWVATISSGCTTYYPDSVKGR 67

Qy 61 FTISRDNKSNILYLQNSLAEDTAVYCAK-----IFGVVWGQGLVTVSSASATKPS 115

Db 68 FTISRDNKSNILYLQNSLAEDTAVYCAK-----IFGVVWGQGLVTVSSASATKPS 127

Qy 116 VFPLAPCSRSTSESTAALGLVDYFPEPVTVSNLGLTSGVHTFPAVLQS 167

Db 128 VFPLAPCSAAQTNSWMTLGLVKGYPFPEPTVTVNWSGLSGVHTFPAVLQS 179

### RESULT 2

S68213

Ig heavy chain (Mab03-1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 29-Jul-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C/Accession: S68213

R/Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Imanaka, T.

FEBS Lett. 375, 273-276, 1995

A/Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin

A/Reference number: S68211; MUID:96085223; PMID:7498516

A/Accession: S68213

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-213 <TAK>

A/Cross-references: UNIPROT:Q91Z05; EMBL:D29667

C/Superfamily: immunoglobulin C region; immunoglobulin homology

F;137-201/Domain: immunoglobulin homology <IMM>

Query Match  
Best Local Similarity 68.1%; Score 590; DB 2; Length 213;  
Matches 115; Conservative 18; Mismatches 34; Indels 2; Gaps 1;

QY 1 GGGLVQPGGSLRLSCAASGTFSSYAMSWVRQAPKGLEWVSTISVGITTYVDVKGR 60  
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
8 GGGLVQPGGSRKLSCAASGTFSSFGMHWRRQAPKEGLEWVAIYSGSSSIYYADIVKGR 67

QY 61 FTISRDNKSNILYLQMNLSRAEDTAVTYCAKR--IFGVVMGQGTLVTVSSASTKGPSVPF 118  
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
68 FTISRDNPKNTLFLQMTSLASEDTAMYCCARSMLLPDYWGQGTLLTVSSAKTTFPSVYP 127

QY 119 LAPCSRSTSESTAALGCLVKDYPPETPVTSWNIGALTSGVHTTPAVLQS 167  
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
128 LAPCGDGTGSSVTLGCLVKGYFPESVTVTNNGSGLSSSVHTFPALLQS 176

RESULT 3  
S23624  
Ig heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
R/Accession: S23624  
R/Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defos, M.; Kozin, F.; Carson, D.A.;  
J. Exp. Med. 175, 831-842, 1992  
A/Ritle: Genetic analysis of self-associated immunoglobulin G rheumatoid factors from  
A/Reference number: S23623; MUID: 92156804; PMID: 1740665  
A/Accession: S23624  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-143 <OLE>  
A/Cross-references: EMBL:X59703; NID:g32012; PIDN:CAA42224.1; PTD:g32013  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.1%; Score 582; DB 2; Length 143;  
Best Local Similarity 84.6%; Pred. No. 1.le-39;  
Matches 115; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 GGGLVQPGGSLRLSCAASGTFSSYAMSWVRQAPKGLEWVSTISVGITTYVDVKGR 60  
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
8 GGGLVQPGGSLRLSCAASGTFSSYNNWRQAPKEGLEWVSISSSSIIYYADSVKGR 67

QY 61 FTISRDNKSNILYLQMNLSRAEDTAVTYCAKRIF--GVVMGQGTLVTVSSASTKGPSVPF 118  
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
68 FTISRDNKNSLYLQMNLSRAEDTAVTYCARSGYRGDYWGQGTLLTVSSASTKGPSVPF 127

QY 119 LAPCSRSTSESTAALG 134  
DB :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
128 LAPCSRSTSGTAALG 143

RESULT 4  
B31790  
Ig heavy chain V region (17/9) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 23-May-1997  
R/Accession: B31790  
R/Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.  
J. Biol. Chem. 263, 17100-17105, 1988  
A/Ritle: Preliminary crystallographic data, primary sequence, and binding data for an anti-  
A/Reference number: A92686; MUID: 89034213; PMID: 31182835  
A/Accession: B31790  
A/Molecule type: mRNA  
A/Residues: 1-254 <SCH>  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.5%; Score 576.5; DB 2; Length 254;  
Best Local Similarity 66.9%; Pred. No. 5.6e-39;

Matches	121;	Conservative	19;	Mismatches	26;	Indels	15;	Gaps	6;
Qy	1	GGGLVQPGGSLRLSCAASGFTSSYAMSVVRQAPGKLEWVSTISVSGITTYVDSVKGR	60						
		:     :     :     :     :     :     :     :     :     :							
Db	8	GGDLVKGPGSLKLSAASGFSFSSYGMVVRQTPDKRLEWVATISNGGGTYYPDSVKGR	67						
		:     :     :     :     :     :     :     :     :							
Qy	61	FTISRDNNSKNILYLQMSNLRADETAVYYCAKRI-----FGVVGGQGLTVTVSSASTKGP	114						
		:     :     :     :     :     :     :     :     :							
Db	68	FTISRDNNAKNTLYLQMSLSKSDSAMYCARERYDENGFA-YWGQGLTVTVSSAAKTAP	126						
		:     :     :     :     :     :     :     :     :							
Qy	115	SVFPLAPCSR--STSESFAALGCLVKDYPPEPTVV-SW----NLGALTSG-VHTEPAVLQ	166						
		:     :     :     :     :     :     :     :     :							
Db	127	SVFPLAPVCGXXDTTGSVTLTGCLVKGYFPEPTVTLTKTWXXXNSGSLSGXVHTFPAVLQ	186						
		:     :     :     :     :     :     :     :     :							
Qy	167	S	167						
Db	187	S	187						
RESULT 5									
S68211									
Ig heavy chain (Wab13-1) - mouse (fragment)									
C;Species: Mus musculus (house mouse)									
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000									
C;Accession: S68211									
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.									
FBS Lett. 375, 273-276, 1995									
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin									
A;Reference number: S68211; MUID:96085223; PMID:7498516									
A;Accession: S68211									
A;Status: preliminary; nucleic acid sequence not shown									
A;Molecule type: mRNA									
A;Residues: 1-220 <TAK>									
A;Cross-references: EMBL:D29669; NID:G473958; PID:BAA06140.1; PID:G473959									
A;Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequence									
C;Superfamily: immunoglobulin C region; immunoglobulin homology									
F;136-200/Domain: immunoglobulin homology <IMM>									
Query Match	64.1%	Score	555.5;	DB 2;	Length	220;			
Best Local Similarity	62.8%	Pred.	No. 2.3e-37;						
Matches	108;	Conservative	22;	Mismatches	37;	Indels	5;	Gaps	3;
Qy	1	GGGLVQPGGSLRLSCAASGFTSSYAMSVVRQAPGKLEWVSTISV--SGITTYVDSVK	58						
		:     :     :     :     :     :     :     :     :							
Db	4	GGGLVRPGNSLKLSCLTSGFTFSNRMHWLRQPPGKRLIEWIAVITKSDNYGAKYAESVR	63						
		:     :     :     :     :     :     :     :     :							
Qy	59	GRFTISRDNNSKNILYLQMSNLRADETAVYYCAKR--IPGV-VWGQGLTVTVSSASTKGPS	115						
		:     :     :     :     :     :     :     :     :							
Db	64	GRFTISRDDSKSSVYLQWNLRLREEDTATYCCRTPMVYAMDCWGQGSVTVSSAKTTTPS	123						
		:     :     :     :     :     :     :     :     :							
Qy	116	VFLAPCSRSTSESFAALGCLVKDYPPEPTVVSNLGLTSGVHTEPAVLQS	167						
		:     :     :     :     :     :     :     :     :							
Db	124	VYPLAPGSAAGTNSMVLTGCLVKGYFPEPTVTVNSGSLSGXVHTFPAVLQS	175						
		:     :     :     :     :     :     :     :     :							
RESULT 6									
PC4436									
monoclonal antibody 13-1 heavy chain - mouse (fragment)									
C;Species: Mus musculus (house mouse)									
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000									
C;Accession: PC4436									
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.									

Query Match 64.1%; Score 555.5; DB 2; Length 444;  
Best Local Similarity 62.8%; Pred. No. 4.7e-37;  
Matches 108; Conservative 22; Mismatches 37; Indels 5; Gaps 3;

QY 1 GGGVQPGGSLRLSCAASGFTFSYAMSVWRQAPKGLVWSTISV--SGITTYVDSVK 58  
DB 8 GGGVVRFGNSLKLSCLSGFTFSYRHWLKPQPKGLEWIAVTKSDNYGAKYASVR 67

QY 59 GRFTISRDNKNIYLQWNSLRADTAIVYCAK--IFGV-VMQGGLTVTVSSASTKGPS 115  
DB 68 GRFTISRDNKSSVYLQWNLREEDTATYYCRRFPWYVANDCWQSGTSVIVSSAKTTPS 127

QY 116 VFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNLGALTSGVHTFPAVLQS 167  
DB 128 VYPLAPGSAQTNSMVLGLCLVKGYFPEPTVTVWNSGSLSSGVHTFPAVLQS 179

RESULT 7  
A49444  
Ig gamma-1 heavy chain (New) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 16-Jul-1999  
C:Accession: A49444  
R:Saul, P.A.; Poljak, R.J.  
Proteins 14, 363-371, 1992  
A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A resolution  
A:Reference number: A49444; MUID:93066153; PMID:1438175  
A:Accession: A49444  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-220 <SAU>  
A:Note: sequence modified after extraction from NCBI backbone  
A:Note: this sequence report includes corrections based on crystal structure refinement  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:137-202/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 546; DB 2; Length 220;  
Best Local Similarity 64.1%; Pred. No. 1.3e-36;  
Matches 109; Conservative 22; Mismatches 35; Indels 4; Gaps 3;

QY 1 GGGVQPGGSLRLSCAASGFTFSYAMSVWRQAPKGLVWSTISVSGITTYVDSVKGR 60  
DB 8 GPGVLRPSQTLSTCTVSGTSFDDYVWTVKQPPGRLGWIYFYTG-TTLDPSPGR 66

QY 61 FTISRDNKNIYLQWNSLRADTAIVYCAKRI--GV-VMQGGLTVTVSSASTKGPSVF 117  
DB 67 VTMLVNTSKQFSLRLSSVTHADTAIVYCANLITAGGIDVWQGSGLTVTVSSASTKGPSVF 126

QY 118 PLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNLGALTSGVHTFPAVLQS 167  
DB 127 PLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNLGALTSGVHTFPAVLQS 176

RESULT 8  
S69131  
Ig heavy chain (DOT) - human (fragment)  
N:Alternate names: anti-riboflavin IGG Fd fragment  
C:Species: Homo sapiens (man)  
C:Date: 12-Feb-1998 #sequence\_revision 22-May-1998 #text\_change 21-Jan-2000  
C:Accession: S69131  
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.  
Eur. J. Biochem. 228, 886-893, 1995  
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins  
A:Reference number: S69130; MUID:95255298; PMID:7737190  
A:Accession: S69131  
A:Molecule type: protein  
A:Residues: 1-241 <STO>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid  
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAT>  
F:140-205/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 61.8%; Score 535.5; DB 2; Length 241;  
Best Local Similarity 63.1%; Pred. No. 9.9e-36;  
Matches 106; Conservative 22; Mismatches 31; Indels 9; Gaps 4;

QY 7 PGCSLRSLSCAASGFTFSYAMSVWRQAPKGLVWSTIS--VSGITTYVDSVKGRFTISR 65  
DB 14 PGASVRISCKASGYAFENYIHWVRQAPKGLVWSTIS--SEKFRDLVWMS 71

QY 66 DNSKNILYLQWNSLRADTAIVYCAK----RIFGV-VMQGGLTVTVSSASTKGPSVPL 119  
DB 72 DTANVTSMQLRNLRSDDTGRYFCARVSYDFSQVGMVWQGITTVIVSSASTKGPSVPL 131

QY 120 APCSRSTSESTAALGCLVKDYFPEPTVSNVNLGALTSGVHTFPAVLQS 167  
DB 132 APCSRSTSESTAALGCLVKDYFPEPTVSNVNLGALTSGVHTFPAVLQS 179

RESULT 9  
S05271  
Ig heavy chain precursor - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: S05271; S04602  
R:Kishimoto, T.  
submitted to the EMBL Data Library, March 1989  
A:Reference number: S05270  
A:Accession: S05271  
A:Molecule type: mRNA  
A:Residues: 1-160 <KIS1>  
A:Cross-references: UNIPROT:Q96BB9; EMBL:X14584  
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.  
Nucleic Acids Res. 17, 4385, 1989  
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a  
A:Reference number: S04601; MUID:89296497; PMID:2500644  
A:Accession: S04602  
A:Molecule type: mRNA  
A:Residues: 1-144 <KIS2>  
A:Cross-references: EMBL:X14584  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 59.7%; Score 518; DB 2; Length 160;  
Best Local Similarity 77.3%; Pred. No. 1.6e-34;  
Matches 102; Conservative 7; Mismatches 13; Indels 10; Gaps 2;

QY 1 GGGVQPGGSLRLSCAASGFTFSYAMSVWRQAPKGLVWSTISVSGITTYVDSVKGR 60  
DB 27 GGGVQPGGSLRLSCAASGFTFSYAMSVWRQAPKGLVWSTISVSGITTYVDSVKGR 86

QY 61 FTISRDNKNIYLQWNSLRADTAIVYCAKRI-----FGV-VMQGGLTVTVSSAS 110  
DB 87 FTISRDNKNTLYLQWNSLRADTAIVYCAKAVRGVVISYIYGMVWQGITTVTVSSGS 146

QY 111 TKGPSVPEPLAPC 122  
DB 147 ASAPTLPPLVSC 158

RESULT 10  
S22080  
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine  
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S22080; S06610; A31303  
R:Sanders, P.G.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S22080

```
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.3%; Score 514.5; DB 2; Length 470;
Best Local Similarity 57.7%; Pred. No. 9.3e-34;
Matches 101; Conservative 23; Mismatches 42; Indels 9; Gaps 2;

Qy 1 GGGIVPQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GPSLVKPSQTLSTCTVSGFSLSSYALTWRQAPGKALEWVGGIT-SGGTTYYPALKSR 85
Qy 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIFGVV-----WGQGLTVTVSSASTK 112
Db 86 LSIKENSQVLSVSVTPEDTATYYCARSTGEVGDGAIDAWQGLLTVTVSSASTT 145
Qy 113 GPSVFPAPCSRSTSESTAALGCLVKDYPFPPTVTSWNLGALTSGVHTFPAVLQS 167
Db 146 APKVYPLSSCGDSSSTVTLGCLVSSYPPEPTVTWNSGALKSGVHTFPAVLQS 200

RESULT 11
Ig heavy chain VHIII-D-JH-CH3 region - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1995 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000
C;Accession: S69340
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69340
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-249 <KHA>
A;Cross-references: EMBL:X81696
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;162-229/Domain: immunoglobulin homology <IMM>

Query Match 57.4%; Score 497.5; DB 2; Length 249;
Best Local Similarity 57.4%; Pred. No. 1.1e-32;
Matches 101; Conservative 19; Mismatches 47; Indels 9; Gaps 2;

Qy 1 GGGIVPQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 86
Qy 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIFGVV-----WGQGLTVTVSSASTK 112
Db 87 FTISRDNKNILYLQMSLRAEDTAVYYCAKDVSVIHLPSAIFHWGQTRVIVSSGQPR 146
Qy 113 GPSVFPAPCSRSTSESTAALGCLVKDYPFPPTVTSW-NLGALTSGVHTFPAVLQS 167
Db 147 EPQVYTLPPSRSEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDS 202

RESULT 12
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: S20782
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of the IGA and IGH rearranged VH repertoire of human cord blood
A;Reference number: S20765
A;Accession: S20782
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-124 <MOR>
A;Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 57.2%; Score 495.5; DB 2; Length 124;
Best Local Similarity 85.5%; Pred. No. 7.8e-33;
Matches 100; Conservative 3; Mismatches 5; Indels 9; Gaps 2;

Qy 1 GGGIVPQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 8 GGGIVPQGGSLRLSCAASGFTFSYAMSWVRQAPGEGLEWVSTISGSDSTYYADSVKGR 67
Qy 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIFGVV-----WGQGLTVTVSS 108
Db 68 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIAFGWIPHFYMGQGLTVTVSS 124

RESULT 13
Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 493.5; DB 2; Length 469;
Best Local Similarity 52.9%; Pred. No. 4.4e-32;
Matches 91; Conservative 34; Mismatches 42; Indels 5; Gaps 1;

Qy 1 GGGIVPQGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db 27 GPDLVPEASVKISCKASGFTFTDYINWVKQPGQGLKWIWYPSAGTKYKNENFGK 86
Qy 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIFGVV-----WGQGLTVTVSSASTKPS 115
Db 87 ATLTVDTSSSTAYMQLSSLTSEDVAVYFCARAMGATATLLDYMGQGLTVTVSSAKTTAPS 146
Qy 116 VFPLAPCSRSTSESTAALGCLVKDYPFPPTVTSWNLGALTSGVHTFPAVLQS 167
Db 147 VYPLAPVCGDITGSSVTGLCLVRGYPPEPTVTLTWNSGSLSSGVHTFPAVLQS 198

RESULT 14
Ig delta chain (WIE) - human
N;Alternate names: myeloma protein WIE
C;Species: Homo sapiens (man)
```



C>Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 26-Apr-1996  
C/Accession: S17597; S06723  
R/Friedrich, R.J.; Baetge, R.; Schranner, I.; Kotucha, U.; Eckart, K.; Hilschmann, N. Biol. Chem. Hoppe-Seyler 372, 795-818, 1991  
A/Title: The complete amino-acid sequence of the heavy chain of the human myeloma protein  
A/Reference number: S17597; MUID:92126236; PMID:1772593  
A/Accession: S17597  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-509 <FRI>  
A/Note: this sequence was determined from the differentiated gene  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: glycoprotein; immunoglobulin; pyroglutamic acid  
F/1-96/Domain: V segment #status predicted <VSE>  
F/15-98/Domain: immunoglobulin homology <IMM>  
F/97-114/Domain: D segment #status predicted <DSE>  
F/115-126/Domain: J segment #status predicted <JSE>  
F/127-509/Domain: C region #status predicted <CRE>  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/141/Disulfide bonds: interchain (to light chain) #status experimental  
F/154-210/Disulfide bonds: #status experimental  
F/239,252,253,257,259/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F/287/Disulfide bonds: interchain (to heavy chain) #status experimental  
F/351,442,493/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F/442/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 56.7%; Score 492; DB 2; Length 509;  
Best Local Similarity 55.7%; Pred. No. 6.3e-32;  
Matches 98; Conservative 15; Mismatches 51; Indels 12; Gaps 2;

QY 1 GGGVLVQGGSLRLSCAASGTFSSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
DB 8 GGGVVPQGRSLRLSCAASGLRFSITYGMFVRQAPGKLEWLAIIWNGSRKHVADSVKGR 67  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 61 FTISRDNKNILYLQNNLSRAEDTAVYCAKRFV-----VWGQGLTVTVSSA 109  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
DB 68 FTISRDNKNILYLQNNLSRAEDTAVYFGSGTTAFSGAAPDNVHIVWGKGTTVTVSSA 127  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 110 STKGPSVFP-LAPCSRSTSESTAALGCLVXDYFPPEVTVSWNLGALTSVHTFPFV 164  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
DB 128 PTRAPDVFIISGCRHPKDSPPVLAQLIYHYFTSVTVTWYNGTQSQPRTPEI 183  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
RESULT 15  
IG gamma-2b chain V-C region Mabb23 - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 21-Jan-2000  
C/Accession: PC4155  
R/Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H. Gene 169, 237-239, 1996  
A/Title: Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody  
A/Reference number: PC4155; MUID:96194809; PMID:8647454  
A/Accession: PC4155  
A/Molecule type: mRNA  
A/Residues: 1-231 <KWA>  
A/Cross-references: GB:U28970; NID:G1262180; PIDN:AAC52489.1; PID:G1262181  
A/Note: This protein has unusual amino acid compared with the conserved sequences of mouse  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
F/1-231/Product: heavy chain #status predicted <MAT>  
F/98-102/Region: unique D sequence  
F/103-119/Region: V region  
F/139-203/Domain: immunoglobulin homology <IMM>

Query Match 56.6%; Score 491; DB 2; Length 231;  
Best Local Similarity 54.7%; Pred. No. 3.4e-32;  
Matches 94; Conservative 28; Mismatches 44; Indels 6; Gaps 2;

QY 1 GGGVLVQGGSLRLSCAASGTFSSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
DB 8 GPGVLAPQSLSITCTVSGFSLTDYGVSWIRPQPGKLEWLGVIWAGG-STFYNALKSR 66  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
QY 61 FTISRDNKNILYLQNNLSRAEDTAVYCAKRFV-----IFGVWGQGLTVTVSSASTKGPS 115  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 62.3661 Seconds  
(without alignments)  
1371.214 Million cell updates/sec

Title: US-09-784-950-40  
Perfect score: 857  
Sequence: 1 GGGLVQGGSLRLSCAASGF.....SWNLGALTSGVHTFPAVLQS 167

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	740	85.4	464	2	Q6MZU6	Q6mz6 homo sapien
2	726.5	83.8	465	2	Q6P6C4	Q6p6c4 homo sapien
3	724	83.5	478	2	Q6PI81	Q6pi81 homo sapien
4	723	83.4	470	2	Q6PJ44	Q6pj44 homo sapien
5	710.5	81.9	475	2	Q6MZD6	Q6mzq6 homo sapien
6	709	81.8	472	2	Q6N089	Q6n089 homo sapien
7	705.5	81.4	473	2	Q6NZV7	Q6nzv7 homo sapien
8	704	81.2	466	2	Q6IN78	Q6in78 homo sapien
9	677.5	78.1	475	2	Q6GMW7	Q6gmw7 homo sapien
10	672.5	77.6	544	2	Q6PJ95	Q6pj95 homo sapien
11	663	76.5	480	2	Q6N094	Q6n094 homo sapien
12	657	75.8	466	2	Q6N096	Q6n096 homo sapien
13	656	75.7	470	2	Q7Z5W1	Q7z5w1 homo sapien
14	654	75.4	493	2	Q68CN4	Q68cn4 homo sapien
15	647.5	74.7	473	2	Q6P055	Q6p055 homo sapien
16	645	74.4	521	2	Q6N4Y9	Q6n4y9 homo sapien
17	641	73.9	482	2	Q7Z351	Q7z351 homo sapien
18	632	72.9	417	2	Q6N093	Q6n093 homo sapien
19	616.5	71.1	481	2	Q6N097	Q6n097 homo sapien
20	597	68.9	458	2	Q65ZQ1	Q65zq1 homo sapien
21	596.5	68.8	473	2	Q91Z05	Q91z05 mus musculus
22	594.5	68.6	471	2	Q66K04	Q66k04 mus musculus
23	585	67.5	464	2	Q6PIB8	Q6pip8 mus musculus
24	577.5	66.6	597	2	Q66BB9	Q66bb9 homo sapien
25	572.5	66.0	473	2	Q6TC63	Q6tc63 homo sapien
26	566	65.3	476	2	Q6GMX1	Q6gmx1 homo sapien
27	565.5	65.2	469	2	Q7Z7P5	Q7z7p5 homo sapien
28	563.5	65.0	518	2	Q6N030	Q6n030 homo sapien
29	563	64.9	613	2	Q6WUK1	Q6wuk1 homo sapien
30	553.5	63.8	465	2	Q6GMX6	Q6gmx6 homo sapien
31	552	63.7	606	2	Q6GMY2	Q6gmy2 homo sapien

32	550	63.4	208	2	Q6ZP87	Q6zpb7 homo sapien
33	549.5	63.4	475	2	Q6N095	Q6n095 homo sapien
34	541	62.4	476	2	Q6MZX7	Q6mzx7 homo sapien
35	539	62.2	480	2	Q6PJF1	Q6pjf1 homo sapien
36	537	61.9	573	2	Q6WU38	Q6wu38 homo sapien
37	522	60.2	493	2	Q6GMX2	Q6gmx2 homo sapien
38	516.5	59.6	494	2	Q6K68	Q6k68 homo sapien
39	513.5	59.2	147	2	Q9Y509	Q9y509 homo sapien
40	510	58.8	473	2	Q9D8L4	Q9d8l4 mus musculus
41	504.5	58.2	463	2	Q99LC4	Q99lc4 mus musculus
42	499.5	57.6	487	2	Q99KA4	Q99ka4 mus musculus
43	498.5	57.5	465	2	Q6PJB2	Q6pjb2 mus musculus
44	497.5	57.4	487	2	Q6ZVX0	Q6zvx0 homo sapien
45	497	57.3	499	2	Q8N5K4	Q8n5k4 homo sapien

ALIGNMENTS

RESULT 1  
Q6MZU6 PRELIMINARY; PRT; 464 AA.  
AC Q6MZU6; 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686C15213.  
GN Name=DKFZp686C15213;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640874; CAB45931.1; -.  
DR HSBP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2; 3.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein\_  
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 85.4%; Score 740; DB 2; Length 464;  
Best Local Similarity 85.4%; Pred. No. 1.4e-62;  
Matches 146; Conservative 9; Mismatches 12; Indels 4; Gaps 3;

Qy	1	GGGLVQGGSLRLSCAASGFTFSYAMSVWRQAPGKGLEWVSTISV-SGITTYVDSVKG	59
Db	27	GGGLVQGGSLRLSCAASGFTFSYAMSVWRQAPGKGLEWVSTISV-SGITTYVDSVKG	86
Qy	60	RFTISRDNKNILYQWNSLRADTAIVYCAKRI--FGV-VWGQGLTVTVSSASTKGPSV	116
Db	87	RFTISRDNKNILYQWNSLRADTAIVYCAKRI--FGV-VWGQGLTVTVSSASTKGPSV	146
Qy	117	FPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWLGALTSGVHTFPAVLQS	167
Db	147	FPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWLGALTSGVHTFPAVLQS	197

RESULT 2

```
Q6P6C4
ID Q6P6C4 PRELIMINARY; PRT; 465 AA.
AC Q6P6C4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RT TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAH62335.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDDB9348ADC37B6D CRC64;

Query Match 83.8%; Score 726.5; DB 2; Length 465;
Best Local Similarity 82.5%; Pred. No. 2.7e-61;
Matches 14; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

Qy 2 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGRF 61
Db GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGRF 87
Qy 62 TISRDNSKNILYQNSLRAEDTAVYCAK-----RIFGVVWGOGTLTVTSSASTKGPSV 116
Db TISRDNSKNILYQNSLRAEDTAVYCAK-----RIFGVVWGOGTLTVTSSASTKGPSV 147
Qy 117 FPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQ 167
Db FPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQ 198
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Q6PI81
ID Q6PI81 PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RT TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 83.5%; Score 724; DB 2; Length 478;
Best Local Similarity 79.0%; Pred. No. 4.9e-61;
Matches 143; Conservative 6; Mismatches 18; Indels 14; Gaps 1;

Qy 1 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 86
Qy 61 FTISRDNSKNILYQNSLRAEDTAVYCAK-----RIFGVVWGOGTLTVT 106
Db FTISRDNSKNILYQNSLRAEDTAVYCAK-----RIFGVVWGOGTLTVT 146
Qy 107 SSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQ 166
Db SSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQ 206
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Qy 167 S 167

Db 207 S 207

## RESULT 4

Q6PJA4 PRELIMINARY; PRT; 470 AA.  
AC Q6PJA4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP TISSUE=Primary B-Cells;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.B., Schnerch A., Schein J.E.,  
RA Jones S.J., Maier M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]

## SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;  
RA Strauberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC018747; AAH18747.1; -;  
DR HSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.cl.  
DR InterPro; IPR003006; Ig.MHC.  
DR InterPro; IPR003596; Ig.v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D99 CRC64;

Query Match 83.4%; Score 723; DB 2; Length 470;  
Best Local Similarity 82.7%; Pred. No. 6e-61;  
Matches 143; Conservative 5; Mismatches 19; Indels 6; Gaps 1;

Qy 1 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60

Db 27 GGGVQPGGSLRLSCWVGFTFSYAMSWVRQAPGKLEWVANIKQDSEKYYVDSVKGR 86

Qy 61 FTISRDNKNLYLQMSLRADTAIVYCAK-----RIFGVVQGGTLVTSSASTKGP 114

Db 87 FTISRDNKNLYLQMSLRADTAIVYCARDGSSWRDVPDPWGQGGTLVTSSASTKGP 146

Qy 115 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNIGALTSGVHTFPAVLQ 167  
Db 147 SVFPLAPSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 199

## RESULT 5

Q6MZQ6 PRELIMINARY; PRT; 475 AA.  
AC Q6MZQ6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKF2p686G11190.  
GN Name=DKF2p686G11190;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human esophagus tumor;  
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
RA Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640947; CAB45972.1; -;  
DR HSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.cl.  
DR InterPro; IPR003006; Ig.MHC.  
DR InterPro; IPR003596; Ig.v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 81.9%; Score 710.5; DB 2; Length 475;  
Best Local Similarity 79.2%; Pred. No. 9.6e-60;  
Matches 141; Conservative 11; Mismatches 15; Indels 11; Gaps 2;

Qy 1 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60

Db 27 GGGVQPGGSLRLSCAASGFTFRYANWVRQAPGKLEWVGSSGVTYYADSVKGR 86

Qy 61 FTISRDNKNLYLQMSLRADTAIVYCAK-----RIFGV-----VWGQGTTLVTSSA 109

Db 87 FTISGDISTNTLYLQMSLRADTAIVYCARADYQVSPAYWYFDWGRGTLVSVSAA 146

Qy 110 STKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNIGALTSGVHTFPAVLQ 167

Db 147 STKGPSVFPPLAPSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 204

## RESULT 6

Q6N089 PRELIMINARY; PRT; 472 AA.  
AC Q6N089;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKF2p686P15220.  
GN Name=DKF2p686P15220;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CA545781.1; -.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 81.8%; Score 709; DB 2; Length 472;
Best Local Similarity 81.1%; Pred. No. 1.3e-59;
Matches 142; Conservative 6; Mismatches 19; Indels 8; Gaps 2;

Qy 1 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITYYVDSVKGR 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 FTISRDNSKNIYLQMSLAEDTAVYYCAKRI-----FGV-VMQQGLVTVTVSSASTK 112
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 113 GPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNWLALGTSGVHFPFPAVLQS 167
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 147 GPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSNWSGALTSGVHFPFPAVLQS 201

RESULT 7
Q6MZV7 PRELIMINARY; PRT; 473 AA.
AC Q6MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZP686C11235.
GN Name=DKFZP686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CA545920.1; -.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.

SQ SEQUENCE 473 AA; 52121 MW; 9476A84C0BFC447 CRC64;

Query Match 81.4%; Score 705.5; DB 2; Length 473;
Best Local Similarity 79.0%; Pred. No. 2.9e-59;
Matches 139; Conservative 11; Mismatches 17; Indels 9; Gaps 1;

Qy 1 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITYYVDSVKGR 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 FTISRDNSKNIYLQMSLAEDTAVYYCAKRI-----IFGVVNGQTLTVTVSSAST 111
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 87 FTISRDNARNSLYLQMSLAEDTAVYYCARQNEHTSPWYPSFFDYWGQGLVTVTVSSAST 146
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 112 KGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNWLALGTSGVHFPFPAVLQS 167
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 147 KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSNWSGALTSGVHFPFPAVLQS 202

RESULT 8
Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RN [1]
RP "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
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DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCDE81076E CRC64;  
Query Match 81.2%; Score 704; DB 2; Length 466;  
Best Local Similarity 82.4%; Pred. No. 4e-59;  
Matches 140; Conservative 6; Mismatches 20; Indels 4; Gaps 2;  
Qy 1 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLGWSTISVSGITTYVDSVKGR 60  
Db 27 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLGWSTISVSGITTYVDSVKGR 85  
Qy 61 FTISRDNKNLYLQMSLRADTAIVYCAKRIQGV---VMGQGLTLVTVSSASTKGPVSF 117  
Db 86 FTISRDNKNLYLQMSLRADTAIVYCAKRIQGV---VMGQGLTLVTVSSASTKGPVSF 145  
Qy 118 PLAPSSKSTSGTAAALGCLVQDYFPEPVTVSNWLGALTSVGHVTFPAVLQS 167  
Db 146 PLAPSSKSTSGTAAALGCLVQDYFPEPVTVSNWLGALTSVGHVTFPAVLQS 195  
RESULT 9  
Q6GMW7  
ID Q6GMW7 PRELIMINARY; PRT; 475 AA.  
AC Q6GMW7  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC073782; AAH73782.1; -.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
KW Hypothetical protein.  
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;  
Query Match 78.1%; Score 677.5; DB 2; Length 475;  
Best Local Similarity 77.0%; Pred. No. 1.4e-56;  
Matches 137; Conservative 8; Mismatches 22; Indels 11; Gaps 2;  
Qy 1 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLGWSTISVSGITTYVDSVKGR 60  
Db 27 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLGWSTISVSGITTYVDSVKGR 86  
Qy 61 FTISRDNKNLYLQMSLRADTAIVYCAKRIQGV---VMGQGLTLVTVSSASTKGPVSF 109  
Db 87 FTISRDNKNLYLQMSLRADTAIVYCAKRIQGV---VMGQGLTLVTVSSASTKGPVSF 146  
Qy 110 STKGPSVFPPLAPCSRSTSESTAALGCLVQDYFPEPVTVSNWLGALTSVGHVTFPAVLQS 167  
Db 147 STKGPSVFPPLAPCSRSTSESTAALGCLVQDYFPEPVTVSNWLGALTSVGHVTFPAVLQS 204  
RESULT 10  
Q6PJ95  
ID Q6PJ95 PRELIMINARY; PRT; 544 AA.  
AC Q6PJ95  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC019046; AAH19046.1; -.  
DR HSPSP; P01861; IADQ.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.

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DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;

Query Match
Best Local Similarity 77.6%; Score 672.5; DB 2; Length 544;
Matches 136; Conservative 5; Mismatches 25; Indels 13; Gaps 2;

QY 1 GGGVOPGSSLRSLSCAASGFTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
DB 27 GGGVOPGSSLRSLSCAASGFTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 86
QY 61 FTISRDNKNILYLQMSLRAEDTAVYYCAK-----RIFGVWVGQGLTVTVSS 108
DB 87 FTISRDNKNILYLQMSLRAEDTAVYYCAKDPWYSNWFLLTNP-SWGRGTLTVTVSS 145
QY 109 ASTKGPSVFLPACSRSTSESTAAALGCLVKDYPPPEVTVSNILGALTSGVHTTTPAVLQS 167
DB 146 ASTKGPSVFLPACSRSTSESTAAALGCLVKDYPPPEVTVSNILGALTSGVHTTTPAVLQS 204

RESULT 11
Q6N094 PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686O01196.
GN Name=DKFZp686O01196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAB45776.1; -.
DR HSP; P01861; IADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match
Best Local Similarity 76.5%; Score 663; DB 2; Length 480;
Matches 131; Conservative 15; Mismatches 21; Indels 16; Gaps 2;

QY 1 GGGVOPGSSLRSLSCAASGFTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
DB 27 GGGVOPGSSLRSLSCAASGFTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 86
QY 61 FTISRDNKNILYLQMSLRAEDTAVYYCAK-----RIFGVW-----WGQGLTV 104
DB 87 FTISRDNKNILYLQMSLRAEDTAVYYCAKRGWVPAGTSTSGPVHRNWFDPWGQGLTV 146
QY 105 TVSSASTKGPSVFLPACSRSTSESTAAALGCLVKDYPPPEVTVSNILGALTSGVHTTTPAV 164
DB 147 TVSSASTKGPSVFLPACSRSTSESTAAALGCLVKDYPPPEVTVSNILGALTSGVHTTTPAV 206
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QY 165 LQS 167  
DB 207 LQS 209

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RESULT 12
Q6N096 PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686I15196.
GN Name=DKFZp686I15196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAB45774.1; -.
DR HSP; P01861; IADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;

Query Match
Best Local Similarity 75.8%; Score 657; DB 2; Length 466;
Matches 131; Conservative 12; Mismatches 24; Indels 2; Gaps 1;

QY 1 GGGVOPGSSLRSLSCAASGFTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
DB 27 GGGVOPGSSLRSLSCAASGFTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 86
QY 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRTFVVV--WGQGLTVTVSSASTKGPSVFP 118
DB 87 FTISRDNKNILYLQMSLRAEDTAVYYCARGFGNPDQMGQGLTVTVSSASTKGPSVFP 146
QY 119 LAPCSRSTSESTAAALGCLVKDYPPPEVTVSNILGALTSGVHTTTPAVLQS 167
DB 147 LAPCSRSTSESTAAALGCLVKDYPPPEVTVSNILGALTSGVHTTTPAVLQS 195

RESULT 13
Q7Z5W1 PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```





RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral Nervous System;  
RA Strausberg R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC065820; AAH65820.1; -.  
DR HSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 74.7%; Score 647.5; DB 2; Length 473;  
Best Local Similarity 73.3%; Pred. No. 1.le-53;  
Matches 129; Conservative 11; Mismatches 27; Indels 9; Gaps 2;  
  
QY 1 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISV--SGITTYVDSVK 58  
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 58  
27 GGLVRFEGGSLTISCTSGFTFSGAWLSWRQAPGKGLEWVARIQTEDDGGTHYGIANK 86  
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 86  
  
QY 59 GRFTISRDNKNIYLQMSLRADTAIVYYCAKRIFGV-----WGQGLTVTVSSAST 111  
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 111  
87 GRFTVSRDSDSRNTLYLQMSDLRTDTAFYFCATGSMNTVGLTGFDSWGQGLTVTVSSAST 146  
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 146  
  
QY 112 KGPSVFPLAFCSRSTSESTAALGCLVKDYFPEPVTVSWNIGALTSGVHTFPAVLQS 167  
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 167  
147 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 202  
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 202

Search completed: March 8, 2005, 06:35:58  
Job time : 63.3661 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 77.4257 Seconds  
(without alignments)  
834.206 Million cell updates/sec

Title: US-09-784-950-40

Perfect score: 867

Sequence: 1 GGLVQGGSLRLSCAASGF.....SWNLGALTSGVHTFPAVLQS 167

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: geneseqp1980s.\*

2: geneseqp1990s.\*

3: geneseqp2000s.\*

4: geneseqp2001s.\*

5: geneseqp2002s.\*

6: geneseqp2003as.\*

7: geneseqp2003bs.\*

8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867	100.0	167	2 AAY34308	Aay34308 Igg antib
2	788	90.9	465	7 ADD93783	Add93783 Monoclonal
3	780	90.0	470	5 ABG77158	Abg77158 Germline
4	780	90.0	470	8 ADR28580	Adr28580 Human ant
5	774.5	89.3	467	6 ABP71365	Abp71365 Anti-OPGL
6	772	89.0	458	8 ADP07903	Adp07903 Human imm
7	769.5	88.8	445	6 AAO31101	Aao31101 Human A2-
8	767	88.5	470	5 ABG77157	Abg77157 Amino aci
9	767	88.3	470	8 ADR28579	Adr28579 Human ant
10	765.5	88.3	443	2 AA113564	Aa113564 Humanised
11	764.5	88.2	466	8 ADL93667	Adl93667 Human CD4
12	764	88.1	217	6 ABR01503	Abr01503 Human ant
13	764	88.1	444	6 ABR55342	Abr55342 Amino aci
14	763.5	88.1	367	6 ABP55467	Abp55467 MAL1A3 pr
15	763.5	88.1	462	8 ADL93670	Adl93670 Human CD4
16	763	88.0	217	6 ABR01505	Abr01505 Human ant
17	762.5	87.9	222	6 ABR01508	Abr01508 Human ant
18	761.5	87.8	220	6 ABR01519	Abr01519 Human ant
19	760.5	87.7	222	6 ABR01515	Abr01515 Human ant
20	760	87.7	217	6 ABR01509	Abr01509 Human ant
21	760	87.7	224	7 ADJ32114	Adj32114 Human int
22	758.5	87.5	224	6 ABR01513	Abr01513 Human ant
23	757.5	87.4	473	5 ABG77162	Abg77162 Germline
24	757.5	87.4	473	8 ADR28584	Adr28584 Human ant
25	757	87.3	221	6 ABR01506	Abr01506 Human ant

ALIGNMENTS

RESULT 1

AAY34308

ID AAY34308 standard; protein; 167 AA.

XX AC AAY34308;

XX DT 19-NOV-1999 (first entry)

XX DE Igg antibody 2.6.1 heavy chain sequence.

XX KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;

XX KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

XX KW organ transplant rejection disease; lymphoma; pancreatic disease;

XX KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.

XX PN WO9945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX PI WPI; 1999-540816/45.

XX PI N-PSDB; AAZ20409.

XX PT New monoclonal antibody, used for treating e.g. graft versus host

XX PT disease, cancer, autoimmune diseases and inflammatory diseases.

XX PS Claim 60; Fig 33; 245pp; English.

XX CC This sequence represents the heavy chain of an antibody of the invention.

XX CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes

XX CC complement and a variable region that binds to the epitope on CD147 bound

XX CC by the Igm Mab ABX-CBL, providing that the antibody is not CBL1. The Mab

XX CC can selectively kill activated T-cells, activated B-cells or resting or

XX CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft

XX CC versus host disease (GVHD), organ transplant rejection diseases (e.g.

XX CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood



AC ABG77158;  
XX  
DT 24-OCT-2002 (first entry)  
XX  
DE Germline protein sequence of anti-IGF-IR antibody DP-47(3-23)/D6-19/JH6.  
XX  
KW Insulin-like growth factor I receptor; antibody; human; cytostatic;  
KW osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour;  
KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;  
KW acromegaly; gigantism; psoriasis; atherosclerosis.  
XX  
OS Homo sapiens.  
XX  
XX WO200253596-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 20-DEC-2001; 2001WO-US051113.  
XX  
XX 05-JAN-2001; 2001US-0259927P.  
XX  
XX (PFIZ ) PFIZER INC.  
XX (ABGE-) ABGENIX INC.  
XX  
XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;  
XX  
XX WPI; 2002-575410/61.  
XX  
XX Novel humanized, chimeric monoclonal antibody that specifically binds to  
XX insulin-like growth factor I (IGF-I) receptor useful for inhibiting  
XX binding of IGF-I or IGF-II to receptor and for treating cancer in humans.  
XX  
XX Disclosure; Fig 19B; 172pp; English.  
XX  
XX This invention relates to a novel humanised, chimeric or human monoclonal  
XX antibody or its antigen binding portion that specifically binds to  
XX insulin-like growth factor I receptor (IGF-IR). The antibodies of the  
XX invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-  
XX IR and can inhibit in vivo tumour growth and IGF-IR tyrosine  
XX phosphorylation. The antibodies of the invention are useful for  
XX diagnosing the presence or location of an IGF-IR-expressing tumour in a  
XX subject. The antibody or its antigen-binding portion is also useful for  
XX treating cancer in a human. The method for this further involves an anti  
XX neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The  
XX antibodies may also be useful for increasing IGF-IR activity and thus  
XX restoring IGF-IR activity in a condition characterised by low IGF-IR  
XX levels e.g. neuropathy, or osteoporosis. An antibody of the invention is  
XX also useful for inducing apoptosis of specific cells in a patient, and to  
XX treat non-cancerous states or disease, e.g. acromegaly, gigantism,  
XX psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies  
XX minimise the immunogenic and allergic responses intrinsic to mouse or  
XX mouse-derived monoclonal antibodies and thus increase the efficacy  
XX and safety of the administered antibodies. The present sequence  
XX represents an anti-insulin-like growth factor I receptor antibody of the  
XX invention  
XX  
SQ Sequence 470 AA;  
Query Match 90.0%; Score 780; DB 5; Length 470;  
Best Local Similarity 87.6%; Pred. No. 8.6e-57;  
Matches 155; Conservative 3; Mismatches 9; Indels 10; Gaps 2;  
QY 1 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITYYVDSVKGR 60  
DB 27 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITYYVDSVKGR 86  
QY 61 FTISRDNKNTLYLQMSLRAEDTAVTYCAK-----RIFGV-VWGQTLTVTSSAS 110  
DB 87 FTISRDNKNTLYLQMSLRAEDTAVTYCAKGYSGGWTYYTYGMDVWGQTLTVTSSAS 146  
QY 111 TKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 167  
DB 147 TKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 203

RESULT 4  
ADR28580  
ID ADR28580 standard; protein; 470 AA.  
XX  
XX ADR28580;  
AC  
XX 18-NOV-2004 (first entry)  
DT  
XX Human anti-IGF-IR antibody DP-47(3-23)/D6-19/JH6 protein SEQ ID NO:46.  
DE  
XX aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;  
KW I-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;  
KW neurodegenerative disorder; human;  
KW anti-insulin-like growth factor I receptor antibody;  
KW anti-IGF-IR antibody; cytostatic; immunosuppressive; endocrine;  
KW vasotropic; neuroprotective; nootropic; antithyroid; vaccine;  
KW gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX WO2004071529-A2.  
XX  
XX 26-AUG-2004.  
PD  
XX 03-FEB-2004; 2004WO-IB000366.  
XX  
XX 13-FEB-2003; 2003US-0447353P.  
XX  
XX (PFIZ ) PFIZER PROD INC.  
PA  
XX Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;  
PI Cusmano JD, Guyot DJ, Page KL;  
PI WPI; 2004-625776/60.  
XX  
XX Treating or preventing aging or a disorder (e.g. multiple myeloma,  
XX autoimmune disease or neurodegenerative disorder) in humans comprises  
XX administering an amount of a human anti-insulin-like growth factor I  
XX receptor antibody.  
XX  
XX Disclosure; SEQ ID NO 46; 105pp; English.  
XX  
XX The present invention describes a method for treating or preventing aging  
XX or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus  
XX disorder, T-cell-mediated autoimmune disease, endocrinological disorder,  
XX ischaemia or neurodegenerative disorder) in a mammal. The method  
XX comprises administering to the mammal an amount of a human anti-insulin-  
XX like growth factor I receptor (IGF-IR) antibody. Also described is a  
XX pharmaceutical composition for treating or preventing the above-mentioned  
XX disorder in a mammal, comprising an amount of the human anti-IGF-IR  
XX antibody and a pharmaceutical carrier. The composition has cytostatic,  
XX immunosuppressive, endocrine, vasotropic, neuroprotective, nootropic and  
XX antithyroid activities, and can be used in vaccines and in gene therapy.  
XX The method and composition are useful for preventing or treating aging or  
XX a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus  
XX disorder, T-cell-mediated autoimmune disease, endocrinological disorder,  
XX ischaemia or neurodegenerative disorder) in mammals, such as humans. The  
XX human IGF-IR antibody is used in preparing a composition for the  
XX treatment or prevention of the above-mentioned disorders. The present  
XX sequence represents a human anti-IGF-IR antibody heavy chain amino acid  
XX sequence, which is used in the exemplification of the present invention.  
XX  
SQ Sequence 470 AA;  
Query Match 90.0%; Score 780; DB 8; Length 470;  
Best Local Similarity 87.6%; Pred. No. 8.6e-57;  
Matches 155; Conservative 3; Mismatches 9; Indels 10; Gaps 2;  
QY 1 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITYYVDSVKGR 60  
DB 27 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITYYVDSVKGR 86

Qy 61 FTISRDNSKNILYLQMNLSRAEDTAVYYCAK-----RIFGV-VWGGTTLVTVSSAS 110  
 |||||  
 Db 87 FTISRDNSKNILYLQMNLSRAEDTAVYYCAKGYSSGWYIIYIGMDVWGGTTLVTVSSAS 146  
 |||||

Qy 111 TKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQS 167  
 |||||  
 Db 147 TKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 203  
 |||||

RESULT 5  
 ABP71365  
 ID ABP71365 standard; protein; 467 AA.  
 AC ABP71365;  
 XX  
 XX  
 DT 28-APR-2003 (first entry)  
 XX  
 DE Anti-OPGL-1 antibody heavy chain.  
 XX Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;  
 KW antiarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "IG2 signal peptide"  
 FT Region 20..141  
 FT /note= "variable region"  
 FT Region 142..467  
 FT /note= "constant region"  
 XX  
 XX WO2003002713-A2.  
 PN  
 XX  
 PD 09-JAN-2003.  
 XX  
 XX 25-JUN-2002; 2002WO-US020181.  
 PF  
 XX 26-JUN-2001; 2001US-0301172P.  
 PR  
 XX (ABGE-) ABGENIX INC.  
 PA (AMGE-) AMGEN INC.  
 PA  
 XX Boyle WJ, Martin FH, Corvalan JR, Davis GC;  
 PI  
 XX WPI; 2003-210262/20.  
 DR N-PSDB; ABZ59147.  
 DR  
 XX New antibodies that interact with osteoprotegerin ligands, useful for  
 PT treating osteopenic disorders, e.g. osteoporosis, bone loss from  
 PT arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and  
 PT osteonecrosis.  
 XX  
 XX Claim 1; Fig 2; 144pp; English.  
 PS  
 XX The invention relates to antibodies that interact with osteoprotegerin  
 CC ligands (OPGL). The antibody is useful for detecting the level of OPGL in  
 CC a biological sample. The antibody, or the pharmaceutical composition  
 CC comprising the antibody, is also useful for treating osteopenic disorder,  
 CC an inflammatory condition with attendant bone loss, an autoimmune  
 CC condition with attendant bone loss in a patient or rheumatoid arthritis  
 CC in a patient. In particular, the antibody or composition is useful for  
 CC treating bone diseases, e.g. osteoporosis, bone loss from arthritis,  
 CC Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's  
 CC syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, Menkes'  
 CC syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or  
 CC osteonecrosis. The present sequence represents an anti-OPGL-1 antibody  
 CC heavy chain  
 XX  
 SQ Sequence 467 AA;

Query Match 89.3%; Score 774.5; DB 6; Length 467;  
 Best Local Similarity 91.0%; Pred. No. 3.9e-56;  
 Matches 152; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

Best Local Similarity 88.5%; Pred. No. 2.5e-56;  
 Matches 154; Conservative 2; Mismatches 11; Indels 7; Gaps 1;

Qy 1 GGLVOPGGSRLRSCAASGFTFSSYAMSVWRQAPGKLEWVSTISVGITTYVDSVKGR 60  
 |||||  
 Db 27 GGLVOPGGSRLRSCAASGFTFSSYAMSVWRQAPGKLEWVSGITSGGTYTADSVKGR 86  
 |||||

Qy 61 FTISRDNSKNILYLQMNLSRAEDTAVYYCAKRIFGVV-----WGQGLTTLVTVSSASTKG 113  
 |||||  
 Db 87 FTISRDNSKNILYLQMNLSRAEDTAVYYCAKDPGTTVMSWFPDPWGQGLTTLVTVSSASTKG 146  
 |||||

Qy 114 PSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQS 167  
 |||||  
 Db 147 PSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 200  
 |||||

RESULT 6  
 ADP07903  
 ID ADP07903 standard; protein; 458 AA.  
 XX  
 AC ADP07903;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human immunoglobulin heavy chain variable region.  
 XX  
 KW monoclonal antibody; tumour growth factor-beta type II receptor;  
 KW TGF-beta type II receptor; kidney disease; nephrosclerosis;  
 KW pulmonary fibrosis; liver cirrhosis; blood-vessel restenosis;  
 KW arteriosclerosis; psoriasis; scleroderma; atopy; keloid; arthritis;  
 KW human; heavy chain variable region.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2004121001-A.  
 XX  
 PD 22-APR-2004.  
 XX  
 XX 07-AUG-2002; 2002JP-00230651.  
 PF  
 XX 07-AUG-2002; 2002JP-00230600.  
 PR  
 XX (NISB ) JAPAN TOBACCO INC.  
 PA  
 XX WPI; 2004-322721/30.  
 DR N-PSDB; ADP07902.  
 DR  
 XX Novel monoclonal antibody coupled with human transforming growth factor  
 PT (TGF)-beta type II receptor, useful for treating or preventing  
 PT arteriosclerosis, psoriasis, scleroderma, atopy, keloid, arthritis.  
 XX  
 PS Claim 29; SEQ ID NO 7; 78pp; Japanese.  
 XX  
 CC The invention comprises a monoclonal antibody coupled with human tumour  
 CC growth factor-beta (TGF-beta) type II receptor. The monoclonal antibody  
 CC coupled with human TGF-beta type II receptor of the invention is useful  
 CC for treating or preventing kidney disease, nephrosclerosis, pulmonary  
 CC fibrosis, liver cirrhosis, blood-vessel restenosis, arteriosclerosis,  
 CC psoriasis, scleroderma, atopy, keloid and arthritis. The present amino  
 CC acid sequence represents a human immunoglobulin heavy chain variable  
 CC region.  
 XX  
 SQ Sequence 458 AA;

Query Match 89.0%; Score 772; DB 8; Length 458;  
 Best Local Similarity 91.0%; Pred. No. 3.9e-56;  
 Matches 152; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

Qy 1 GGLVOPGGSRLRSCAASGFTFSSYAMSVWRQAPGKLEWVSTISVGITTYVDSVKGR 60  
 |||||  
 Db 27 GGLVOPGGSRLRSCAASGFTFSSYAMSVWRQAPGKLEWISVISVGGSTYADSVKGR 86  
 |||||

Qy 61 FTISRDNSKNILYLQMNLSRAEDTAVYYCAKRIFGVVWGQGLTTLVTVSSASTKGSPVPLA 120  
 |||||

```

Db      87 FTISRDNSKNTLYLQMSLRADTAHYC--EIAARLGGQGLTVTVSSASTKGSVPFPLA 144
Qy      121 PCSRSTSESTAALGCLVKDYPPPEPTVTVSNLGLTSGVHTTFFAVLQS 167
Db      145 PCSRSTSESTAALGCLVKDYPPPEPTVTVSNLGLTSGVHTTFFAVLQS 191

RESULT 7
AAO31101
ID      AAO311101 standard; protein; 445 AA.
AC      AAO311101;
XX
DT      06-OCT-2003 (first entry)
DE      Human A2-G8 SCF antibody heavy chain variable and constant region.
KW      Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;
KW      steel factor; c-kit ligand; gene therapy.
OS      Homo sapiens.
XX
FN      WO2003051311-A2.
XX
PD      26-JUN-2003.
XX
PF      16-DEC-2002; 2002WO-US040227.
XX
PR      17-DEC-2001; 2001US-0342174P.
XX
PA      (FARB ) BAYER. CORP.
XX
PI      Takeuchi T, Tomkinson A, Neben S;
XX
WPI; 2003-523500/49.
XX
PT      New purified human antibody that binds to stem cell factor protein,
PT      useful for preparing a composition for treating asthma.
XX
PS      Claim 9; Page 47; 94pp; English.
XX
CC      The invention provides human antibodies that bind to stem cell factor
CC      (SCF) protein. SCF is also known as mast cell growth factor, steel factor
CC      or c-kit ligand. Antibodies of the invention are useful for preparing
CC      compositions for treating asthma. They are also used in gene therapy. The
CC      present sequence is human SCF antibody heavy chain variable and constant
CC      region
XX
SQ      Sequence 445 AA;
Query Match      88.8%; Score 769.5; DB 6; Length 445;
Best Local Similarity 89.4%; Pred. No. 6.1e-56;
Matches 152; Conservative 3; Mismatches 12; Indels 3; Gaps 1;

Qy      1 GGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db      5 GGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 64
Qy      61 FTISRDNSKNTLYLQMSLRADTAHYCAKRIFGV---VWGQGLTVTVSSASTKGSVPF 117
Db      65 FTISRDNSKNTLYLQMSLRADTAHYCAKRIFGV---VWGQGLTVTVSSASTKGSVPF 124
Qy      118 PLAPCSRSTSESTAALGCLVKDYPPPEPTVTVSNLGLTSGVHTTFFAVLQS 167
Db      125 PLAPCSRSTSESTAALGCLVKDYPPPEPTVTVSNLGLTSGVHTTFFAVLQS 174

RESULT 8
ABG77157
ID      ABG77157 standard; protein; 470 AA.
XX
AC      ABG77157;

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XX
DT      24-OCT-2002 (first entry)
XX
DE      Amino acid sequence of anti-IGF-1R antibody 2.13.2 Vh domain.
XX
KW      Insulin-like growth factor I receptor; antibody; human; cytostatic;
KW      osteopathic; antiatherosclerotic; antiapoptotic; IGF-1R; tumour;
KW      anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
KW      acromegaly; gigantism; psoriasis; atherosclerosis.
XX
OS      Homo sapiens.
XX
FN      WO200253596-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-US051113.
XX
PR      05-JAN-2001; 2001US-0259927P.
XX
PA      (PFIZ ) PFIZER INC.
XX
PA      (ABGE-) ABGENIX INC.
XX
PI      Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
WPI; 2002-575410/61.
XX
DR      Novel humanized, chimeric monoclonal antibody that specifically binds to
XX      insulin-like growth factor I (IGF-1) receptor useful for inhibiting
XX      binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
XX
PS      Claim 16; Fig 19B; 172pp; English.
XX
CC      This invention relates to a novel humanised, chimeric or human monoclonal
CC      antibody or its antigen binding portion that specifically binds to
CC      insulin-like growth factor I receptor (IGF-1R). The antibodies of the
CC      invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
CC      IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
CC      phosphorylation. The antibodies of the invention are useful for
CC      diagnosing the presence or location of an IGF-IR-expressing tumour in a
CC      subject. The antibody or its antigen-binding portion is also useful for
CC      treating cancer in a human. The method for this further involves an anti
CC      neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
CC      antibodies may also be useful for increasing IGF-IR activity and thus
CC      restoring IGF-IR activity in a condition characterised by low IGF-IR
CC      levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
CC      also useful for inducing apoptosis of specific cells in a patient, and to
CC      treat non-cancerous states or disease, e.g. acromegaly, gigantism,
CC      psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
CC      minimise the immunogenic and allergic responses intrinsic to mouse or
CC      mouse-derived monoclonal antibodies and thus increase the efficacy
CC      and safety of the administered antibodies. The present sequence
CC      represents an anti-insulin-like growth factor I receptor antibody of the
CC      invention
XX
SQ      Sequence 470 AA;
Query Match      88.5%; Score 767; DB 5; Length 470;
Best Local Similarity 85.3%; Pred. No. 1e-55;
Matches 151; Conservative 6; Mismatches 10; Indels 10; Gaps 2;

Qy      1 GGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db      27 GGGLVQPGGSLRLSCTASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 86
Qy      61 FTISRDNSKNTLYLQMSLRADTAHYCAKRI-----FGV-VWGQGLTVTVSSAS 110
Db      87 FTISRDNSRTTLYLQMSLRADTAHYCAKLDGWSDSYTYGMDVWGQGLTVTVSSAS 146
Qy      111 TKGPSVFPPLAPCSRSTSESTAALGCLVKDYPPPEPTVTVSNLGLTSGVHTTFFAVLQS 167
Db      147 TKGPSVFPPLAPCSRSTSESTAALGCLVKDYPPPEPTVTVSNLGLTSGVHTTFFAVLQS 203

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Db 67 FTISRDNKNTLYLQMSLRADTAAYVYCAKRDYDYGFDYWGQGLTVTVSSASTKGPVFP 126

Qy 119 LAPCSRSTSESTAALGCLVKDYFFPEPVTVSNWLGALTSVGHVTFPAVLQS 167

Db 127 LAPCSRSTSESTAALGCLVKDYFFPEPVTVSNWLGALTSVGHVTFPAVLQS 175

RESULT 11

ADL93667

ID ADL93667 standard; protein; 466 AA.

XX AC ADL93667;

XX DT 17-JUN-2004 (first entry)

XX DE Human CD44-binding antibody heavy chain HAE-F1-heavy SEQ ID NO:162.

XX KW human; CD44; light chain immunoglobulin variable domain;

XX KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;

XX KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;

XX KW dermatological; vasotropic; neuroprotective; antibody therapy;

XX KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;

XX KW graft versus host response; multiple sclerosis; neoplastic disorder;

XX KW cancer; antibody.

XX OS Homo sapiens.

XX PN WO2004024750-A2.

XX PD 25-MAR-2004.

XX PF 15-SEP-2003; 2003WO-US029318.

XX PR 13-SEP-2002; 2002US-0410758P.

XX PR 09-MAY-2003; 2003US-0469123P.

XX PA (DYAX-) DYAX CORP.

XX PI Rondon IJ, Edge A, Baribault Kent R;

XX DR WPI; 2004-270003/25.

XX PT New protein comprising a light chain (LC) immunoglobulin variable domain

XX PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,

XX PT useful for preparing a composition for treating inflammatory or

XX PT neoplastic disorders.

XX PS Disclosure; SEQ ID NO 162; 128pp; English.

XX CC The invention relates to a novel isolated protein comprising a light

XX CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)

XX CC immunoglobulin variable domain sequence that form an antigen binding site

XX CC with binding affinity for the human CD44 extracellular domain and where

XX CC CDR3 of the LC variable domain sequence. A protein of the invention has

XX CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,

XX CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,

XX CC and may have a use in antibody therapy. The protein is useful for

XX CC preparing a composition for treating inflammatory disorders, e.g.,

XX CC rheumatoid arthritis, lupus, restenosis, graft versus host response or

XX CC multiple sclerosis or neoplastic disorder, which is a malignant or

XX CC metastatic cancer. The present sequence represents a human CD44-binding

XX CC antibody heavy chain.

XX SQ Sequence 466 AA;

Query Match 88.2%; Score 764.5; DB 8; Length 466;

Best Local Similarity 87.2%; Pred. No. 1.7e-55;

Matches 150; Conservative 5; Mismatches 12; Indels 5; Gaps 2;

Qy 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60

Db 27 GGGVLVQPGGSLRLSCAASGFTFSYPGMWVRQAPGKGLEWVSSISPSGTTLYADSVKGR 86

Qy 61 FTISRDNKNTLYLQMSLRADTAAYVYCAKRDYDYGFDYWGQGLTVTVSSASTKGPS 115

Db 87 FTISRDNKNTLYLQMSLRADTAAYVYCAKRDYDYGFDYWGQGLTVTVSSASTKGPS 146

Qy 116 VFPLAPCSRSTSESTAALGCLVKDYFFPEPVTVSNWLGALTSVGHVTFPAVLQS 167

Db 147 VFPLAPCSRSTSESTAALGCLVKDYFFPEPVTVSNWLGALTSVGHVTFPAVLQS 198

RESULT 12

ABR01503

ID ABR01503 standard; protein; 217 AA.

XX AC ABR01503;

XX DT 16-APR-2003 (first entry)

XX DE Human anti-TIMP-1 antibody heavy chain #1.

XX KW Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;

XX KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;

XX KW variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis;

XX KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;

XX KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;

XX KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.

XX OS Homo sapiens.

XX PN WO200286085-A2.

XX PD 31-OCT-2002.

XX PF 24-APR-2002; 2002WO-US012801.

XX PR 24-APR-2001; 2001US-0285683P.

XX PA (FARB ) BAYER CORP.

XX PA (MORP-) MORPHOSYS AG.

XX PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;

XX DR WPI; 2003-129114/12.

XX DR N-PSDB; ABZ74774.

XX PT New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies,

XX PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1

XX PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung

XX PT cancer.

XX PS Claim 20; Page 148; 228pp; English.

XX CC The invention relates to a novel purified preparation of a human

XX CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)

XX CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP

XX CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a

XX CC variable light chain (VLC)DR3 region. An antibody preparation of the

XX CC invention has hepatotropic, cytostatic, nephrotropic and cardiant

XX CC activity. The human antibody is useful for decreasing an MMP-inhibiting

XX CC activity of a TIMP-1. It is especially useful for ameliorating the

XX CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,

XX CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus

XX CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary

XX CC fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The

XX CC antibody is also useful for detecting a TIMP-1 in a test preparation, or

XX CC in diagnosing a disorder in which a TIMP-1 level is elevated. The

XX CC sequences shown in ABR01502-ABR01545 represent the heavy chain regions of

XX CC a human anti-TIMP-1 antibody of the invention

XX SQ Sequence 217 AA;

Query Match 88.1%; Score 764; DB 6; Length 217;

Best Local Similarity 89.8%; Pred. No. 8e-56;

Matches 150; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVSTISVSGITTYVDSVKGR 60  
DB 8 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVSAISGGSTTYADSVKGR 67  
QY 61 FTISRDNSKNILYLQMSLRAEDTAVYCAKRIFGVVMVGQGLTVTVSSASTKGPSVPLA 120  
DB 68 FTISRDNSKNILYLQMSLRAEDTAVYCAR--FMDIWGQGLTVTVSSASTKGPSVPLA 125  
QY 121 PCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQS 167  
DB 126 PSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 172  
RESULT 13  
ABR55342  
ID ABR55342 standard; protein; 444 AA.  
XX  
AC ABR55342;  
XX  
DT 29-JUL-2003 (first entry)  
XX  
DE Amino acid sequence of a grafted VH chaine for anti-KDR antibody.  
XX  
KW Antibody; kinase insert domain-containing receptor; KDR; antibody VR165;  
KW complementarity determining region; vascular endothelial growth factor;  
KW CDR; VEGF; inflammation; psoriasis; rheumatoid arthritis; tumour.  
XX  
OS Synthetic.  
XX  
PN WO2003031475-A2.  
XX  
PD 17-APR-2003.  
XX  
PF 10-OCT-2002; 2002WO-GB004619.  
XX  
PR 10-OCT-2001; 2001GB-00024317.  
XX  
PA (CELL-) CELTECH R & D LTD.  
XX  
PI Popplewell AG, Tickle SP, Zinkewich-Peotti K, Morrison RK;  
XX  
DR WPI; 2003-441133/41.  
XX  
PT Novel antibody molecules having specificity for human kinase insert  
PT domain-containing receptors, useful for treating inflammation, psoriasis,  
PT rheumatoid arthritis, tumor growth and metastasis.  
XX  
PS Claim 16; Fig 21; 57pp; English.  
XX  
CC The specification describes an antibody molecule which has specificity  
CC for human kinase insert domain-containing receptor (KDR). The antibody  
CC comprises complementarity determining regions (CDRs) from the heavy and  
CC light chain variable domains of the murine monoclonal antibody VR165.  
CC This antibody is specific for human KDR. The antibody of the invention  
CC blocks vascular endothelial growth factor (VEGF) binding to KDR.  
CC Antibodies of the invention are useful for treating a pathology in which  
CC VEGF and/or KDR are implicated, and in the manufacture of a medicament  
CC for the treatment of a pathology in which VEGF and/or KDR are implicated.  
CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour  
CC growth or metastasis. The present sequence represents a grafted VH chain,  
CC comprising a VR165 CDR regions and a human framework. It is used to  
CC produce antibody molecules of the invention  
XX  
SQ Sequence 444 AA;  
Query Match 88.1%; Score 764; DB 6; Length 444;  
Best Local Similarity 87.7%; Pred. No. 1.8e-55;  
Matches 150; Conservative 4; Mismatches 11; Indels 6; Gaps 2;  
QY 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVSTISVSGITTYVDSVKGR 60  
DB 8 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVATITSGGYTVDYVKGR 67

QY 61 FTISRDNSKNILYLQMSLRAEDTAVYCAKRIFGV---VMGQGLTVTVSSASTKGPSV 116  
DB 68 FTISRDNAKNTLYLQMSLRAEDTAVYCYVR--IGEDALDYWGQGLTVTVSSASTKGPSV 125  
QY 117 FPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQS 167  
DB 126 FPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 176  
RESULT 14  
ABP55467  
ID ABP55467 standard; protein; 367 AA.  
XX  
AC ABP55467;  
XX  
DT 18-FEB-2003 (first entry)  
XX  
DE MALLA3 protein sequence SEQ ID NO:453.  
XX  
KW Library; cleavage; display; diverse family.  
XX  
OS Synthetic.  
XX  
PN WO200283872-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 17-APR-2002; 2002WO-US012405.  
XX  
PR 17-APR-2001; 2001US-00837306.  
PR 24-OCT-2001; 2001US-00000516.  
PR 25-OCT-2001; 2001US-00045674.  
XX  
PA (LADN/) LADNER R C.  
PA (COHE/) COHEN E H.  
PA (NAST/) NASTRI H G.  
PA (ROOK/) ROOKEY K L.  
PA (HOET/) HOET R.  
PA (HOOG/) HOOGENBOOM H R J M.  
XX  
PI Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;  
PI Hoogenboom HRJM;  
XX  
DR WPI; 2003-093015/08.  
XX  
PT Cleaving single-stranded nucleic acid sequences at a desired location by  
PT contacting the nucleic acid with an single strand oligonucleotide  
PT complementary to a nucleic acid region where cleavage is desired.  
XX  
PS Disclosure; Page 400-401; 485pp; English.  
XX  
CC The present invention describes a method for cleaving single-stranded  
CC nucleic acid sequences at a desired location. Also described: (1) methods  
CC for displaying or expressing a member of a diverse family of peptides,  
CC polypeptides or proteins on the surface of a genetic package and  
CC collectively displaying at least a part of the diversity of the family,  
CC where the displayed or expressed peptide, polypeptide or protein is  
CC encoded at least in part by a nucleic acid that has been cleaved at a  
CC desired location; (2) a method for preparing single-stranded nucleic  
CC acids; (3) a method for preparing a library comprising a collection of  
CC genetic packages that display a member of a diverse family of peptides,  
CC polypeptides or proteins and that collectively display at least a portion  
CC of the family; (4) a vector comprising a DNA sequence encoding an  
CC antibody variable region linked to a version of F101 anchor which does  
CC not mediate infection of phage particles, and wild-type gene III; (5) a  
CC method for producing a population or a library of immunoglobulin genes;  
CC and (6) a library of immunoglobulins that comprise members having at  
CC least one variable domain in which at least one of CDR1 and CDR2 contain  
CC synthetic diversity and CDR3 diversity is captured from B cells. The  
CC method is useful for cleaving single-stranded nucleic acid sequences at a  
CC desired location, which can be subsequently used to produce libraries or  
CC genetic packages that display and/or express a diverse family of

CC peptides, polypeptides or proteins. ABZ36912 to ABZ37510 and ABP55464 to  
CC ABP55499 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 367 AA;  
  
Query Match 88.1%; Score 763.5; DB 6; Length 367;  
Best Local Similarity 87.2%; Pred. No. 1.6e-55;  
Matches 150; Conservative 4; Mismatches 13; Indels 5; Gaps 1;  
  
Qy 1 GGGVLVQPGGSLRLSCAASGFTFFSSYAMSVWVRAQPGKGLEWVSTISVSGITTYVDSVKGR 60  
Db 30 GGGVLVQPGGSLRLSCAASGFTFFSSYAMSVWVRAQPGKGLEWVSTISVSGITTYVDSVKGR 89  
  
Qy 61 FTISRDNKNILYLQMNLSRAEDTAVYYCAKRIFGV-----VWGQGLTVTVSSASTKGPS 115  
Db 90 FTISRDNKNILYLQMNLSRAEDTAVYYCAKRIFGV-----VWGQGLTVTVSSASTKGPS 149  
  
Qy 116 VPELAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 167  
Db 150 VPELAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 201

RESULT 15  
ADL93670  
ID ADL93670 standard; protein; 462 AA.  
XX  
AC ADL93670;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human CD44-binding antibody heavy chain BE-A11-heavy SEQ ID NO:165.  
XX  
KW human; CD44; light chain immunoglobulin variable domain;  
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;  
KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;  
KW dermatological; vasotropic; neuroprotective; antibody therapy;  
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;  
KW graft versus host response; multiple sclerosis; neoplastic disorder;  
KW cancer; antibody.  
XX  
OS Homo sapiens.  
XX  
PN WO2004024750-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 15-SEP-2003; 2003WO-US029318.  
XX  
PR 13-SEP-2002; 2002US-0410758P.  
PR 09-MAY-2003; 2003US-0469123P.  
XX  
PA (DYAX-) DYAX CORP.  
XX  
PI Rondon IJ, Edge A, Baribault Kent R;  
XX  
DR WPI; 2004-270003/25.  
XX  
PT New protein comprising a light chain (LC) immunoglobulin variable domain  
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,  
PT useful for preparing a composition for treating inflammatory or  
PT neoplastic disorders.  
XX  
PS Disclosure; SEQ ID NO 165; 128pp; English.

XX  
CC The invention relates to a novel isolated protein comprising a light  
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)  
CC immunoglobulin variable domain sequence that form an antigen binding site  
CC with binding affinity for the human CD44 extracellular domain and where  
CC CD44 of the LC variable domain sequence. A protein of the invention has  
CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,  
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,  
CC and may have a use in antibody therapy. The protein is useful for

CC preparing a composition for treating inflammatory disorders, e.g.,  
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
CC multiple sclerosis or neoplastic disorder, which is a malignant or  
CC metastatic cancer. The present sequence represents a human CD44-binding  
CC antibody heavy chain.  
XX  
SQ Sequence 462 AA;  
  
Query Match 88.1%; Score 763.5; DB 8; Length 462;  
Best Local Similarity 88.7%; Pred. No. 2e-55;  
Matches 149; Conservative 4; Mismatches 14; Indels 1; Gaps 1;  
  
Qy 1 GGGVLVQPGGSLRLSCAASGFTFFSSYAMSVWVRAQPGKGLEWVSTISVSGITTYVDSVKGR 60  
Db 27 GGGVLVQPGGSLRLSCAASGFTFFSKYSMEWVRAQPGKGLEWVSTISVSGITTYVDSVKGR 86  
  
Qy 61 FTISRDNKNILYLQMNLSRAEDTAVYYCAKRIFGV-VWGQGLTVTVSSASTKGPSVPPL 119  
Db 87 FTISRDNKNILYLQMNLSRAEDTAVYYCARDSTGMDVWGQGLTVTVSSASTKGPSVPPL 146  
  
Qy 120 APCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 167  
Db 147 APCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 194

Search completed: March 8, 2005, 06:17:24  
Job time : 78.4257 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 88.6225 Seconds  
(without alignments)  
620.051 Million cell updates/sec

Title: US-09-784-950-40  
Perfect score: 867  
Sequence: 1 GGGLVQPGGSLRLSCAASGP.....SWNLGALTSGVHTFPAVLQS 167

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	788	90.9	465	14	US-10-401-344-2
2	780	90.0	470	15	US-10-038-591-46
3	774.5	89.3	467	15	US-10-180-648-2
4	769.5	88.8	445	14	US-10-320-231A-79
5	767	88.5	470	15	US-10-038-591-45
6	765.5	88.3	443	9	US-09-917-410-4
7	764.5	88.2	466	16	US-10-663-244-162
8	764	88.1	217	16	US-10-128-520-140
9	763.5	88.1	367	15	US-10-045-674-453
10	763.5	88.1	368	11	US-09-837-306-196
11	763.5	88.1	462	16	US-10-663-244-165
12	763	88.0	217	16	US-10-128-520-142
13	762.5	87.9	222	16	US-10-128-520-145

14	761.5	87.8	220	16	US-10-128-520-156	Sequence 156, App
15	760.5	87.7	222	16	US-10-128-520-152	Sequence 152, App
16	760	87.7	217	16	US-10-128-520-146	Sequence 146, App
17	760	87.7	224	10	US-09-972-656-68	Sequence 68, Appl
18	758.5	87.5	224	16	US-10-128-520-150	Sequence 150, App
19	757.5	87.4	473	15	US-10-038-591-50	Sequence 50, Appl
20	757	87.3	221	16	US-10-128-520-143	Sequence 143, App
21	756.5	87.3	218	16	US-10-128-520-144	Sequence 144, App
22	756	87.2	221	16	US-10-128-520-171	Sequence 171, App
23	755	87.1	217	16	US-10-128-520-141	Sequence 141, App
24	754.5	87.0	220	16	US-10-128-520-154	Sequence 154, App
25	754.5	87.0	462	16	US-10-663-244-163	Sequence 163, App
26	754.5	87.0	464	16	US-10-663-244-156	Sequence 156, App
27	753.5	86.9	462	16	US-10-663-244-155	Sequence 155, App
28	752.5	86.8	224	16	US-10-128-520-148	Sequence 148, App
29	752	86.7	470	15	US-10-292-088-78	Sequence 78, Appl
30	751	86.6	463	16	US-10-663-244-160	Sequence 160, App
31	749.5	86.4	223	10	US-09-972-656-86	Sequence 86, Appl
32	749.5	86.4	460	16	US-10-663-244-159	Sequence 159, App
33	749.5	86.4	468	16	US-10-663-244-161	Sequence 161, App
34	748.5	86.3	464	16	US-10-663-244-158	Sequence 158, App
35	747	86.2	469	16	US-10-663-244-164	Sequence 164, App
36	745	85.9	449	9	US-09-736-371B-21	Sequence 21, Appl
37	745	85.9	449	15	US-10-463-442-21	Sequence 21, Appl
38	745	85.9	451	9	US-09-822-698A-26	Sequence 26, Appl
39	743	85.7	470	15	US-10-292-088-62	Sequence 62, Appl
40	743	85.7	470	15	US-10-038-591-49	Sequence 49, Appl
41	742	85.6	469	16	US-10-663-244-157	Sequence 157, App
42	742	85.6	474	10	US-09-848-832-3	Sequence 3, Appli
43	742	85.6	474	14	US-10-225-108A-3	Sequence 3, Appli
44	742	85.6	474	15	US-10-461-148-1	Sequence 1, Appli
45	742	85.6	519	16	US-10-312-354-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1  
US-10-401-344-2  
; Sequence 2, Application US/10401344  
; Publication No. US20030194404A1  
; GENERAL INFORMATION:  
; APPLICANT: Schering Corporation and Abgenix, Inc.  
; APPLICANT: Greenfeder, Scott  
; APPLICANT: Corvalan, Jose  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COMPC  
; TITLE OF INVENTION: COMPRISING SAME  
; FILE REFERENCE: L101564W1  
; CURRENT APPLICATION NUMBER: US/10/401,344  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)..(19)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: Variable Region  
; LOCATION: (20)..(138)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: CH1 Region  
; LOCATION: (139)..(236)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: Hinge Region  
; LOCATION: (237)..(248)  
; OTHER INFORMATION:  
; FEATURE:

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; NAME/KEY: CH2 Region
; LOCATION: (249)..(358)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CH3 Region
; LOCATION: (359)..(465)
; OTHER INFORMATION:
US-10-401-344-2

Query Match      90.9%; Score 788; DB 14; Length 465;
Best Local Similarity 90.6%; Pred. No. 1.2e-50;
Matches 155; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

Qy 1 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 27 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISGSGSTYYADSVKGR 86

Qy 61 FTISRDNSKNTLYLQWNSLRADTAIVYCAKRIFG-----VWGGTTLVTVSSASTKGPSV 116
Db 87 FTISRDNSKNTLYLQWNSLRADTAIVYCAKERYNNYLYHWGGTTLVTVSSASTKGPSV 146

Qy 117 FPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 167
Db 147 FPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 197

RESULT 2
US-10-038-591-46
; Sequence 46, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-46

Query Match      90.0%; Score 780; DB 15; Length 470;
Best Local Similarity 87.6%; Pred. No. 4.6e-50;
Matches 155; Conservative 3; Mismatches 9; Indels 10; Gaps 2;

Qy 1 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 27 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSAISGSGSTYYADSVKGR 86

Qy 61 FTISRDNSKNTLYLQWNSLRADTAIVYCAK-----RIFGV-VWGGTTLVTVSSAS 110
Db 87 FTISRDNSKNTLYLQWNSLRADTAIVYCAKGYSSGWYVYVYVYVYVYVYVYVYVYVYV 146

Qy 111 TKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 167
Db 147 TKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 203

RESULT 3
US-10-180-648-2
; Sequence 2, Application US/10180648
; Publication No. US20040033535A1
; GENERAL INFORMATION:
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; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvalan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPG
; FILE REFERENCE: 06843.0049-00000
; CURRENT APPLICATION NUMBER: US/10/180,648
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/301,172
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-648-2

Query Match      89.3%; Score 774.5; DB 15; Length 467;
Best Local Similarity 88.5%; Pred. No. 1.2e-49;
Matches 154; Conservative 2; Mismatches 11; Indels 7; Gaps 1;

Qy 1 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 27 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSGITGSGSTYYADSVKGR 86

Qy 61 FTISRDNSKNTLYLQWNSLRADTAIVYCAKRIFGV-----WGOGTTLVTVSSASTKG 113
Db 87 FTISRDNSKNTLYLQWNSLRADTAIVYCAKDPGTTVMSWFDPMGGGTLVTVSSASTKG 146

Qy 114 PSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 167
Db 147 PSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 200

RESULT 4
US-10-320-231A-79
; Sequence 79, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-79

Query Match      88.8%; Score 769.5; DB 14; Length 445;
Best Local Similarity 89.4%; Pred. No. 2.6e-49;
Matches 152; Conservative 3; Mismatches 12; Indels 3; Gaps 1;

Qy 1 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 5 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSAISGSGSTYYADSVKGR 64

Qy 61 FTISRDNSKNTLYLQWNSLRADTAIVYCAKRIFGV---VWGGTTLVTVSSASTKGPSVF 117
Db 65 FTISRDNSKNTLYLQWNSLRADTAIVYCARROFFFAHFDVWGGTTLVTVSSASTKGPSVF 124

Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 167
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|||||:|||||
Db 125 PLAPSSKTSCTAALGCLVKDYFPEPVTVSNWNGALTSVHTTTPAVLQS 174

RESULT 5
US-10-038-591-45
; Sequence 45, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-45

Query Match 88.5%; Score 767; DB 15; Length 470;
Best Local Similarity 85.3%; Pred. No. 4.3e-49;
Matches 151; Conservative 6; Mismatches 10; Indels 10; Gaps 2;

Qy 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVLVQPGGSLRLSCTASGFTFSYAMWVRQAPGKGLEWVSAISGSGITTFYADSVKGR 86
Qy 61 FTISRDNSKNILYLQMSLRAEDTAVYYCAKRI-----FGV-VWGQGLTVTVSSAS 110
Db 87 FTISRDNSRTLYLQMSLRAEDTAVYYCAKDLGWSDSYVYVYGVWVGQGTTVTVSSAS 146
Qy 111 TKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSVHTTTPAVLQS 167
Db 147 TKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSVHTTTPAVLQS 203

RESULT 6
US-09-917-410-4
; Sequence 4, Application US/09917410
; Patent No. US20020098183A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
; CO, Man S.
; TITLE OF INVENTION: ANTI-I-SELECTIN ANTIBODIES FOR PREVENTION OF
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER
; EXTRACORPOREAL BLOOD CIRCULATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pelfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII, WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,410
; FILING DATE: 26-Jul-2001

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020098183A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-917-410-4

Query Match 88.3%; Score 765.5; DB 9; Length 443;
Best Local Similarity 88.8%; Pred. No. 5.2e-49;
Matches 150; Conservative 6; Mismatches 10; Indels 3; Gaps 2;

Qy 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 8 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVASISTGG-STIYPDSVKGR 66
Qy 61 FTISRDNSKNILYLQMSLRAEDTAVYYCAKRIFGV--VWGQGLTVTVSSASTKGPSVFP 118
Db 67 FTISRDNAKNTLYLQMSLRAEDTAVYYCARDYDGYDYGQGLTVTVSSASTKGPSVFP 126
Qy 119 LAPCSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSVHTTTPAVLQS 167
Db 127 LAPCSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSVHTTTPAVLQS 175

RESULT 7
US-10-663-244-162
; Sequence 162, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-162

Query Match 88.2%; Score 764.5; DB 16; Length 466;
Best Local Similarity 87.2%; Pred. No. 6.5e-49;
Matches 150; Conservative 5; Mismatches 12; Indels 5; Gaps 2;

Qy 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVLVQPGGSLRLSCAASGFTFSYGMWVRQAPGKGLEWVSSISPSTGTTLYADSVKGR 86
```

```
QY 61 FTISRDNKNTLYLQMSLRAEDTAVYYCAKRIFGV--VMQGTLVTVSSASTKGPS 115
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 87 FTISRDNKNTLYLQMSLRAEDTAVYYCARQKRESSIGAFDINGQGTMTVTSSASTKGPS 146
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 116 VFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNWLGLTSGVHTFPAVLQS 167
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 147 VFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNWSGALTSGVHTFPAVLQS 198
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

RESULT 8
US-10-128-520-140
; Sequence 140, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-140

Query Match 88.1%; Score 764; DB 16; Length 217;
Best Local Similarity 89.8%; Pred. No. 3.4e-49;
Matches 150; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY 1 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWWSITISVSGITTYVDSVKGR 60
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 8 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWWSAISGSGSTTYADSVKGR 67
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 61 FTISRDNKNTLYLQMSLRAEDTAVYYCAKRIFGVVMQGTLVTVSSASTKGPSVFPLA 120
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 68 FTISRDNKNTLYLQMSLRAEDTAVYYCAR--FMDIWGGQTLVTVSSASTKGPSVFPLA 125
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 121 PCSRSTSESTAALGCLVKDYFPEPTVTSNWLGLTSGVHTFPAVLQS 167
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 126 PSSKSTSGTAAALGCLVKDYFPEPTVTSNWSGALTSGVHTFPAVLQS 172
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

RESULT 9
US-10-045-674-453
; Sequence 453, Application US/10045674
; Publication No. US2003023233A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: DYAX/002 CIP2
; CURRENT APPLICATION NUMBER: US/10/045,674
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 09/837,306
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 635
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 453
; LENGTH: 367
```

```
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: MALIA3 protein
; OTHER INFORMATION: sequence
US-10-045-674-453

Query Match 88.1%; Score 763.5; DB 15; Length 367;
Best Local Similarity 87.2%; Pred. No. 6.1e-49;
Matches 150; Conservative 4; Mismatches 13; Indels 5; Gaps 1;

QY 1 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWWSITISVSGITTYVDSVKGR 60
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 30 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWWSAISGSGSTTYADSVKGR 89
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 61 FTISRDNKNTLYLQMSLRAEDTAVYYCAKRIFGV-----VMQGTLVTVSSASTKGPS 115
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 90 FTISRDNKNTLYLQMSLRAEDTAVYYCAKDYEGTGAFDINGQGTMTVTSSASTKGPS 149
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 116 VFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNWLGLTSGVHTFPAVLQS 167
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 150 VFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSNWSGALTSGVHTFPAVLQS 201
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

RESULT 10
US-09-837-306-196
; Sequence 196, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; FILE REFERENCE: DYAX/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 196
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: MALIA3
US-09-837-306-196

Query Match 88.1%; Score 763.5; DB 11; Length 368;
Best Local Similarity 87.2%; Pred. No. 6.1e-49;
Matches 150; Conservative 4; Mismatches 13; Indels 5; Gaps 1;

QY 1 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWWSITISVSGITTYVDSVKGR 60
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 30 GGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWWSAISGSGSTTYADSVKGR 89
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 61 FTISRDNKNTLYLQMSLRAEDTAVYYCAKRIFGV-----VMQGTLVTVSSASTKGPS 115
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 90 FTISRDNKNTLYLQMSLRAEDTAVYYCAKDYEGTGAFDINGQGTMTVTSSASTKGPS 149
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

QY 116 VFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNWLGLTSGVHTFPAVLQS 167
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 150 VFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSNWSGALTSGVHTFPAVLQS 201
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

RESULT 11
US-10-663-244-165
; Sequence 165, Application US/10663244
; Publication No. US20040110933A1
```



```
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
; US-10-663-244-165

Query Match      88.1%; Score 763.5; DB 16; Length 462;
Best Local Similarity 88.7%; Pred. No. 7.6e-49;
Matches 149; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

QY 1 GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 27 GGGLVQPGGSLRLSCAASGFTFSSYMEWVRQAPGKGLWVSRIPYSGGPTLYADSVKGR 86
QY 61 FTISRDNSKNTLYLQWNSLRAEDTAVYYCAKRIQGV-VWGQGLTVTVSSASTKGPSVFPL 119
Db 87 FTISRDNSKNTLYLQWNSLRAEDTAVYYCARDYSYGMVWGQGLTVTVSSASTKGPSVFPL 146
QY 120 APCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQ 167
Db 147 APCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 194

RESULT 12
US-10-128-520-142
; Sequence 142, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-128-520-142

Query Match      88.0%; Score 763; DB 16; Length 217;
Best Local Similarity 89.8%; Pred. No. 4e-49;
Matches 150; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY 1 GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 8 GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWVSAISGSGSTYYADSVKGR 67
QY 61 FTISRDNSKNTLYLQWNSLRAEDTAVYYCAKRIQGVVWGQGLTVTVSSASTKGPSVFPL 120
Db 68 FTISRDNSKNTLYLQWNSLRAEDTAVYYCAR--FLDWGQGLTVTVSSASTKGPSVFPL 125
QY 121 PCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQ 167
| :||| |
```

```
Db 126 PSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 172

RESULT 13
US-10-128-520-145
; Sequence 145, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-128-520-145

Query Match      87.9%; Score 762.5; DB 16; Length 222;
Best Local Similarity 88.2%; Pred. No. 4.5e-49;
Matches 150; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 1 GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 8 GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWVSAISGSGSTYYADSVKGR 67
QY 61 FTISRDNSKNTLYLQWNSLRAEDTAVYYCAKRIQGV---VWGQGLTVTVSSASTKGPSVF 117
Db 68 FTISRDNSKNTLYLQWNSLRAEDTAVYYCARYRGLSFDIWGQGLTVTVSSASTKGPSVF 127
QY 118 PLAPCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQ 167
Db 128 PLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 177

RESULT 14
US-10-128-520-156
; Sequence 156, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-128-520-156

Query Match      87.8%; Score 761.5; DB 16; Length 220;
Best Local Similarity 89.3%; Pred. No. 5.3e-49;
Matches 150; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 8 GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLWVSAISGSGSTYYADSVKGR 67
QY 61 FTISRDNSKNTLYLQWNSLRAEDTAVYYCAKRI--FGVWGQGLTVTVSSASTKGPSVFPL 119
Db 68 FTISRDNSKNTLYLQWNSLRAEDTAVYYCARLICYFDLWGQGLTVTVSSASTKGPSVFPL 127
QY 120 APCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQ 167
```

Db 128 APSSKSTGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 175

RESULT 15

US-10-128-520-152  
; Sequence 152, Application US/10128520  
; Publication No. US20040105862A1  
; GENERAL INFORMATION:  
; APPLICANT: PAN et al.  
; TITLE OF INVENTION: Human TIMP-1 Antibodies  
; FILE REFERENCE: 02973.00073  
; CURRENT APPLICATION NUMBER: US/10/128,520  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 60/285,683  
; PRIOR FILING DATE: 2001-04-24  
; NUMBER OF SEQ ID NOS: 381  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 152  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-128-520-152

Query Match 87.7%; Score 760.5; DB 16; Length 222;  
Best Local Similarity 88.8%; Pred. No. 6.3e-49;  
Matches 151; Conservative 4; Mismatches 12; Indels 3; Gaps 2;  
Qy 1 GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60  
Db 8 GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGSTYYADSVKGR 67  
Qy 61 FTISRDNSKNTLYLQMSLRAEDTAVYYCAK--RIFGV-VWGQGLTVTVSSASTKGPSVF 117  
Db 68 FTISRDNSKNTLYLQMSLRAEDTAVYYCARYGAYFGLDYWGQGLTVTVSSASTKGPSVF 127  
Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGALTSGVHTFPAVLQS 167  
Db 128 PLAPSSKSTGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 177

Search completed: March 8, 2005, 07:05:59  
Job time : 89.6225 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 18.3627 Seconds  
(without alignments)  
678.897 Million cell updates/sec

Title: US-09-784-950-40

Perfect score: 867

Sequence: 1 GGGVQPGGSLRLSCAASG.....SWNLGALTGVHTFPAVLQS 167

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	765.5	88.3	443	5	PCT-US96-13152-4
2	742	85.6	467	1	US-08-704-744-81
3	741	85.5	451	4	US-09-472-087-70
4	729.5	84.1	248	4	US-09-315-926A-80
5	727.5	83.9	463	4	US-09-472-087-1
6	727.5	83.9	463	4	US-09-472-087-63
7	727.5	83.9	463	4	US-09-472-087-64
8	726.5	83.8	463	4	US-09-472-087-4
9	726.5	83.8	463	4	US-09-472-087-68
10	724.5	83.6	169	4	US-09-472-087-5
11	724.5	83.6	169	4	US-09-472-087-73
12	719	82.9	464	4	US-09-472-087-2
13	719	82.9	464	4	US-09-472-087-66
14	718	82.8	225	4	US-09-456-090A-56
15	718	82.8	225	4	US-09-456-090A-60
16	718	82.8	225	4	US-09-456-090A-70
17	718	82.8	225	4	US-09-456-090A-92
18	718	82.8	225	4	US-09-453-234-56
19	718	82.8	225	4	US-09-453-234-60
20	718	82.8	225	4	US-09-453-234-70
21	718	82.8	225	4	US-09-453-234-92
22	717.5	82.8	174	4	US-09-472-087-12
23	717	82.7	470	4	US-09-859-053-32
24	717	82.7	470	4	US-09-859-053-36
25	715	82.5	225	4	US-09-456-090A-68
26	715	82.5	225	4	US-09-456-090A-106
27	715	82.5	225	4	US-09-453-234-68

28	715	82.5	225	4	US-09-453-234-106	Sequence 106, App
29	712	82.1	225	4	US-09-456-090A-108	Sequence 108, App
30	712	82.1	225	4	US-09-453-234-108	Sequence 108, App
31	711.5	82.1	167	4	US-09-472-087-74	Sequence 74, Appl
32	709	81.8	225	4	US-09-456-090A-94	Sequence 94, Appl
33	709	81.8	225	4	US-09-453-234-94	Sequence 94, Appl
34	708	81.7	225	4	US-09-456-090A-58	Sequence 58, Appl
35	708	81.7	225	4	US-09-456-090A-110	Sequence 110, App
36	708	81.7	225	4	US-09-453-234-58	Sequence 58, Appl
37	708	81.7	225	4	US-09-453-234-110	Sequence 110, App
38	706.5	81.5	233	2	US-08-480-753-2	Sequence 2, Appli
39	706.5	81.5	233	3	US-09-041-889-9	Sequence 9, Appli
40	706.5	81.5	233	3	US-08-837-058-9	Sequence 9, Appli
41	706.5	81.5	233	4	US-09-417-264-9	Sequence 9, Appli
42	706	81.4	225	4	US-09-456-090A-102	Sequence 102, App
43	706	81.4	225	4	US-09-453-234-102	Sequence 102, App
44	705.5	81.4	171	4	US-09-472-087-83	Sequence 83, Appl
45	704	81.2	225	4	US-09-456-090A-98	Sequence 98, Appl

#### ALIGNMENTS

RESULT 1  
PCT-US96-13152-4  
; Sequence 4, Application PC/TUS9613152  
; GENERAL INFORMATION:  
; APPLICANT: Martin, Ulrich, et al.  
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; ADDRESSEE: Attn: Norman D. Hanson  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Computer Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/13152  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/578,953  
; FILING DATE: 27-Dec-95  
; APPLICATION NUMBER: EP 95 112 895.8  
; FILING DATE: 17-Aug-95  
; APPLICATION NUMBER: EP 95 114 969.9  
; FILING DATE: 19-Sep-95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Norman D. Hanson  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 688-3884  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 443  
; TYPE: amino acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US96-13152-4

Query Match 88.3% Score 765.5; DB 5; Length 443;  
Best Local Similarity 88.8%; Pred. No. 2.4e-62;  
Matches 150; Conservative 6; Mismatches 10; Indels 3; Gaps 2;

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QY 1 GGGLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 8 GGGLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 66
QY 61 FTISRDNKNILYLQNMNLSRAEDTAVYYCAKRIFGV--VWGQGLTVTVSSASTKGPSVFP 118
Db 67 FTISRDNKNILYLQNMNLSRAEDTAVYYCAKRIFGV--VWGQGLTVTVSSASTKGPSVFP 126
QY 119 LAPCSRSTSESTAALGCLVKDYRPEPTVSWNLSGALTSGVHTFPAVLQ 167
Db 127 LAPCSRSTSESTAALGCLVKDYRPEPTVSWNLSGALTSGVHTFPAVLQ 175

RESULT 2
US-08-704-744-81
; Sequence 81, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalié, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-704-744-81

Query Match 85.6%; Score 742; DB 1; Length 467;
Best Local Similarity 83.2%; Pred. No. 3.7e-60;
Matches 14; Conservative 10; Mismatches 13; Indels 6; Gaps 1;

QY 1 GGGLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGGLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 86
QY 61 FTISRDNKNILYLQNMNLSRAEDTAVYYCAKRIFGV-----VWGQGLTVTVSSASTKGP 114
Db 87 FTISRDNKNILYLQNMNLSRAEDTAVYYCAKRIFGV-----VWGQGLTVTVSSASTKGP 146
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QY 115 SVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNLSGALTSGVHTFPAVLQ 167
Db 147 SVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNLSGALTSGVHTFPAVLQ 199

RESULT 3
US-09-472-087-70
; Sequence 70, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-70

Query Match 85.5%; Score 741; DB 4; Length 451;
Best Local Similarity 82.5%; Pred. No. 4.4e-60;
Matches 146; Conservative 3; Mismatches 18; Indels 10; Gaps 1;

QY 1 GGGLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 8 GGGLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 67
QY 61 FTISRDNKNILYLQNMNLSRAEDTAVYYCAKRIFGV-----VWGQGLTVTVSSAS 110
Db 68 FTISRDNKNILYLQNMNLSRAEDTAVYYCAKRIFGV-----VWGQGLTVTVSSAS 127
QY 111 TKGPSVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNLSGALTSGVHTFPAVLQ 167
Db 128 TKGPSVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNLSGALTSGVHTFPAVLQ 184

RESULT 4
US-09-315-926A-80
; Sequence 80, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmut
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
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Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNIGALTSGVHTFPAVLQ 167
Db 147 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNIGALTSGVHTFPAVLQ 196

RESULT 8
US-09-472-087-4
; Sequence 4, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-4

Query Match      83.8%; Score 726.5; DB 4; Length 463;
Best Local Similarity 83.5%; Pred. No. 9.6e-59;
Matches 142; Conservative 6; Mismatches 19; Indels 3; Gaps 2;

Qy 1 GGGVLQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWSTISVSGITTYVDSVKGR 60
Db 27 GGGVVEPGRSLRLSCTASGFTFSYGMHWVRQAPGKGLVWVAVIWDGSKNHYADSAKGR 86
Qy 61 FTISRDNSKNTLYLQMNLSRAEDTAVYYCAKR-IFGV--VWGQGLTVTVSSASTKGPSVF 117
Db 87 FTISRDNSKNTLYLQMNLSRAEDTAVYYCARAGLLGYFDYWGQGLTVTVSSASTKGPSVF 146
Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNIGALTSGVHTFPAVLQ 167
Db 147 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNIGALTSGVHTFPAVLQ 196

RESULT 9
US-09-472-087-68
; Sequence 68, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-68

Query Match      83.8%; Score 726.5; DB 4; Length 169;
Best Local Similarity 85.2%; Pred. No. 4.4e-59;
Matches 144; Conservative 3; Mismatches 17; Indels 5; Gaps 2;

Qy 3 GLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWSTISVSGITTYVDSVKGRFT 62
Db 1 GVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKGLVWVAVIWDGSKNHYADSVKGRFT 60
Qy 63 ISRDNSKNTLYLQMNLSRAEDTAVYYCAK--RIFGV---VWGQGLTVTVSSASTKGPSVF 117
Db 61 ISRDNSKNTLYLQMNLSRAEDTAVYYCARGARIITPCMDVWGQGLTVTVSSASTKGPSVF 120
Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNIGALTSGVHTFPAVLQ 166
Db 121 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNIGALTSGVHTFPAVLQ 169

RESULT 11
US-09-472-087-73
; Sequence 73, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY

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US-09-472-087-68

Query Match      83.8%; Score 726.5; DB 4; Length 463;
Best Local Similarity 83.5%; Pred. No. 9.6e-59;
Matches 142; Conservative 6; Mismatches 19; Indels 3; Gaps 2;

Qy 1 GGGVLQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWSTISVSGITTYVDSVKGR 60
Db 27 GGGVVEPGRSLRLSCTASGFTFSYGMHWVRQAPGKGLVWVAVIWDGSKNHYADSAKGR 86
Qy 61 FTISRDNSKNTLYLQMNLSRAEDTAVYYCAKR-IFGV--VWGQGLTVTVSSASTKGPSVF 117
Db 87 FTISRDNSKNTLYLQMNLSRAEDTAVYYCARAGLLGYFDYWGQGLTVTVSSASTKGPSVF 146
Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNIGALTSGVHTFPAVLQ 167
Db 147 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNIGALTSGVHTFPAVLQ 196

RESULT 10
US-09-472-087-5
; Sequence 5, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-5

Query Match      83.6%; Score 724.5; DB 4; Length 169;
Best Local Similarity 85.2%; Pred. No. 4.4e-59;
Matches 144; Conservative 3; Mismatches 17; Indels 5; Gaps 2;

Qy 3 GLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWSTISVSGITTYVDSVKGRFT 62
Db 1 GVVQPGGSLRLSCAASGFTFSYGMHWVRQAPGKGLVWVAVIWDGSKNHYADSVKGRFT 60
Qy 63 ISRDNSKNTLYLQMNLSRAEDTAVYYCAK--RIFGV---VWGQGLTVTVSSASTKGPSVF 117
Db 61 ISRDNSKNTLYLQMNLSRAEDTAVYYCARGARIITPCMDVWGQGLTVTVSSASTKGPSVF 120
Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNIGALTSGVHTFPAVLQ 166
Db 121 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNIGALTSGVHTFPAVLQ 169

RESULT 11
US-09-472-087-73
; Sequence 73, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY

```

```
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-472-087-73

Query Match      83.6%; Score 724.5; DB 4; Length 169;
Best Local Similarity 85.2%; Pred. No. 4.4e-59;
Matches 144; Conservative 3; Mismatches 17; Indels 5; Gaps 2;

Qy 3 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGKFT 62
Db 1 GWVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGKFT 60

Qy 63 ISRDNSKNILYLQMSLRADTAIVYCAK--RIFGV---VWGQGLTVTVSSASTKGPSV 117
Db 61 ISRDNSKNILYLQMSLRADTAIVYCAKRIITPCMDVWGQGLTVTVSSASTKGPSV 120

Qy 118 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGALTSGVHTFPAVLQ 166
Db 121 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 169

RESULT 12
US-09-472-087-2
; Sequence 2, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-2

Query Match      82.9%; Score 719; DB 4; Length 464;
Best Local Similarity 83.0%; Pred. No. 4.7e-58;
Matches 142; Conservative 7; Mismatches 18; Indels 4; Gaps 2;

Qy 1 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGK 60
Db 27 GGVVQPGSLRLSCTASGFTFSYGMHVRQAPGKGLEWVAVIWDGSKNKHGDSVKGR 86

Qy 61 FTISRDNKNILYLQMSLRADTAIVYCAK--RI--FGVWGQGLTVTVSSASTKGPSV 116
Db 87 FTISRDNKNILYLQMSLRADTAIVYCAKRIITPCMDVWGQGLTVTVSSASTKGPSV 146

Qy 117 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGALTSGVHTFPAVLQ 167
Db 147 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 197

RESULT 13
US-09-472-087-66
; Sequence 66, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-66

Query Match      82.9%; Score 719; DB 4; Length 464;
Best Local Similarity 83.0%; Pred. No. 4.7e-58;
Matches 142; Conservative 7; Mismatches 18; Indels 4; Gaps 2;

Qy 1 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGR 60
Db 27 GGVVQPGSLRLSCTASGFTFSYGMHVRQAPGKGLEWVAVIWDGSKNKHGDSVKGR 86

Qy 61 FTISRDNKNILYLQMSLRADTAIVYCAK--RI--FGVWGQGLTVTVSSASTKGPSV 116
Db 87 FTISRDNKNILYLQMSLRADTAIVYCAKRIITPCMDVWGQGLTVTVSSASTKGPSV 146

Qy 117 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGALTSGVHTFPAVLQ 167
Db 147 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 197

RESULT 14
US-09-456-090A-56
; Sequence 56, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkira, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nile
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-3H
US-09-456-090A-56

Query Match      82.8%; Score 718; DB 4; Length 225;
Best Local Similarity 83.4%; Pred. No. 2.4e-58;
Matches 141; Conservative 5; Mismatches 21; Indels 2; Gaps 1;

Qy 1 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGR 60
Db 147 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 197
```

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; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-472-087-73

Query Match      83.6%; Score 724.5; DB 4; Length 169;
Best Local Similarity 85.2%; Pred. No. 4.4e-59;
Matches 144; Conservative 3; Mismatches 17; Indels 5; Gaps 2;

Qy 3 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGKFT 62
Db 1 GWVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGKFT 60

Qy 63 ISRDNSKNILYLQMSLRADTAIVYCAK--RIFGV---VWGQGLTVTVSSASTKGPSV 117
Db 61 ISRDNSKNILYLQMSLRADTAIVYCAKRIITPCMDVWGQGLTVTVSSASTKGPSV 120

Qy 118 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGALTSGVHTFPAVLQ 166
Db 121 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 169

RESULT 12
US-09-472-087-2
; Sequence 2, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-2

Query Match      82.9%; Score 719; DB 4; Length 464;
Best Local Similarity 83.0%; Pred. No. 4.7e-58;
Matches 142; Conservative 7; Mismatches 18; Indels 4; Gaps 2;

Qy 1 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGR 60
Db 27 GGVVQPGSLRLSCTASGFTFSYGMHVRQAPGKGLEWVAVIWDGSKNKHGDSVKGR 86

Qy 61 FTISRDNKNILYLQMSLRADTAIVYCAK--RI--FGVWGQGLTVTVSSASTKGPSV 116
Db 87 FTISRDNKNILYLQMSLRADTAIVYCAKRIITPCMDVWGQGLTVTVSSASTKGPSV 146

Qy 117 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGALTSGVHTFPAVLQ 167
Db 147 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 197
```

Db 8 GGGVVQFGRSLRLSCAASGFTFSYGMHWRQAFPGKLEWTLITYDGNKYADSVKGR 67  
Qy 61 FTISRDNKNTLYLQMNLSRAEDTAVYYCAKRIFGV--VMQGQTLVTVSSASTKGPSVFP 118  
Db 68 FTISRDNKNTLYLQMNLSRAEDTAVYYCARDGIGYFDYMGQGLTIVTSSASTKGPSVFP 127  
Qy 119 LAPCSRSTSESTAALGCLVKDYFPEPPTVSNLIGALTSGVHTFPAVLQS 167  
Db 128 LAPSKSTSGGTAALGCLVKDYFPEPPTVSNLIGALTSGVHTFPAVLQS 176

RESULT 15  
US-09-456-090A-60  
; Sequence 60, Application US/09456090A  
; Patent No. 6680209  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS  
; FILE REFERENCE: 020015-000200US  
; CURRENT APPLICATION NUMBER: US/09/456,090A  
; CURRENT FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 60  
; LENGTH: 225  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-5H  
US-09-456-090A-60

Query Match 82.8%; Score 718; DB 4; Length 225;  
Best Local Similarity 83.4%; Pred. No. 2.4e-58;  
Matches 141; Conservative 5; Mismatches 21; Indels 2; Gaps 1;  
Qy 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVVDVSVKGR 60  
Db 8 GGGVVQFGRSLRLSCAASGFTFSYGMHWRQAFPGKLEWTLITYDGNKYADSVKGR 67  
Qy 61 FTISRDNKNTLYLQMNLSRAEDTAVYYCAKRIFGV--VMQGQTLVTVSSASTKGPSVFP 118  
Db 68 FTISRDNKNTLYLQMNLSRAEDTAVYYCARDGIGYFDYMGQGLTIVTSSASTKGPSVFP 127  
Qy 119 LAPCSRSTSESTAALGCLVKDYFPEPPTVSNLIGALTSGVHTFPAVLQS 167  
Db 128 LAPSKSTSGGTAALGCLVKDYFPEPPTVSNLIGALTSGVHTFPAVLQS 176

Search completed: March 8, 2005, 05:54:15  
Job time : 19.3627 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 06:39:37 ; Search time 39 Seconds  
(without alignments)  
404.604 Million cell updates/sec

Title: US-09-784-950-41  
Perfect score: 849  
Sequence: 1 GIRLDIQLTQSPSLSASVG.....PREAKVQWKVDNALQSKPN 164

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	639.5	75.3	215	2 JE0242	Ig kappa chain NIG
2	636.5	75.0	215	2 JE0244	Ig kappa chain NIG
3	608.5	71.7	215	2 A23746	Ig kappa chain V-I
4	596.5	70.3	215	2 JE0243	Ig kappa chain NIG
5	564	66.4	216	2 JE0241	Ig kappa chain Am3
6	558.5	65.8	234	2 S14237	Ig kappa chain pre
7	540	63.6	230	2 S33161	Ig kappa chain - s
8	531.5	62.6	234	2 S01320	Ig kappa chain pre
9	524.5	61.8	214	2 S68212	Ig kappa chain (Ma
10	524	61.7	141	2 A49134	Ig kappa chain V-I
11	521	61.4	240	2 S06084	Ig kappa chain pre
12	514	60.5	129	2 S40369	Ig kappa chain - h
13	514	60.5	132	2 S40334	Ig kappa chain - h
14	513.5	60.5	210	2 A56169	Ig kappa chain V-I
15	509.5	60.0	218	2 JC5810	monoclonal antibod
16	507.5	59.8	220	2 A31790	Ig kappa chain V r
17	505.5	59.5	218	2 S68241	Ig kappa chain V r
18	501	59.0	225	2 S37484	Ig kappa chain - m
19	494	58.2	125	2 S40349	Ig kappa chain V-J
20	493	58.1	125	2 S40353	Ig kappa chain V-J
21	493	58.1	235	2 S25058	Ig kappa chain - m
22	492	58.0	108	1 K1HUBN	Ig kappa chain V-I
23	492	58.0	117	2 S46376	Ig kappa chain V-J
24	490.5	57.8	124	2 S40336	Ig kappa chain V-J
25	490	57.7	125	2 S40333	Ig kappa chain V-J
26	490	57.7	127	2 S40367	Ig kappa chain - h
27	490	57.7	139	2 S40365	Ig kappa chain pre
28	489	57.6	144	2 P40106	Ig kappa chain V-J
29	488	57.5	131	2 S40352	Ig kappa chain V-J

30	487.5	57.4	107	2 S47183	Ig kappa chain - h
31	486	57.2	107	2 S36264	Ig lambda chain V
32	484	57.0	125	2 S40316	Ig kappa chain - h
33	483	56.9	107	2 169017	anti-HIV1 envelope
34	483	56.9	128	2 S46372	Ig light chain var
35	482	56.8	117	2 C21056	Ig kappa chain pre
36	482	56.8	130	2 S40368	Ig kappa chain - h
37	480	56.5	123	2 S40331	Ig kappa chain - h
38	478	56.3	108	2 B49047	Ig kappa chain V r
39	478	56.3	132	2 S38646	Ig kappa chain V r
40	477	56.2	117	2 S46371	Ig kappa chain V-J
41	477	56.2	219	2 S38865	Ig kappa chain - m
42	476	56.1	124	2 S40318	Ig kappa chain V r
43	476	56.1	219	2 FC4203	Ig kappa chain (mo
44	475	55.9	123	2 S40313	Ig kappa chain V-J
45	474	55.8	127	2 S11240	Ig kappa chain V r

ALIGNMENTS

RESULT 1

JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mult  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 639.5; DB 2; Length 215;  
Best Local Similarity 77.2%; Pred. No. 6.3e-42;  
Matches 122; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

Qy	5	DIQLTQSPSLSASVGRVTITCRASQGIS-IYLAWFQORPGKAPKSLIYAASSLSQSGVP	63
Db	1	EIVLTQSPGTLISLSPGERATLSCRASQSVSNVYLAWYQQKPGQAPSLIYDASRRATGIP	60
Qy	64	SKFSGSGGTDFTLTITSSLOPEDPATYCCQYNISYPTFGPTKVDIKRTVAAPSVFIFP	123
Db	61	DRFSGSGSGTDFTLTISGLSPEDFAVYCCQYDRPPWTFGGQTKVEIKRTVAAPSVFIFP	120
Qy	124	PSDEQLKSGTASVVCVLLNNFPYPREAKVQWKVDNALQSG	161
Db	121	PSDEQLKSGTASVVCVLLNNFPYPREAKVQWKVDNALQSG	158

RESULT 2

JE0244  
Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yanagata, F.; Yamaki, S.; Kazi, H.; T  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 636.5; DB 2; Length 215;  
Best Local Similarity 75.9%; Pred. No. 1.1e-41;  
Matches 120; Conservative 20; Mismatches 17; Indels 1; Gaps 1;



Db 137 IFPPSEQLTGGASVCFLNFPKD INVKWIDGSE RONGVLN 181

## RESULT 7

S33161  
IG kappa chain - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S33161  
R:Foley, R.C.; Beh, K.J.  
submitted to the EMBL Data Library, July 1990  
A:Description: Isolation and characterisation of sheep kappa light chain cDNA.  
A:Reference number: S33161  
A:Accession: S33161  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-230 <POL>  
A:Cross-references: EMBL:X54110; NID:G297103; PID:CAA38046.1; PID:gl354221  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
P:143-212/Domain: immunoglobulin homology <IMM>

RESIT.T 8

S01320  
 Ig kappa chain precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 21-Jan-2000  
 C:Accession: S01320  
 R:De Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
 Eur. J. Biochem. 176: 287-295, 1988  
 A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a  
 A:Reference number: S01320; MUID:98329081; PMID:3138116  
 A:Accession: S01320  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <DE1>  
 A:Cross-references: EMBL:X13187; NID:G51784; PIDN:CAA31579.1; PID:G51785  
 A:Note: this sequence was determined from the differentiated gene  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-234/Product: Ig kappa chain #status predicted <MAT>  
 F:36-110/Domain: immunoglobulin homology <IMW>

**Qy** 123 PPSEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSCKPN 164  
||| ||| ||| ||| ||| ||| ||| : ||| : |||  
**Db** 139 PPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRONGVLN 181

## RESULT 9

S68212  
IG kappa chain (Mab03-1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 29-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 11-Jan-2000  
C:Accession: S68212  
R:Takegi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
FEBS Lett. 375, 273-276, 1995  
A:Title: Thermosable peroxidase activity with a recombinant antibody L chain-porphyrin  
A:Reference number: S68211; MUID:96085223; PMID:7498516  
A:Accession: S68212  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-214 <TAK>  
A:Cross-references: EMBL:D29668  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

DEPT. 10

A49134  
IG kappa chain V-I region (ISE) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: A49134; S25115  
R:Rocca, A.; Khamlichi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.L.  
Clin. Exp. Immunol. 91, 506-509, 1993  
A:title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light  
A:Reference number: A49134; MUID:93185310; PMID:7680298  
A:Accession: A49134  
A>Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-141 <ROC>  
A:Cross-references: EMBL:X67322; NID:g33268; PIDN:CAA47736.1; PID:g33269  
A>Note: sequence extracted from NCBI backbone (NCBIP:127088)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-112/Domain: immunoglobulin homology <IMM>

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Db      139 IFP 141

RESULT 11
S06084
Ig kappa chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C/Accession: S06084
R/Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A/Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A/Reference number: S06084; MUID:90016888; PMID:2508067
A/Accession: S06084
A/Molecule type: mRNA
A/Residues: 1-240 <CRO>
A/Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:133-222/Domain: immunoglobulin homology <IMM>

Query Match      61.4%; Score 521; DB 2; Length 240;
Best Local Similarity 62.4%; Pred. No. 7.6e-33;
Matches 98; Conservative 23; Mismatches 30; Indels 6; Gaps 1;

Qy      5 DIQLTQSPSSLSASVGRVVTITCRASQGI-----SIYLAWFQORPGKAPKSLIYAASL 58
Db      21 DFVMTQSPSSLSASVGRVVTITCRASHVITINCKSSQSLFYSGNKNYLAWYQKPGQSPKLLIYWA 80
Qy      59 QSGVPKFSGSGGTDTLTITSSLOPEDFATYVCOQYNSVPFTFGPTKVDIKRTVAAPS 118
Db      81 QSGVDFRIFGSGGTDTLTITSSVQASDLAIYCLQYETPYTFGAGTKLEKRAAPT 140
Qy      119 VFIPPPDEQLKSGTASVWCLNNFYPREAKVQMKVD 155
Db      141 VSIFFPSTEQLATGASVWCLNNFYPRDISVKWKID 177

RESULT 12
S40369
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40369
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40369
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-129 <KLE>
A/Cross-references: EMBL:X72479; NID:9441426; PIDN:CAA51147.1; PID:g441427
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match      60.5%; Score 514; DB 2; Length 129;
Best Local Similarity 88.4%; Pred. No. 1.4e-32;
Matches 99; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy      1 GIRLDIQLTQSPSSLSASVGRVVTITCRASQGISIYLAWFQORPGKAPKSLIYAASLS 60
Db      18 GARCIDIQLTQSPSSLSASVGRVVTITCRASHVITINHLVWFQKPGKAPKSLIYAASLS 77
Qy      61 GVPSKFSGSGGTDTLTITSSLOPEDFATYVCOQYNSVPFTFGPTKVDIKRTVA 112
Db      78 GVPSKFSGSGGTDTLTITSSLOPEDFATYVCOQYNSVPFTFGPTKVDIKRTVA 129

RESULT 13
S40334
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40334
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40334
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-132 <KLE>
A/Cross-references: EMBL:X72444
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match      60.5%; Score 514; DB 2; Length 132;
Best Local Similarity 84.3%; Pred. No. 1.4e-32;
Matches 97; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy      1 GIRLDIQLTQSPSSLSASVGRVVTITCRASQGISIYLAWFQORPGKAPKSLIYAASLS 60
Db      18 GARCIDIQLTQSPSSLSASVGRVVTITCRASQGISIYLAWFQORPGKAPKSLIYVASTLS 77
Qy      61 GVPSKFSGSGGTDTLTITSSLOPEDFATYVCOQYNSVPFTFGPTKVDIKRTVA 115
Db      78 GVPSKFSGSGGTDTLTITSSLOPEDFATYVCOQYNSVPFTFGPTKVDIKRTVA 132

RESULT 14
A56169
Ig kappa chain V region (clone 23.2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C/Accession: A56169
R/Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godillc
J. Biol. Chem. 270, 6628-6638, 1995
A/Title: Recombinant antibodies in bioactive peptide design.
A/Reference number: A56169; MUID:95204454; PMID:7896802
A/Accession: A56169
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-210 <MON>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query Match      60.5%; Score 513.5; DB 2; Length 210;
Best Local Similarity 60.0%; Pred. No. 2.5e-32;
Matches 99; Conservative 26; Mismatches 35; Indels 5; Gaps 2;

Qy      5 DIQLTQSPSSLSASVGRVVTITCRASQGIS-----IYLAWFQORPGKAPKSLIYAASLS 60
Db      1 DIVLTQSPASLTVSLGORATISCRASKSVSSSGSYNMHWYQKPGQPKVLIYLASNLS 60
Qy      61 GVPSKFSGSGGTDTLTITSSLOPEDFATYVCOQYNSVPFTFGPTKVDIKRTVAAPS 120
Db      61 GVPSKFSGSGGTDTLTITSSLOPEDFATYVCOQYNSVPFTFGPTKVDIKRTVAAPS 120
Qy      121 IFPPSEQLKSGTASVWCLNNFYPREAKVQMKVDNA-LQSGKPN 164
Db      121 IFPPSEQLTSGGASVWCLNNFYPRDINVKWKIDGSEKQNGVLN 165

RESULT 15
JC5810
monoclonal antibody 13-1 light chain - mouse
C/Species: Mus musculus (house mouse)
C/Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C/Accession: JC5810
R/Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.;
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
```

A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin  
A;Reference number: JC5810; MUID:98063277; PMID:9398605  
A;Accession: JC5810  
A;Molecule type: protein  
A;Residues: 1-218 <AKA>  
C;Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match	60.0%;	Score	509.5;	DB	2;	Length	218;
Best Local Similarity	59.4%;	Pred. NO.	5.2e-32;				
Matches	98;	Conservative	27;	Mismatches	35;	Indels	5;
						Gaps	2;

  

Qy	5	DIQLTQSPSSLSASVGDRTTITCRASQGIS----	IYLAWFOORPKAPKSLIYAASSLQS	60
Db	1	NIVLTQSPASLAVSLGQRATISCRASKSVASGYIMHWYQQKPKLISLASNLES	60	
Qy	61	GVPSKFGSGSGTDFTLTITSLQPEDFATYYCQQVNSYPFTFGPCTKVDIKRTVAAPSVF	120	
Db	61	GVPARFSGSGSGTDFTLTINHPVEEDVATYYCQHSRELPLTFGAGTKLELRADAAFTVS	120	
Qy	121	IFPPSDEQLKSGTASVVCCLNNFYPREAKVQMKVDNA-LQSGKPN	164	
Db	121	IFPPSSEQLTSGGASVVCFLNNFYPKDINVWKIDGSRQNGVLN	165	

Search completed: March 8, 2005, 07:13:12  
Job time : 41 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 8, 2005, 06:36:06 ; Search time 174 Seconds  
(without alignments)  
482.649 Million cell updates/sec

Title: US-09-784-950-41

Perfect score: 849

Sequence: 1 GILDLTQLTQSPSLASVG.....PREAKVQKVDNALQSGKN 164

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	771	90.8	236	2 Q6GMX8	Q6gmX8 homo sapien
2	756	89.0	236	2 Q7Z3Y4	Q7z3Y4 homo sapien
3	748	88.1	236	2 Q6GMX9	Q6gmX9 homo sapien
4	742	87.4	236	2 Q6PIH7	Q6piH7 homo sapien
5	730	86.0	236	2 Q6GMW1	Q6gmW1 homo sapien
6	711	83.7	236	2 Q6GMX0	Q6gmX0 homo sapien
7	710	83.6	234	2 Q7Z473	Q7z473 homo sapien
8	709	83.5	236	2 Q6PIT5	Q6pit5 homo sapien
9	693	81.6	236	2 Q6PIH4	Q6piH4 homo sapien
10	642.5	75.7	235	2 Q6PJF2	Q6pjF2 homo sapien
11	632	74.4	236	2 Q6PIL8	Q6piL8 homo sapien
12	630.5	74.3	235	2 Q6GMW0	Q6gmW0 homo sapien
13	625.5	73.7	235	2 Q6GMV9	Q6gmV9 homo sapien
14	624	73.5	236	2 Q6P588	Q6p588 homo sapien
15	568.5	67.0	239	2 Q8TCD0	Q8tcd0 homo sapien
16	559.5	65.9	236	2 Q7TS98	Q7ts98 mus musculus
17	552.5	65.1	239	2 Q6P491	Q6p491 homo sapien
18	549.5	64.7	239	2 Q6NEK0	Q6nek0 homo sapien
19	545	64.2	240	2 Q6PIH6	Q6piH6 homo sapien
20	504.5	59.4	238	2 Q66JS7	Q66jS7 mus musculus
21	497	58.5	108	2 Q9UL70	Q9ul70 homo sapien
22	492	58.0	108	1 KV1V_HUMAN	P04430 homo sapien
23	473	55.7	237	2 Q7SZ36	Q7sz36 xenopus lae
24	472.5	55.7	107	1 KV1D_HUMAN	P01596 homo sapien
25	472	55.6	219	2 Q65ZC0	Q65zc0 mus musculus
26	468	55.1	244	2 Q65ZC8	Q65zc8 homo sapien
27	467	55.0	108	2 Q9UL77	Q9ul77 homo sapien
28	466	54.9	116	2 Q96PP6	Q96pf6 homo sapien
29	462	54.4	108	1 KV1R_HUMAN	P01610 homo sapien
30	462	54.4	117	1 KV1I_HUMAN	P01601 homo sapien
31	461.5	54.4	107	2 Q96SA9	Q96sa9 homo sapien

32	461	54.3	108	1 KV1G_HUMAN	P01599 homo sapien
33	460	54.2	108	1 KV1I_HUMAN	P00362 homo sapien
34	460	54.2	240	2 Q65ZC9	Q65zc9 homo sapien
35	457.5	53.9	243	2 Q6NTU5	Q6ntu5 xenopus lae
36	457	53.8	108	1 KV1H_HUMAN	P01600 homo sapien
37	457	53.8	108	1 KV1L_HUMAN	P01604 homo sapien
38	455	53.6	108	2 Q9UL79	Q9ul79 homo sapien
39	453.5	53.4	107	2 Q9UL81	Q9ul81 homo sapien
40	452	53.2	108	1 KV1P_HUMAN	P01608 homo sapien
41	451	53.1	108	1 KV1S_HUMAN	P01611 homo sapien
42	450	53.0	129	1 KV1W_HUMAN	P04431 homo sapien
43	447.5	52.7	241	2 Q63ZK4	Q63zk4 mus musculus
44	446	52.5	108	1 KV1E_HUMAN	P01597 homo sapien
45	445	52.4	108	1 KV1W_HUMAN	P01605 homo sapien

#### ALIGNMENTS

#### RESULT 1

ID	Q6GMX8	PRELIMINARY;	PRT;	236 AA.
AC	Q6GMX8;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DB	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uadin T.B., Tohiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mull�hy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villal�n D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalka U., Smailus D.E., Schnrerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RA	Strausberg R.;			
RL	EMBL; BC073764; AAH73764.1; -.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig cl.			
DR	InterPro; IPR003006; Ig MHC.			
DR	InterPro; IPR003596; Ig v.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN1.			

KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;  
Query Match 90.8%; Score 771; DB 2; Length 236;  
Best Local Similarity 91.9%; Pred. No. 4.5e-65;  
Matches 146; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GIRLDIQLTQSPSSLSASVGDRTVITICRASQGISIYLAWFQQRPGKAPKLLIYAASLSQS 60  
DB 19 GSRCDIQMTQSPSSLSASVGDRTVITICRASQGISIYLAWFQQRPGKAPKLLIYAASLSQS 78  
QY 61 GVPKSGSGSGGTDFTLTISLQPEDPATYCCQYNSYPTFGPTGKVDIKRTVAAPSVF 120  
DB 79 GVPKSGSGSGGTDFTLTISLQPEDPATYCCQYNSYPTFGPTGKVDIKRTVAAPSVF 138  
QY 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161  
DB 139 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 179  
RESULT 2  
Q6GMX9 PRELIMINARY; PRT; 236 AA.  
ID Q6GMX9  
AC Q6GMX9  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal Muscle;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal Muscle;  
RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC005332; AAH05332.1; -.  
DR HSP; P01834; IHEZ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IGV; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25702 MW; 7FBFB4ED23084BC6 CRC64;

Query Match 89.0%; Score 756; DB 2; Length 236;  
Best Local Similarity 91.3%; Pred. No. 1.2e-63;  
Matches 147; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
QY 1 GIRLDIQLTQSPSSLSASVGDRTVITICRASQGISIYLAWFQQRPGKAPKLLIYAASLSQS 60  
DB 19 GARCIDIQMTQSPSSLSASVGDRTVITICRASQGISIYLAWFQQRPGKAPKLLIYAASLSQS 78  
QY 61 GVPKSGSGSGGTDFTLTISLQPEDPATYCCQYNSYPTFGPTGKVDIKRTVAAPSVF 120  
DB 79 GVPKSGSGSGGTDFTLTISLQPEDPATYCCQYNSYPTFGPTGKVDIKRTVAAPSVF 138  
QY 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161  
DB 139 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 179  
RESULT 3  
Q6GMX9 PRELIMINARY; PRT; 236 AA.  
ID Q6GMX9  
AC Q6GMX9  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073763; AAH73763.1; -.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IGV; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.



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SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;
Query Match 88.1%; Score 748; DB 2; Length 236;
Best Local Similarity 89.4%; Pred. No. 6.8e-63;
Matches 144; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQISIIYLAWFOORPKAPKSLIYAASSLQS 60
Db 19 GARCIDIQLTQSPSSLSASVGDRTVITCRASQISIIYLAWFOORPKAPKSLIYAASSLQS 78
QY 61 GVPKFSGSGSGTGDTFTLTISLQPEDFATYYCQVNSVPFTFGPTKVDIKRTVAAPSVF 120
Db 79 GVPKFSGSGSGTGDTFTLTISLQPEDFATYYCQVNSVPFTFGPTKVDIKRTVAAPSVF 138
QY 121 IFPPSDEQLKSGTASVVCLLNFPYKQVQKVDNALQSG 161
Db 139 IFPPSDEQLKSGTASVVCLLNFPYKQVQKVDNALQSG 179

RESULT 4
Q6PIH7 PRELIMINARY; PRT; 236 AA.
ID Q6PIH7
AC Q6PIH7
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
Query Match 87.4%; Score 742; DB 2; Length 236;
Best Local Similarity 90.1%; Pred. No. 2.5e-62;
Matches 145; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQISIIYLAWFOORPKAPKSLIYAASSLQS 60
Db 19 GARCIDIQLTQSPSSLSASVGDRTVITCRASQISIIYLAWFOORPKAPKSLIYAASSLQS 78
QY 61 GVPKFSGSGSGTGDTFTLTISLQPEDFATYYCQVNSVPFTFGPTKVDIKRTVAAPSVF 120
Db 79 GVPKFSGSGSGTGDTFTLTISLQPEDFATYYCQVNSVPFTFGPTKVDIKRTVAAPSVF 138
QY 121 IFPPSDEQLKSGTASVVCLLNFPYKQVQKVDNALQSG 161
Db 139 IFPPSDEQLKSGTASVVCLLNFPYKQVQKVDNALQSG 179

RESULT 5
Q6GMW1 PRELIMINARY; PRT; 236 AA.
ID Q6GMW1
AC Q6GMW1
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
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DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25751 MW; 5BFEGA087AFAC437 CRC64;  
  
Query Match 86.0%; Score 730; DB 2; Length 236;  
Best Local Similarity 88.8%; Pred. No. 3.5e-61;  
Matches 143; Conservative 7; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASOGISIVLAWFOQRPKAPKSLIIYAASLSQS 60  
DB 19 GARCAIQMTQSPSSLSASVGDRTVITCRASQISNDLIGWQKPKAPKLIIIYAASLSQS 78  
QY 61 GVPKFSGSGSGTDTLTITSSLPQEPATYCCQYNSYPTFGTGVKVDIKRTVAAPSVF 120  
DB 79 GVPKFSGSGSGTDTLTITSSLPQEPATYCCQYNSYPTFGTGVKVDIKRTVAAPSVF 138  
QY 121 IFPPSDQLKSGTGASVVCLLNNFYPREAKVQMKVDNALQSG 161  
DB 139 IFPPSDQLKSGTGASVVCLLNNFYPREAKVQMKVDNALQSG 179  
  
RESULT 6  
Q6GMX0  
ID Q6GMX0 PRELIMINARY; PRT; 236 AA.  
AC Q6GMX0;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RA Strausberg R.;  
RL EMBL; BC073775; AAH73775.1; -.  
DR InterPro; IPR003599; IG-like.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG v.  
DR Pfam; PF07654; Cl-set; 1.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;  
  
Query Match 83.7%; Score 711; DB 2; Length 236;  
Best Local Similarity 85.7%; Pred. No. 2.2e-59;  
Matches 138; Conservative 9; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASOGISIVLAWFOQRPKAPKSLIIYAASLSQS 60  
DB 19 GARCAIQMTQSPSSLSASVGDRTVITCRASQINNNLNMWYQLKPKAPNLIIIYAASLSQS 78  
QY 61 GVPKFSGSGSGTDTLTITSSLPQEPATYCCQYNSYPTFGTGVKVDIKRTVAAPSVF 120  
DB 79 GVPKFSGSGSGTDTLTITSSLPQEPATYCCQYNSYPTFGTGVKVDIKRTVAAPSVF 138  
QY 121 IFPPSDQLKSGTGASVVCLLNNFYPREAKVQMKVDNALQSG 161  
DB 139 IFPPSDQLKSGTGASVVCLLNNFYPREAKVQMKVDNALQSG 179  
  
RESULT 7  
Q7Z473  
ID Q7Z473 PRELIMINARY; PRT; 234 AA.  
AC Q7Z473;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
RA Strausberg R.;  
RL EMBL; BC056256; AAH56256.1; -.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IGv; 1.  
DR SMART; PS50835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25674 MW; 1A2C359BAB51BC0F CRC64;  
Query Match 83.6%; Score 710; DB 2; Length 234;  
Best Local Similarity 84.5%; Pred. No. 2.8e-59;  
Matches 136; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQIGISYILAWFOQRGKAPKSLIYAASLSQS 60  
DB 17 GARCAIRMTQSPSSFSASTGDRVTITCRASQISGYSILAWYQOKPGKAPQLLIYAASLTQS 76  
QY 61 GVPKFSGSGSGTDTLTITSSLOPEDPATYCCQYNSYPTFTGKTVDIKRTVAAPSVF 120  
DB 77 GVPKFSGSGSGTDTLTISICLOSEDPATYCCQYNYPTFTGQGTKEIKRTVAAPSVF 136  
QY 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161  
DB 137 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 177

RESULT 8  
Q6PIT5 PRELIMINARY; PRT; 236 AA.  
AC Q6PIT5  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC029444; AAH29444.1; -;  
DR HSSP; P01607; 1AR2.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003596; Ig\_MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FBEES51 CRC64;  
Query Match 83.5%; Score 709; DB 2; Length 236;  
Best Local Similarity 85.1%; Pred. No. 3.5e-59;  
Matches 137; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQIGISYILAWFOQRGKAPKSLIYAASLSQS 60  
DB 19 GARCAIQLTQSPSSLSASVGERVTITCRASQIGISSALAWYQOKPGKPKLLIYDASTMES 78  
QY 61 GVPKFSGSGSGTDTLTITSSLOPEDPATYCCQYNSYPTFTGKTVDIKRTVAAPSVF 120  
DB 79 GVPKFSGSGSGTDTLTITSSLOPEDPATYCCQYNSYPTFTGQGTKEIKRTVAAPSVF 138  
QY 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161  
DB 139 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 179

RESULT 9  
Q6PIH4 PRELIMINARY; PRT; 236 AA.  
AC Q6PIH4  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC034146; AAH34146.1; -;  
DR HSSP; P01607; 1AR2.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003596; Ig\_MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGv; 1.

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DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 236 AA; 25871 MW; BE01A28CD06EE26 CRC64;

Query Match      81.6%; Score 693; DB 2; Length 236;
Best Local Similarity 83.2%; Pred. No. 1.1e-57;
Matches 134; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GIRLDIOLTSPSSLSASVGDRTVITCRASQGISYILAWFQORPGKAPKSLIYAASLSQS 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 19 GAKCDIQMTOSPSTLSASVGDRTVITCRASQGISDNLAWYQKPGKAPKLLIYDASRLS 78
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 GVPKFGSGSGGDTFTLTISLQPEDFATYVCQYNSYPTFGTGKVDIKRTVAAPSVP 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 79 GVPKFGSGSGGDTFTLTISLQPEDFATYVCQYNSYPTFGTGKVDIKRTVAAPSVP 138
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 121 IFPPSDQLKSGTASVCLNNFYPREAKVQKVDNALQSG 161
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 139 IFPPSDQLKSGTASVCLNNFYPREAKVQKVDNALQSG 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
Q6PJF2 ID Q6PJF2 PRELIMINARY; PRT; 235 AA.
AC Q6PJF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Ioquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAL16380.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match      75.7%; Score 642.5; DB 2; Length 235;
Best Local Similarity 77.2%; Pred. No. 7.2e-53;
Matches 122; Conservative 18; Mismatches 17; Indels 1; Gaps 1;

Qy 5 DIOLTSPSSLSASVGDRTVITCRASQGISYILAWFQORPGKAPKSLIYAASLSQSGVP 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 21 EIVLTOSPSTLSASVGDRTVITCRASQGISYILAWYQKPGQAPRLMFGSSSRATGIP 80
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 64 SKFGSGSGGDTFTLTISLQPEDFATYVCQYNSYPTFGTGKVDIKRTVAAPSVPFI 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 81 DRFGSGSGGDTFTLTISRLEPFAVYVCQYSGSGTGFGTGKVDIKRTVAAPSVPFI 140
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 124 PSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSG 161
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 141 PSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSG 178
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
Q6PIL8 ID Q6PIL8 PRELIMINARY; PRT; 236 AA.
AC Q6PIL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Ioquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC02451; AAL2451.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
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```
DR SMART; SMO0407; IGC1; 1.  
DR SMART; SMO0406; IGV; 1.  
DR PROSITE; PS0835; IG LIKE; 2.  
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.  
KW Hypothetical protein.  
SQ SEQUENCE      236 AA;   6647A9E77A3C0053 CRC64;  
  
Query Match          74.4%; Score 632; DB 2; Length 236;  
Best Local Similarity 77.6%; Pred. No. 7.2e-52;  
Matches 121; Conservative 15; Mismatches 18; Indels 2; Gaps 2  
  
Qy      8 LTQSPSSLSASGVRVTITCRASQGI-SIYLAWFQOREKAPKSLIIYAASSLSQSGVPSKF 66  
        ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Db      24 LTQPGTLLSIPGRATLSCRASQSLSSSYLAWYQQKFGQAPRLLIYGVSRRATGIDPRF 83  
        ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Qy     67 SGSGSGTDFTLTISSLPEDEPATTYYCQY-QNSYPPTFGTGKVIDIKRTVAAPSFIPPPS 125  
        ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Db     84 SGSGSGTDFTLTISLEPEDFAVYYCQYGTSRPTTFGGQTGLDIKRIVAAPSVFIFPPS 143  
        ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Qy    126 DEQLKSGGTASVCLLNFPYPEAKVKQVDNALQSG 161  
        ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Db    144 DEQLKSGGTASVCLLNFPYPEAKVKQVDNALQSG 179  
        ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
```

RESULT 12

Q6GMW0 Q6GMW0 PRELIMINARY; PRT; 235 AA.

AC Q6GMW0;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

DE Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxId=9606;

RN [1]

SEQUENCE FROM N.A.

RP RP

RC TISSUE=Spleen;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rhee S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL [2]

SEQUENCE FROM N.A.

RP RP

RC TISSUE=Spleen;

RC Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC073792; AAH73792.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG cl.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG v.

DR Pfam; PF07654; Cl-set; 1.

DR Pfam; PF00047; iq; 2.

DR	SMART; SMO0409; IG; 2.
DR	SMART; SMO0407; IGC1; 1.
DR	SMART; SMO0406; IGV; 1.
DR	PROSITE; PS0835; IG LIKE; 2.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE    235 AA;    25765 MW;    4360C36B6D4133F5 CRC64;
 Query Match Best Local Similarity    74.3%;    Score 630.5; DB 2; Length 235; Matches 120; Conservative    20; Mismatches 17; Indels    1; Gaps    1;	
Qy	5 DIQLTQPSSLSASVGRDVITTCRASQCISIIYLAWFORPKAKPSLIYAASSLQSGLGPS 64
Dd	21 EIVMTOSPATLVSPGSRATILSCRSQSIINNLAWYQQRPQGAPRLIITYGASRRVTGI GP 80
Qy	65 KFGSGSGTGDTTLTISSLQDEDFATYYCCQNS;-PTFTGGTKVDIKRTVAAPSVFIP 123
Dd	81 RFSGSGSGGTFTLTISSLQSEDFAVYCQQNDMLLYTFGGTGKLEIKRTVAAPSVFIPP 140
Qy	124 PSEDLKSAGTSVVCLLNFFYPREARKVMKDVALQSG 161
Dd	141 PSEDLLKSAGTSVVCLLNFFYPREARKVMKDVALQSG 178
 <b>RESULT 13</b> O6GMV9 PRELIMINARY;                 PRT;      235 AA. ID O6GMV9 AC O6GMV9 CD O6GMV9-2004 (TrEMBLrel. 27, Created) DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update) DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) DS Hypoethical protein. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_Taxid=9606; [1] RN RNP RP SEQUENCE FROM N.A. RC TISSUE=Spleen; RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., RA Raja S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., RA Krzywinski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E., RA Jones S.J., Marra M.A.; RT "generation and initial analysis of more than 15,00 full-length human RT and mouse cDNA sequences;" RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2] RN RNP RP SEQUENCE FROM N.A. RC TISSUE=Spleen; RX Strausberg R.; RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC073793; AAAH7393.1; -. DR InterPro; IPRO03599; Ig. DR InterPro; IPRO07110; Ig-like. DR InterPro; IFPO03597; Ig-cl. DR InterPro; IFPO03006; Ig_MHC. DR InterPro; IPRO03596; Ig_v. DR Pfam; PF07654; Cl-set; 1.	



```

DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSP; P01834; 1172.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match      67.0%; Score 568.5; DB 2; Length 239;
Best Local Similarity 66.0%; Pred. No. 7.8e-46;
Matches 107; Conservative 22; Mismatches 28; Indels 5; Gaps 1;

QY 5 DIQLTQSPSSLSASVGRVTITCRASOGI-----SIVLWFOQRPGRKAPKSLIYAASLQ 59
Db 21 DVNMTQGPLSLPVTIGQPASISCRSTOSLVYSDGNTLYLWFFQRPQSPRLIYKVSNRD 80

QY 60 SGVPSKFSFGSGSGTDFLTITSSLOPEDFATYYCOQYNSYPFTFGTGKVDIKRTVAAPSV 119
Db 81 SGVDPDRFSGSGSGTDFLTITREVAEDVGYYFCMQGTHWPSTFGGTGKLEIKRTVAAPSV 140

QY 120 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSG 161
Db 141 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSG 182

```

Search completed: March 8, 2005, 07:12:26  
Job time : 175 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 06:17:32 ; Search time 164 Seconds  
(without alignments)

386.760 Million cell updates/sec

Title: US-09-784-950-41

Perfect score: 849

Sequence: 1 GIBLDTQLTQSPSSLSASVG.....PREAKVQWKVDNALQSGKPN 164

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	849	100.0	164	2 AAY34317	Aay34317 IGF antib
2	777	91.5	224	2 AAB75040	Aab75040 TRO005 Hu
3	763	89.9	233	8 ADR46823	Adr46823 Human ant
4	761	89.6	214	7 ADF11431	Adf11431 18B2 anti
5	754	88.8	236	3 AAY96297	Aay96297 Human IGF
6	753	88.7	214	3 AAY93735	Aay93735 The kappa
7	753	88.7	214	6 AAE35890	Aae35890 Human 11.
8	753	88.7	234	8 ADS84446	Ads84446 Human ant
9	753	88.7	234	8 ADS84464	Ads84464 Human ant
10	753	88.7	234	8 ADR68588	Adr68588 Human ant
11	753	88.7	234	8 ADR68606	Adr68606 Human ant
12	751	88.5	236	5 AAU74297	Aau74297 Anti-huma
13	746	87.9	214	7 ADF11423	Adf11423 2B11 anti
14	746	87.9	234	7 ADM47073	Adm47073 Mouse ant
15	746	87.9	236	5 AAG77164	Aag77164 Germline
16	746	87.9	236	8 ADR28586	Adr28586 Human ant
17	745	87.8	233	8 ADL93655	Adl93655 Human CD4
18	745	87.8	236	5 ABG77160	Abg77160 Germline
19	745	87.8	236	8 ADR28582	Adr28582 Human ant
20	743.5	87.6	234	2 AAR38162	Aar38162 Human imm
21	742	87.4	224	4 AAB75043	Aab75043 TRO005 Hu
22	740	87.2	224	4 AAB75044	Aab75044 TRO005 Hu
23	739	87.0	214	8 ADF11669	Adf11669 anti-CD11
24	739	87.0	224	4 AAB75041	Aab75041 TRO005 Hu
25	737	86.8	184	8 ADS84439	Ads84439 Human ant

#### ALIGNMENTS

##### RESULT 1

AAAY34317  
ID AAY34317 standard; protein; 164 AA.

XX AC AAY34317;

XX DT 19-NOV-1999 (first entry)

XX DE IGF antibody 2.6.1 kappa chain sequence.

XX KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;  
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;  
KW organ transplant rejection disease; lymphoma; pancreatic disease;  
KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

XX PN WO9945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;  
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX N-PSDB; AAZ20418.

XX PT New monoclonal antibody, used for treating e.g. graft versus host  
PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 61; Fig 33; 245pp; English.

XX CC This sequence represents the kappa chain of an antibody of the invention.  
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes  
CC complement and a variable region that binds to the epitope on CD147 bound  
CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB  
CC can selectively kill activated T-cells, activated B-cells or resting or  
CC activated monocytes. The products and methods can be used for treating  
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft  
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.  
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

26	737	86.8	184	8	ADR68581	Adr68581 Human ant
27	737	86.8	234	7	ADE28413	Ade28413 Human ant
28	737	86.8	234	8	ADS84452	Ads84452 Human ant
29	737	86.8	234	8	ADR68594	Adr68594 Human ant
30	736	86.7	223	6	ABJ36940	Abj36940 Anti-CD40
31	736	86.7	234	8	ADS84470	Ads84470 Human ant
32	736	86.7	234	8	ADS84476	Ads84476 Human ant
33	736	86.7	234	8	ADR68618	Adr68618 Human ant
34	736	86.7	234	8	ADR68612	Adr68612 Human IGF
35	733.5	86.4	237	3	AAY96298	Aay96298 Human imm
36	733.5	86.4	241	4	AAB82912	Aab82912 Human imm
37	733	86.3	212	6	AAQ31100	Aao31100 Human A2-
38	733	86.3	214	2	AAY08600	Aay08600 JP1112785
39	733	86.3	234	2	AAR20058	Aar20058 Light cha
40	733	86.3	234	7	ADE28429	Ade28429 Human ant
41	733	86.3	236	8	ADP07905	Adp07905 Human imm
42	731	86.1	152	8	ADK52390	Adk52390 Human ant
43	730	86.0	212	8	ADF76324	Adf76324 M16-L lig
44	730	86.0	234	8	ADS84458	Ads84458 Human ant
45	730	86.0	234	8	ADR68600	Adr68600 Human ant

CC	(e.g. leukemia's and lymphomas) and pancreatic), autoimmune diseases
CC	(e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX	
SQ	Sequence 164 AA;
	Query Match 100.0%; Score 849; DB 2; Length 164;
	Best Local Similarity 100.0%; Pred. No. 2.8e-48;
	Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GIRLDIQLTQSPSSLSASVGRVITTCRASOGISIIYLAWFQQRPGKAPKSLIYAASSLOS 60
Db	1 GIRLDIQLTQSPSSLSASVGRVITTCRASOGISIIYLAWFQQRPGKAPKSLIYAASSLOS 60
QY	61 GVPSPKPSGSGGTDTFTLISSLPQEDFATYYCQOYNSYPTFGTKVDIKRTVAAPSVF 120
Db	61 GVPSPKPSGSGGTDTFTLISSLPQEDFATYYCQOYNSYPTFGTKVDIKRTVAAPSVF 120
QY	121 IFPPSDEQLKSGTASVWCLLNNFYPREAKQWKVDNALQSGKN 164
Db	121 IFPPSDEQLKSGTASVWCLLNNFYPREAKQWKVDNALQSGKN 164
RESULT 2	
AAB75040	
ID	AAB75040 standard; protein; 224 AA.
XX	
AC	AAB75040;
XX	
DT	19-JUL-2001 (first entry)
XX	
DE	TRO005 HuMab kappa chain protein sequence 3E2K.
XX	
KW	Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW	human antibody phage display library; immunisation; transgenic animal.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200125492-A1.
XX	
PD	12-APR-2001.
XX	
PF	02-OCT-2000; 2000WO-US027237.
XX	
PR	02-OCT-1999; 99US-0157415P.
PR	01-DEC-1999; 99US-00453234.
XX	
PA	(BIOS-) BIOSITE DIAGNOSTICS INC.
PA	(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX	
PI	Buechler J, Valkirs G, Gray J, Lonberg N;
XX	
DR	WPI; 2001-335567/35.
XX	
PT	Producing a human antibody phage display library comprises providing a
PT	transgenic animal whose genome comprises human immunoglobulin genes and
PT	isolating nucleic acids encoding antibody chains from lymphatic cells.
XX	
PS	Example 37; Page 121-122; 161pp; English.
XX	
CC	The present invention describes a method (M1) for producing a human
CC	antibody phage display library (I), comprising: (1) providing a nonhuman
CC	transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC	(2) isolating nucleic acids encoding human antibody chains (III) from
CC	lymphatic cells; and (3) forming a library of display packages whose
CC	members comprise a nucleic acid encoding (III) which is displayed from
CC	the package. The method is used for producing a human antibody display
CC	library, e.g., a Fab phage display library. The display method may be
CC	used to screen nucleic acids encoding antibody chains obtained from
CC	immunised nonhuman transgenic animals, and from this a population of
CC	antibodies may be prepared. Production of a human monoclonal antibodies
CC	display library using this method means there is no need to immunise
CC	humans with antigens, and the difficulties faced with immortalising B

CC	cells are avoided.	AHH29958 to AAH30066 and AAB74994 to AAB75056
XX	represent sequences used in the exemplification of the present invention	
XX	Sequence 224 AA;	
Query Match	91.5%; Score 777; DB 4; Length 224;	
Best Local Similarity	94.9%; Pred. No.1.9e-43;	
Matches 149; Conservative 6; Mismatches 2; Indels 0; Gaps 0		
QY	5 DIQLTQPSSLSASGVRVITTCRASOGISITYLAWFOORGPKAPKSILIYAASSLSQGVS 64	
Dd	1 NIQWTQPSSLSASGVRVITTCRASOGISSWLAWYQQKPEKAPKSILIYAASSLSQGVS 60	
QY	65 KFGSGSGTGDTFTLTIISSLQPEDFATYYCQQNSYPFTFGPGTKVDIKRTVAAPSVEIFPP 124	
Dd	: ~~~~~~	
QY	125 SDEOLKGTASVVCLNNFYPREAKVQWKVNALQSG 161	
Dd	121 SDEOLKGTASVVCLNNFYPREAKVQWKVNALQSG 157	
RESULT 3		
ADR46823	ID ADR46823 standard; protein; 233 AA.	
XX	AC ADR46823;	
XX	DT 18-NOV-2004 (first entry)	
XX	Human antibody B11 light chain variable region protein SEQ ID NO:6.	
OS	molecular conjugate; monoclonal antibody; human antigen presenting cell;	
KW	antigen presenting cell; APC; human; beta human chorionic gonadotropin;	
KW	betaHCG; beta chorionic gonadotropin; antibody;	
KW	T cell-mediated immune response; immunisation; cytostatic; antimicrobial;	
KW	immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;	
KW	C8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;	
KW	melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;	
KW	antibody B11; light chain variable region.	
XX	Homo sapiens.	
XX	WO2004074432-A2.	
Pf	02-SEP-2004.	
XX	30-JAN-2004; 2004WO-US002725.	
XX	31-JAN-2003; 2003US-0443979P.	
PA	(MEDA-) MEDAREX INC.	
PI	Keler T, Endres M, He L, Ramakrishna V;	
XX	WPI; 2004-635555/61.	
N-PSDB:	ADR46822.	
New molecular conjugate having a monoclonal antibody that binds to human APCs linked to a beta human chorionic gonadotropin, useful for inducing a cytotoxic T cell response in cancers and infectious diseases.		
Claim 14; SEQ ID NO 6; 82pp; English.		
The present invention describes a molecular conjugate comprising a monoclonal antibody that binds to human antigen presenting cells (APCs) linked to beta human chorionic gonadotropin (betaHCG), where the antibody comprises a heavy and/or light chain variable region derived from a human VH5-51 or Vk-L15 germline sequence with the 98 or 95 amino acid sequences of SEQ ID NO:30 or 32 (ADR46847, or ADR46849), respectively. Also described: (1) a molecular conjugate comprising a human antibody heavy chain and a human antibody light chain, where either or both chains are linked to betaHCG; (2) a molecular conjugate comprising a human single chain and a human antibody light chain, where either or both chains are		



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FT      /label= Ig_domain
XX      WO200029583-A2.
XX      25-MAY-2000.
XX      19-NOV-1999; 99WO-US027566.
XX      19-NOV-1998; 98US-00195853.
XX      22-DEC-1998; 98US-0113635P.
XX      07-APR-1999; 99US-0128194P.
XX      (INCY-) INCYTE PHARM INC.
XX
XX      Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
XX      Lu DAM, Lal P, Hillman JL, Yang J;
XX
XX      WPI; 2000-387796/33.
XX      N-PSDB; AAA27389.
XX
XX      Immunoglobulin superfamily proteins, the agonist and antagonist of the
XX      protein is useful for preventing and treating disorders associated with
XX      altered levels of the protein such as cancer, immune system disorders.
XX
XX      Claim 1; Page 85; 105pp; English.
XX
XX      The present sequence is the human immunoglobulin superfamily protein
XX      IGFAM-9. Its gene was isolated from a cDNA library of breast tumour
XX      tissue. It is expressed in reproductive, gastrointestinal and immune and
XX      haematopoietic tissue, where cancer and inflammation are common. The
XX      gene, protein, its antibodies, agonists and antagonists are suitable for
XX      diagnosing and treating many diseases, including cancer, immune system
XX      disorders (such as inflammation, AIDS, allergies, anaemia, Crohn's
XX      arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
XX      disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
XX      multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
XX      systemic lupus erythematosus and ulcerative colitis), complications of
XX      cancer, haemodialysis and extracorporeal circulation, trauma and
XX      haematopoietic cancer (such as leukaemia) and infections caused by
XX      bacteria, viruses, fungi or parasites
XX
XX      Query Match      88.8%; Score 754; DB 3; Length 236;
XX      Best Local Similarity 90.7%; Pred. No. 6.4e-42;
XX      Matches 146; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
XX
XX      1 GIRDILQTSPLSASVGDRTVITCRASQGISIYLAWFQQRPGKAPKSLIYAASLSQS 60
XX      19 GARCDIQMTQSPSLSASVGDRTVITCRASQDISNYLAWFQQRPGTAPKSLIYDTSLSQS 78
XX
XX      61 GVPSKFGSGSGTDFTLTISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 120
XX      79 GVPSKFGSGSGTDFTLTISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 138
XX
XX      121 IFPPSDQLKSGTASVCLNNFYPRKQVQKVDNALQSG 161
XX      139 IFPPSDQLKSGTASVCLNNFYPRKQVQKVDNALQSG 179
XX
XX      RESULT 6
XX      ID AAY93735
XX      AC AAY93735 standard; protein; 214 AA.
XX
XX      AAY93735;
XX
XX      03-OCT-2000 (first entry)
XX
XX      The kappa chain of immunoglobulin clone 11.2.1.
XX
XX      Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX      hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX      proliferative disorder; cancer; immunodeficient disorder.
```

```
XX      Homo sapiens.
XX      WO200037504-A2.
XX      29-JUN-2000.
XX      23-DEC-1999; 99WO-US030895.
XX      23-DEC-1998; 98US-0113647P.
XX      (PFIZ ) PFIZER INC.
XX      (ABGE-) ABGENIX INC.
XX
XX      Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
XX      Corvalan JR;
XX
XX      WPI; 2000-442647/38.
XX      N-PSDB; AAA46899.
XX
XX      Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
XX      -4 containing specified heavy and light chain sequences, useful for
XX      treating, e.g. immune disorders.
XX
XX      Claim 3; Fig 22a; 157pp; English.
XX
XX      The present sequence represents a kappa chain of an antibody of the
XX      invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
XX      -4. Antibodies of the invention are composed of a heavy chain variable
XX      region, comprising a modified contiguous sequence from a FRI-FR3 sequence
XX      encoded by a human VH3-33 family gene. The modifications are contained in
XX      CDR1, CDR2 and/or framework regions. The antibodies may be used to
XX      inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
XX      disorders (e.g. autoimmune disease, diabetes and graft rejection) and
XX      proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
XX      used to up-regulate immune system to up-regulate immunodeficient
XX      disorders
XX
XX      Sequence 214 AA;
XX
XX      Query Match      88.7%; Score 753; DB 3; Length 214;
XX      Best Local Similarity 92.4%; Pred. No. 6.8e-42;
XX      Matches 145; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
XX
XX      5 DIQLTQSPSLSASVGDRTVITCRASQGISIYLAWFQQRPGKAPKSLIYAASLSQSVPS 64
XX      1 DIQMTQSPSLSASVGDRTVITCRASQDISNYLAWFQQRPGKAPKSLIYAASLSQSVPS 60
XX
XX      65 KFGSGSGSGTDFTLTISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVFIFPP 124
XX      61 RFSGSGSGTDFTLTISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVFIFPP 120
XX
XX      125 SDEQLKSGTASVCLNNFYPRKQVQKVDNALQSG 161
XX      121 SDEQLKSGTASVCLNNFYPRKQVQKVDNALQSG 157
XX
XX      RESULT 7
XX      ID AAE35890
XX      AC AAE35890 standard; protein; 214 AA.
XX
XX      AAE35890;
XX
XX      17-JUN-2003 (first entry)
XX
XX      Human 11.2.1 anti-CTLA-4 antibody mature kappa chain.
XX
XX      Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
XX      cancer.
XX
XX      Homo sapiens.
XX      EP1262193-A1.
```

XX PD 04-DEC-2002.  
 XX XX  
 XX PF 23-MAY-2002; 2002EP-00253652.  
 XX XX  
 XX PR 23-MAY-2001; 2001US-0293042P.  
 XX XX  
 XX PA (PFIZ ) PFIZER PROD INC.  
 XX XX  
 XX PI Hanson DC, Mueller EE;  
 XX XX  
 XX DR WPI; 2003-131215/13.  
 XX DR N-PSDB; AAD54350.  
 XX XX  
 XX PT Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the  
 XX PT preparation of medicament for the treatment of cancer.  
 XX XX  
 XX PS Disclosure; Fig 1S; 76pp; English.  
 XX XX  
 XX CC The invention relates to the use of human anti-cytotoxic T lymphocyte  
 XX CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for  
 XX CC the treatment of cancer such as bone cancer, pancreatic cancer, skin  
 XX CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian  
 XX CC cancer, cancer of the anal region, stomach cancer, breast cancer,  
 XX CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.  
 XX CC The present sequence is human anti-CTLA-4 antibody mature kappa chain  
 XX CC  
 XX SQ Sequence 214 AA;  
 Query Match 88.7%; Score 753; DB 6; Length 214;  
 Best Local Similarity 92.4%; Pred. No. 6.8e-42;  
 Matches 145; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 QY 5 DIQTQSPSSLSASVGRVITTCRASQGISIYLAWFQORPKAPKSLIYAASSLSQGVPS 64  
 DB 1 DIQTQSPSSLSASVGRVITTCRASQGISIYLAWFQORPKAPKSLIYAASSLSQGVPS 60  
 QY 65 KFGSGSGTDFTLTISLQPEDFATYCCQYNSVPFTFGPTKVDIKRTVAAPSVFIPPP 124  
 DB 61 RFSGSGSGTDFTLTISLQPEDFATYCCQYNSVPFTFGPTKVDIKRTVAAPSVFIPPP 120  
 QY 125 SDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 161  
 DB 121 SDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 157  
 RESULT 8  
 ADS84446  
 ID ADS84446 standard; protein; 234 AA.  
 XX AC  
 XX AC ADS84446;  
 XX XX  
 XX DT 18-NOV-2004 (first entry)  
 XX XX  
 XX DE Human anti-EPO-R antibody Ab198 light chain SEQ ID NO:85.  
 XX XX  
 XX KW human; erythropoietin receptor; EPO receptor;  
 XX KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 XX KW antianaemic; neuroprotective; vulnerable; gene therapy; aplasia; anaemia;  
 XX KW wound healing; neural cell damage protection;  
 XX KW neural tissue damage protection; brain injury; spinal cord injury;  
 XX KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.  
 XX XX  
 XX OS Homo sapiens.  
 XX XX  
 XX PN W02004035603-A2.  
 XX XX  
 XX PD 29-APR-2004.  
 XX XX  
 XX PP 14-OCT-2003; 2003WO-US032243.  
 XX XX  
 XX XX 14-OCT-2002; 2002US-00269711.  
 XX PR 10-OCT-2003; 2003US-00684109.

XX PA (ABBO ) ABBOTT LAB.  
 XX PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;  
 XX XX  
 XX DR WPI; 2004-348433/32.  
 XX DR N-PSDB; ADS84444, ADS84445.  
 XX XX  
 XX PT New antibodies that bind to or activate an endogenous human  
 XX PT erythropoietin receptor, useful for diagnosing, preventing or treating  
 XX PT disorders associated with dysfunctional erythropoietin receptor, e.g.  
 XX PT anemia.  
 XX XX  
 XX PS Disclosure; SEQ ID NO 85; 192pp; English.  
 XX XX  
 XX CC The present invention describes an antibody or its fragment that binds to  
 XX CC or activates an endogenous activity of a human erythropoietin (EPO)  
 XX CC receptor in a mammal, but does not interact with a peptide having a  
 XX CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)  
 XX CC methods of modulating or activating an endogenous activity of a human EPO  
 XX CC receptor in a mammal, comprising administering to the mammal a  
 XX CC therapeutic amount of the above antibody or its fragment to modulate or  
 XX CC activate the receptor; (2) a method of treating a mammal suffering from  
 XX CC aplasia, comprising administering to the mammal a therapeutic amount of  
 XX CC the above antibody or its fragment to modulate or activate the receptor;  
 XX CC (3) a pharmaceutical composition comprising a therapeutic amount of the  
 XX CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)  
 XX CC an isolated and purified polynucleotide sequence, and their fragments,  
 XX CC complements and degenerate codon equivalents; and (5) an isolated and  
 XX CC purified amino acid sequence, and their fragments. The EPO receptor  
 XX CC binding antibody has antianaemic, neuroprotective and vulnerary  
 XX CC activities, and can be used in gene therapy. The compositions and methods  
 XX CC from the present invention can be used for modulating an endogenous  
 XX CC activity of a human EPO receptor or for treating mammals suffering from  
 XX CC aplasia or anaemia. They may also be used for identifying mammals having  
 XX CC a dysfunctional EPO receptor. The composition may also be used in  
 XX CC promoting wound healing or in protecting against neural cell and/or  
 XX CC tissue damage resulting from brain/spinal cord injury, stroke and the  
 XX CC like. The present sequence represents a human anti-EPO-R antibody light  
 XX CC chain, which is given in the exemplification of the present invention.  
 XX XX  
 XX SQ Sequence 234 AA;  
 Query Match 88.7%; Score 753; DB 8; Length 234;  
 Best Local Similarity 88.8%; Pred. No. 7.4e-42;  
 Matches 143; Conservative 11; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 GIRLDIQLTQSPSSLSASVGRVITTCRASQGISIYLAWFQORPKAPKSLIYAASSLSQ 60  
 DB 17 GSRCDIQMTQSPSSVSASIGRVSITCRASQGISIYLAWFQORPKAPKSLIYAASSLSQ 76  
 QY 61 GVPKFSFGSGSGTDFTLTISLQPEDFATYCCQYNSVPFTFGPTKVDIKRTVAAPSVF 120  
 DB 77 GVPKFSFGSGSGTDFTLTISLQPEDFATYCCQYNSVPFTFGPTKVDIKRTVAAPSVF 136  
 QY 121 IFPPSDBQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 161  
 DB 137 IFPPSDBQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 177  
 RESULT 9  
 ADS84464  
 ID ADS84464 standard; protein; 234 AA.  
 XX AC  
 XX AC ADS84464;  
 XX XX  
 XX DT 18-NOV-2004 (first entry)  
 XX XX  
 XX DE Human anti-EPO-R antibody Ab430 light chain SEQ ID NO:103.  
 XX XX  
 XX KW human; erythropoietin receptor; EPO receptor;  
 XX KW erythropoietin receptor binding antibody; EPO receptor binding antibody;  
 XX KW antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;

KW	wound healing; neural cell damage protection;	
KW	neural tissue damage protection; brain injury;	spinal cord injury;
KW	stroke; anti-erythropoietin receptor antibody;	anti-EPO-R antibody.
OS	Homo sapiens.	
XX		
XX		
PN	WO2004035603-A2.	
XX		
PD	29-APR-2004.	
XX		
XX	14-OCT-2003; 2003WO-US032243.	
PF		
XX	14-OCT-2002; 2002US-00269711.	
PR		
XX	10-OCT-2003; 2003US-00684109.	
PR		
XX		
PA	(ABBO ) ABBOTT LAB.	
XX		
PI	Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;	
XX		
DR	WPI; 2004-348433/32.	
XX	N-PSDB; ADS84462, ADS84463.	
DR		
XX		
PT	New antibodies that bind to or activate an endogenous human	
PT	erythropoietin receptor, useful for diagnosing, preventing or treating	
PT	disorders associated with dysfunctional erythropoietin receptor, e.g.	
PT	anemia.	
XX		
PS	Disclosure; SEQ ID NO 103; 192pp; English.	
XX		
CC	The present invention describes an antibody or its fragment that binds to	
CC	or activates an endogenous activity of a human erythropoietin (EPO)	
CC	receptor in a mammal, but does not interact with a peptide having a	
CC	sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)	
CC	methods of modulating or activating an endogenous activity of a human EPO	
CC	receptor in a mammal, comprising administering to the mammal a	
CC	therapeutic amount of the above antibody or its fragment to modulate or	
CC	activate the receptor; (2) a method of treating a mammal suffering from	
CC	aplasia, comprising administering to the mammal a therapeutic amount of	
CC	the above antibody or its fragment to modulate or activate the receptor;	
CC	(3) a pharmaceutical composition comprising a therapeutic amount of the	
CC	above antibody or antibody fragment, and a pharmaceutical excipient; (4)	
CC	an isolated and purified polynucleotide sequence, and their fragments,	
CC	complements and degenerate codon equivalents; and (5) an isolated and	
CC	purified amino acid sequence, and their fragments. The EPO receptor	
CC	binding antibody has antianaemic, neuroprotective and vulnerary	
CC	activities, and can be used in gene therapy. The compositions and methods	
CC	from the present invention can be used for modulating an endogenous	
CC	activity of a human EPO receptor or for treating mammals suffering from	
CC	aplasia or anaemia. They may also be used for identifying mammals having	
CC	a dysfunctional EPO receptor. The composition may also be used in	
CC	promoting wound healing or in protecting against neural cell and/or	
CC	tissue damage resulting from brain/spinal cord injury, stroke and the	
CC	like. The present sequence represents a human anti-EPO-R antibody light	
CC	chain, which is given in the exemplification of the present invention.	
XX		
SQ	Sequence 234 AA;	
	Query Match 88.7%; Score 753; DB 8; Length 234;	
	Best Local Similarity 90.7%; Pred. No. 7.4e-42;	
	Matches 146; Conservative 6; Mismatches 9; Indels 0; Gaps 0	
QY	1 GIRLDIQLTQSPSSLASVGRDVTITCRASGISIYLAWFOORPGKAPKSLIYAASSLQS 60	
DB	17 GARCDIQWTSPPSSLASVGRDVTITCRASGIRNDLGWYQQKPGKAPKRLIYAASSLQS 76	
QY	61 GVPSKFGSGSGTDFTLTISLQPEDFATYYCQQVNSYPPTFGPGTKVDIKRTVAAPSVF 120	
DB	77 GVPSRFSGSGSGTEFTLTISLQPEDFATYYICLQHSYPTFGPGTKVDIKRTVAAPSVF 136	
QY	121 IFPPSDQLKSGTASVVCLLNNFVPRAKVGQKVDNALQSG 161	
DB	137 IFPPSDQLKSGTASVVCLLNNFVPRAKVGQKVDNALQSG 177	

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XX SQ Sequence 234 AA;
Query Match 88.7%; Score 753; DB 8; Length 234;
Best Local Similarity 88.8%; Pred. No. 7.4e-42;
Matches 143; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDVRVITTCRASQGISIYLAWFOQRGKAPKSLIYAASSLSQS 60
Db 17 GSRCDIQMTQSPSSVSASIGDRVSIITCRASQGISLSLAWYQQRKPKAPTLIIYAASLTQR 76

Qy 61 GVPKFSGSGSGTDTLTITISLQPEDFATYICQOYNSVPFTFGPTKVDIKRTVAAPSVF 120
Db 77 GVPKFSGSGSGTDTLTITISLQPEDFATYICQOYNSVPFTFGPTKVDIKRTVAAPSVF 136

Qy 121 IFPPSDEQLKSGTASVCLLNFPYKQVQKVDNALQSG 161
Db 137 IFPPSDEQLKSGTASVCLLNFPYKQVQKVDNALQSG 177

RESULT 11
ADR68606
ID ADR68606 standard; protein; 234 AA.
AC ADR68606;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human antibody Ab430 light chain polypeptide seqid 103.
XX
KW antianemic; respiratory; vulnery; gene therapy; vaccine;
KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
KW wound healing; neural cell damage; tissue damage; brain injury;
KW spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;
KW AB430.
XX
OS Homo sapiens.
XX
XX US2004175379-A1.
XX
PD 09-SEP-2004.
XX
PF 10-OCT-2003; 2003US-00684109.
XX
PR 14-OCT-2002; 2002US-0418031P.
XX
PA (DEVIR/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREEN/) GREEN L L.
PA (WIEL/) WIELER J.
XX
PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
XX
DR WPI; 2004-661369/64.
DR N-ESDB; ADR68604.
XX
PT New antibody or its antibody fragment that activates an endogenous
PT activity or is capable of binding to a human erythropoietin receptor in a
PT mammal, useful for treating a mammal suffering aplasia or anemia.
XX
PS Disclosure; SEQ ID NO 103; 156pp; English.
XX
XX The invention describes an antibody or its fragment that activates an
CC endogenous activity or capable of binding to a human erythropoietin
CC receptor in a mammal, or that comprises at least one heavy or light chain
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
CC ID NO: 3 or 5) given in the specification or its fragment, but does not
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
CC given in the specification. Also described are: a method of activating or
CC modulating an endogenous activity of a human erythropoietin receptor in a
CC mammal; a pharmaceutical composition comprising a therapeutic amount of
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CC an antibody or antibody fragment above and a pharmaceutical excipient; an
CC isolated and purified polynucleotide sequence selected from 28 sequences
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
CC the specification, and their fragments, complements, and degenerate codon
CC equivalents; and an isolated and purified amino acid sequence selected
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
CC their fragments. The antibody or its antibody fragment that activates or
CC modulates the activity of the receptor is useful in a method of treating
CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
CC treating disorders characterised by decreased or subnormal levels of
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
CC hypoxia and/or diseases characterised by inadequate blood circulation or
CC reduced blood flow. They are also useful for promoting wound healing or
CC for protecting against neural cell and/or tissue damage, resulting from
CC brain/spinal cord injury, stroke and the like. The antibodies are also
CC useful for identifying or diagnosing mammals having dysfunctional
CC erythropoietin receptor. This sequence represents a human Ab430 antibody
CC light chain polypeptide.
XX
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SQ Sequence 234 AA;

Query Match 88.7%; Score 753; DB 8; Length 234;  
Best Local Similarity 90.7%; Pred. No. 7.4e-42;  
Matches 146; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

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Qy 1 GIRLDIQLTQSPSSLSASVGDVRVITTCRASQGISIYLAWFOQRGKAPKSLIYAASSLSQS 60
Db 17 GARCIDIQMTQSPSSLSASVGDVRVITTCRASQGISIRNDLGWYQQRKPKAPKRLIYAASSLSQS 76

Qy 61 GVPKFSGSGSGTDTLTITISLQPEDFATYICQOYNSVPFTFGPTKVDIKRTVAAPSVF 120
Db 77 GVPKFSGSGSGTDTLTITISLQPEDFATYICQOYNSVPFTFGPTKVDIKRTVAAPSVF 136

Qy 121 IFPPSDEQLKSGTASVCLLNFPYKQVQKVDNALQSG 161
Db 137 IFPPSDEQLKSGTASVCLLNFPYKQVQKVDNALQSG 177
```

RESULT 12  
AAU74297

ID AAU74297 standard; protein; 236 AA.

AC AAU74297;

DT 12-MAR-2002 (first entry)

DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain.

Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic;  
immunosuppressive; dermatological; antiinflammatory; hepatotropic;  
activation inducible lymphocyte immunomodulatory molecule; AILIM;  
monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;  
multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;  
allergic contact-type dermatitis; chronic inflammatory dermatosis;  
systemic lupus erythematosus; autoimmune disorder; inflammation;  
graft versus host reaction; immune rejection; intestinal immunity;  
ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.

OS Homo sapiens.

XX WO200187981-A2.

XX 22-NOV-2001.

XX 15-MAY-2001; 2001WO-JP004035.

XX 18-MAY-2000; 2000JP-00147116.

XX 30-MAR-2001; 2001JP-00099508.

XX (NIBS ) JAPAN TOBACCO INC.

XX

PI Teuji T, Tezuka K, Hori N;  
 XX WPI; 2002-075313/10.  
 DR N-PSDB; AAS99473.  
 XX  
 PT New human monoclonal antibody that binds to activation inducible  
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid  
 PT arthritis, multiple sclerosis and inflammation.  
 XX  
 XX Claim 30; Page 270-271; 300pp; English.  
 XX  
 CC The invention relates to a novel human antibody (I), preferably a human  
 CC monoclonal antibody which binds to an activation inducible lymphocyte  
 CC immunomodulatory molecule (AIIIM). (I) is useful for modulating signal  
 CC transduction into a cell mediated by AIIIM, for modulating proliferation  
 CC of AIIIM-expressing cells, for modulating production of a cytokine from  
 CC AIIIM-expressing cells, and for inducing antibody-dependent cytotoxicity  
 CC against AIIIM-expressing cells and/or immune cytotoxicity or apoptosis of  
 CC AIIIM-expressing cells. (I) is useful for treating, preventing or  
 CC prophylaxis of delayed type allergy. (I) is useful for treating and  
 CC preventing various diseases associated with AIIIM-mediated costimulatory  
 CC transduction, and for inhibiting the onset and/or advancement of the  
 CC diseases. (I) is useful for suppression, prevention and/or treatment of  
 CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,  
 CC allergic contact-type dermatitis, chronic inflammatory dermatosis,  
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,  
 CC psoriasis, autoimmune or allergic disorders, inflammation, disorders  
 CC caused by abnormal intestinal immunity, specifically inflammatory  
 CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,  
 CC nephritis, vasculitis, and pancreatitis. (I) induces no serious  
 CC immunorejection due to antigenicity to human, i.e., human anti-mouse  
 CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human  
 CC AIIIM monoclonal antibody amino acid sequences of the invention  
 XX  
 SQ Sequence 236 AA;

Query Match 88.5%; Score 751; DB 5; Length 236;  
 Best Local Similarity 90.1%; Pred. No. 1e-41;  
 Matches 145; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLANFQORPGKAPKSLIYAASLSQS 60  
 DB 19 GSRCDIQMTQSPSSVSASVGDRTVITCRASQGISRLLAWYQQKPKAPKLLIYVASSLSQS 78  
 QY 61 GVPSKFSGSGTDFTLTISLQPEDFATYYCQYNSVPFTFGPTKVDIKRTVAAPSVF 120  
 DB 79 GVPSRFSGSGTDFTLTISLQPEDFATYYCQANSFPWTFGGTKVETIKRTVAAPSVF 138  
 QY 121 IFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSG 161  
 DB 139 IFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSG 179  
 RESULT 13  
 ADF11423  
 ID ADF11423 standard; protein; 214 AA.  
 XX  
 AC ADF11423;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE 2E11 anti-OPGL antibody light chain SEQ ID NO:36.  
 XX  
 KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;  
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;  
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.  
 OS Homo sapiens.  
 XX  
 PN WO2003086289-A2.  
 XX  
 PD 23-OCT-2003.

XX 07-APR-2003; 2003WO-US010749.  
 XX  
 XX 05-APR-2002; 2002US-0370407P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;  
 XX  
 XX WPI; 2003-845253/78.  
 XX N-PSDB; ADF11422.  
 DR  
 XX New isolated antibody that specifically binds osteoprotegerin ligand,  
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,  
 PT bone loss from arthritis, Paget's disease or osteopenia.  
 XX  
 XX Claim 18; SEQ ID NO 36; 156pp; English.  
 XX  
 CC The present invention describes an isolated human antibody (I) that  
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a  
 CC pharmaceutical composition comprising a pharmaceutical carrier and a  
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder  
 CC in a patient, comprising administering to a patient the pharmaceutical  
 CC composition of (1) or a pharmaceutical amount of (I); and (3) a method  
 CC for detecting OPGL in a biological sample, comprising contacting the  
 CC sample with (I) under conditions that allow for binding of the antibody  
 CC to OPGL, and measuring the level of bound antibody in the sample. (I) has  
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in  
 CC gene therapy. The composition and methods are useful in diagnosing or  
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,  
 CC Paget's disease or osteopenia. The antibody (I) may also be used for  
 CC detecting OPGL in biological samples and in identifying cells or tissues  
 CC that produce the protein. The present sequence represents a sequence  
 CC which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 214 AA;

Query Match 87.9%; Score 746; DB 7; Length 214;  
 Best Local Similarity 91.7%; Pred. No. 1.9e-41;  
 Matches 144; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 5 DIQLTQSPSSLSASVGDRTVITCRASQGISIYLANFQORPGKAPKSLIYAASLSQS 64  
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQGISISLLAWYQQKPKAPKSLIYAASLSQS 60  
 QY 65 KFSGSGSGTDFTLTISLQPEDFATYYCQYNSVPFTFGPTKVDIKRTVAAPSVF 124  
 DB 61 RFSGSGSGTDFTLTISLQPEDFATYYCQYNSVPFTFGPTKVDIKRTVAAPSVF 120  
 QY 125 SDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSG 161  
 DB 121 SDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSG 157  
 RESULT 14  
 ADF47073  
 ID ADF47073 standard; protein; 234 AA.  
 XX  
 AC ADF47073;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Mouse anti-human G-CSF antibody light chain protein.  
 XX  
 KW methylothroph yeast; mammalian sugar chain; OCH1; alpha-1;  
 KW 6-mannosyl transferase; alpha-1; 2-mannosidase;  
 KW orotidin-5'-phosphate decarboxylase; URA3;  
 KW phosphoribosyl-amino-imidazole succinocarboxamide synthase; ADE1;  
 KW imidazole-glycerol-phosphate dehydratase; HIS3;  
 KW 3-isopropyl malate dehydrogenase; LEU2; proteinase A; proteinase B; PRB1;  
 KW PEP4; YPS1; KTR1; MN9; AOX; GAPDH; mannosyl transferase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; mannose glycoprotein.  
 XX



```

OS Mus sp.
XX WO2003091431-A1.
XX
XX 06-NOV-2003.
XX
XX 28-APR-2003; 2003WO-JP005464.
XX
XX 26-APR-2002; 2002JP-00127677.
XX
XX (KIRI ) KIRIN BEER KK.
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
XX Kobayashi K, Kitagawa Y, Kameda T, Kawashima N, Jigami Y;
XX Chiba Y;
XX
XX WPI; 2003-854401/79.
XX
XX Producing methylotroph yeast that expresses mammalian sugar chains by
XX disrupting the OCH1 gene and inserting an alpha-1,2-mannosidase gene.
XX
XX Example 28; SEQ ID NO 92; 247pp; Japanese.
XX
XX The invention relates to the production of a methylotroph yeast that
XX produces mammalian sugar chains, comprising disrupting the OCH1 gene in
XX the yeast that encodes for alpha-1,6-mannosyl transferase and inserting
XX and expressing the alpha-1,2-mannosidase gene. The specification also
XX includes DNA sequences encoding: (a) orotidin-5'-phosphate decarboxylase
XX (URA3); (b) phosphoribosyl-amino-imidazole succinocarboxamide synthase
XX (ADE1); (c) imidazole-glycerol-phosphate dehydratase (HIS3); (d) 3-
XX isopropyl malate dehydrogenase (LEU2); (e) alpha-1,6-mannosyl transferase
XX (OCH1); (f) proteinase A (PEP4); (g) proteinase B (PRB1); and (h)
XX aspartic protease (YPS1), mannosyl transferase (KTR1 or MNN9), alcohol
XX oxidase (AOX) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene
XX sequences. The yeast is used for the production of human and mammalian
XX high mannose glycoproteins with high yield and purity. The method is also
XX useful for producing hybrid or complex sugar chains containing mammalian
XX type chains. This sequence represents a mouse anti-human G-CSF antibody
XX light chain used in the invention.
XX
XX Sequence 234 AA;
XX
Query Match 87.9%; Score 746; DB 7; Length 234;
Best Local Similarity 90.1%; Pred. No. 2.1e-41;
Matches 145; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GIRDLIQLTQSPSSLSASVGDRTVITCRASOGISYLAWFQORPKGAPKSLIYAASLSQS 60
Db 17 GARDIQMTQSPSSVSASVGDRTVITCRASQVSSWLAWYQOKPKGAPKSLIYAASLSQS 76
Qy 61 GVPSKFGSGSGTDFTLTISLQPEDFATYYCQQYNSYPFFGPGTKVDIKRTVAAPSVF 120
Db 77 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQANSFPFFGPGTKVEIKRTVAAPSVF 136
Qy 121 IFPPSDEQLKSGTASVVCLLNFPYPRKQVQKVDNALQSG 161
Db 137 IFPPSDEQLKSGTASVVCLLNFPYPRKQVQKVDNALQSG 177

RESULT 15
ABG77164
ID ABG77164 standard; protein; 236 AA.
XX
XX ABG77164;
XX
XX 24-OCT-2002 (first entry)
XX
XX Germline protein sequence of anti-IGF-1R antibody AJ30/Jk1.
XX
XX Insulin-like growth factor I receptor; antibody; human; cytostatic;
XX osteopathic; antiatherosclerotic; antipsoriatic; IGF-1R; tumour;
XX anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
XX acromegaly; gigantism; psoriasis; atherosclerosis.

```

```

XX Homo sapiens.
XX OS
XX WO200253596-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-US051113.
XX
XX 05-JAN-2001; 2001US-0259927P.
XX
XX (PFIZ ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX
XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX WPI; 2002-575410/61.
XX
XX Novel humanized, chimeric monoclonal antibody that specifically binds to
XX insulin-like growth factor I (IGF-I) receptor useful for inhibiting
XX binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
XX
XX Disclosure; Fig 198; 172pp; English.
XX
XX This invention relates to a novel humanised, chimeric or human monoclonal
XX antibody or its antigen binding portion that specifically binds to
XX insulin-like growth factor I receptor (IGF-IR). The antibodies of the
XX invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
XX IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
XX phosphorylation. The antibodies of the invention are useful for
XX diagnosing the presence or location of an IGF-IR-expressing tumour in a
XX subject. The antibody or its antigen-binding portion is also useful for
XX treating cancer in a human. The method for this further involves an anti
XX neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
XX antibodies may also be useful for increasing IGF-IR activity and thus
XX restoring IGF-IR activity in a condition characterised by low IGF-IR
XX levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
XX also useful for inducing apoptosis of specific cells in a patient, and to
XX treat non-cancerous states or disease, e.g. acromegaly, gigantism,
XX psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
XX minimise the immunogenic and allergic responses intrinsic to mouse or
XX mouse-derivatised monoclonal antibodies and thus increase the efficacy
XX and safety of the administered antibodies. The present sequence
XX represents an anti-insulin-like growth factor I receptor antibody of the
XX invention
XX
XX Sequence 236 AA;
XX
Query Match 87.9%; Score 746; DB 5; Length 236;
Best Local Similarity 89.4%; Pred. No. 2.1e-41;
Matches 144; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GIRDLIQLTQSPSSLSASVGDRTVITCRASOGISYLAWFQORPKGAPKSLIYAASLSQS 60
Db 19 GARDIQMTQSPSSLSASVGDRTVITCRASQIRNDLWYQOKPKGAPKRLIYAASLSQS 78
Qy 61 GVPSKFGSGSGTDFTLTISLQPEDFATYYCQQYNSYPFFGPGTKVDIKRTVAAPSVF 120
Db 79 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQQHNSYPFFGPGTKVEIKRTVAAPSVF 138
Qy 121 IFPPSDEQLKSGTASVVCLLNFPYPRKQVQKVDNALQSG 161
Db 139 IFPPSDEQLKSGTASVVCLLNFPYPRKQVQKVDNALQSG 179

Search completed: March 8, 2005, 07:09:26
Job time : 165 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 07:06:05 ; Search time 133 Seconds  
(without alignments)  
405.739 Million cell updates/sec

Title: US-09-784-950-41

Perfect score: 849

Sequence: 1 GIRLDQLTQSPSLASVG.....PREAKVQKVDNALQSKPN 164

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	761	89.6	214	15	US-10-408-901-44
2	753	88.7	214	14	US-10-153-382-19
3	753	88.7	234	16	US-10-684-109-85
4	753	88.7	234	16	US-10-684-109-103
5	751	88.5	236	9	US-09-859-053-30
6	751	88.5	236	16	US-10-625-105-30
7	746	87.9	214	15	US-10-408-901-36
8	746	87.9	236	15	US-10-408-901-52
9	745	87.8	233	16	US-10-663-244-150
10	745	87.8	236	15	US-10-663-244-150
11	739	87.0	214	15	US-10-423-299-3
12	737	86.8	184	16	US-10-684-109-78
13	737	86.8	234	15	US-10-292-088-24
					Sequence 44, Appl
					Sequence 19, Appl
					Sequence 85, Appl
					Sequence 103, Appl
					Sequence 30, Appl
					Sequence 30, Appl
					Sequence 36, Appl
					Sequence 52, Appl
					Sequence 150, Appl
					Sequence 48, Appl
					Sequence 3, Appl
					Sequence 78, Appl
					Sequence 24, Appl

14	737	86.8	234	16	US-10-684-109-91	Sequence 91, Appl
15	736	86.7	223	16	US-10-693-629-66	Sequence 66, Appl
16	736	86.7	234	16	US-10-684-109-109	Sequence 109, Appl
17	736	86.7	234	16	US-10-684-109-115	Sequence 115, Appl
18	733.5	86.4	241	14	US-10-221-945-1	Sequence 1, Appl
19	733	86.3	212	14	US-10-320-231A-77	Sequence 77, Appl
20	733	86.3	234	15	US-10-292-088-48	Sequence 48, Appl
21	730	86.0	234	16	US-10-684-109-97	Sequence 97, Appl
22	730	86.0	363	15	US-10-291-265-335	Sequence 335, Appl
23	729.5	85.9	211	9	US-09-974-449-36	Sequence 36, Appl
24	729	85.9	367	15	US-10-291-265-899	Sequence 899, Appl
25	723	85.2	213	16	US-10-379-392-135	Sequence 135, Appl
26	723	85.2	214	15	US-10-364-953-1	Sequence 1, Appl
27	723	85.2	237	14	US-10-020-786-10	Sequence 10, Appl
28	722	85.0	208	15	US-10-634-581-1	Sequence 1, Appl
29	722	85.0	214	9	US-09-949-559-128	Sequence 128, Appl
30	722	85.0	214	10	US-09-875-221A-128	Sequence 4, Appl
31	722	85.0	214	14	US-10-310-454-4	Sequence 113, Appl
32	722	85.0	214	17	US-10-728-420B-113	Sequence 62, Appl
33	721	84.9	223	16	US-10-693-629-62	Sequence 137, Appl
34	720	84.8	213	16	US-10-379-392-137	Sequence 100, Appl
35	720	84.8	237	9	US-09-056-160B-100	Sequence 100, Appl
36	720	84.8	237	14	US-10-234-671-100	Sequence 2, Appl
37	720	84.8	491	13	US-10-011-125-2	Sequence 155, Appl
38	719	84.7	213	16	US-10-379-392-155	Sequence 2, Appl
39	717	84.5	215	16	US-10-462-040A-2	Sequence 68, Appl
40	716	84.3	233	15	US-10-404-724-68	Sequence 47, Appl
41	715	84.2	236	15	US-10-038-591-47	Sequence 88, Appl
42	715	84.2	502	16	US-10-679-620-88	Sequence 245, Appl
43	714	84.1	153	15	US-10-309-762-245	Sequence 21, Appl
44	714	84.1	164	15	US-10-364-743-21	Sequence 23, Appl
45	714	84.1	164	15	US-10-364-743-23	

#### ALIGNMENTS

#### RESULT 1

US-10-408-901-44  
; Sequence 44, Application US/10408901  
; Publication No. US20040023313A1  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William  
; APPLICANT: Huang, Haichun  
; APPLICANT: Elliot, Robin  
; APPLICANT: Sullivan, John  
; APPLICANT: Medlock, Eugene  
; APPLICANT: Martin, Francis  
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway  
; TITLE OF INVENTION: Inhibitors  
; FILE REFERENCE: MBHB 01-1145-A  
; CURRENT APPLICATION NUMBER: US/10/408,901  
; CURRENT FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 44  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-901-44

Query Match 89.6%; Score 761; DB 15; Length 214;  
Best Local Similarity 93.6%; Pred. No. 3.8e-48;  
Matches 147; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 5 DIQLTQSPSLASVGDRTVITCRASQGISYILAWFOORCKAPKSLIYRAASSLSQGVPS 64  
Db 1 DIQMTQSPSLASVGDRTVITCRASQGISYILAWFOORCKAPKSLIYRAASSLSQGVPS 60  
Qy 65 KFGSGSGTDTLTITISSLPQEDFATYCCQVNSVPTFFGQTKVDIKRTVAAPSVFPP 124  
Db 61 RFSGSGSGTDTLTITISSLPQEDFATYCCQVNSVPTFFGQTKVDIKRTVAAPSVFPP 120



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; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Query Match      88.5%; Score 751; DB 9; Length 236;
Best Local Similarity 90.1%; Pred. No. 2.3e-47;
Matches 145; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GIRDILQTSPPSSLSASVGDRTVITCRASQGISIYLAWFOORPGKAPKSLIYAASLSQS 60
Db 19 GSRCDIQWTSPPSSVSASVGDRTVITCRASQGISRLAWYQKPGKAPKLLIYVASSLSQS 78

Qy 61 GVPSKFGSGSGTDFTLTISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 120
Db 79 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQYNSFPFTFGQGTKEIKRTVAAPSVF 138

Qy 121 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 139 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 179

RESULT 6
US-10-625-105-30
; Sequence 30, Application US/10625105
; Publication No. US20040180052A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; FILE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT FILING DATE: US/10/625,105
; PRIOR FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-625-105-30

Query Match      88.5%; Score 751; DB 16; Length 236;
Best Local Similarity 90.1%; Pred. No. 2.3e-47;
Matches 145; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GIRDILQTSPPSSLSASVGDRTVITCRASQGISIYLAWFOORPGKAPKSLIYAASLSQS 60
Db 19 GSRCDIQWTSPPSSVSASVGDRTVITCRASQGISRLAWYQKPGKAPKLLIYVASSLSQS 78

Qy 61 GVPSKFGSGSGTDFTLTISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 120
Db 79 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQYNSFPFTFGQGTKEIKRTVAAPSVF 138

Qy 121 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 139 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 179

RESULT 7
US-10-408-901-36
; Sequence 36, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-36

Query Match      87.9%; Score 746; DB 15; Length 214;
Best Local Similarity 91.7%; Pred. No. 4.8e-47;
Matches 144; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 5 DIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOORPGKAPKSLIYAASLSQGVPS 64
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISISLAWYQKPEKAPKSLIYAASLSQGVPS 60

Qy 65 KFGSGSGTDFTLTISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVFIPPP 124
Db 61 RFGSGSGTDFTLTISLQSEDATYYCQYNSYPFTFGQGTREIKRTVAAPSVFIPPP 120

Qy 125 SDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 121 SDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 157

RESULT 8
US-10-038-591-52
; Sequence 52, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-52

Query Match      87.9%; Score 746; DB 15; Length 236;
Best Local Similarity 89.4%; Pred. No. 5.3e-47;
Matches 144; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GIRDILQTSPPSSLSASVGDRTVITCRASQGISIYLAWFOORPGKAPKSLIYAASLSQS 60
Db 19 GARCDIQMTQSPSSLSASVGDRTVITCRASQGISRLNDLGMWYQKPGKAPKLLIYAASLSQS 78

Qy 61 GVPSKFGSGSGTDFTLTISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 120
Db 79 GVPSRFGSGSGTEFTLTISLQPEDFATYYCLOHNSYPWTFGQGTKEIKRTVAAPSVF 138
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; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-78

Query Match      86.8%; Score 737; DB 16; Length 184;
Best Local Similarity 89.9%; Pred. No. 1.9e-46;
Matches 143; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPKAPKSLIYAASLSQGV 62
Db 21 KLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPKAPKSLIYAASLSQGV 80
Qy 63 PSKPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVFIF 122
Db 81 PSRPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVFIF 140
Qy 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161
Db 141 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 179

RESULT 13
US-10-292-088-24
; Sequence 24, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PP/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-24

Query Match      86.8%; Score 737; DB 15; Length 234;
Best Local Similarity 88.2%; Pred. No. 2.4e-46;
Matches 142; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPKAPKSLIYAASLSQ 60
Db 17 GSRCDIQMTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPKAPKSLIYAASLSQ 76
Qy 61 GVPKPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 120
Db 77 GVPKPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 136
Qy 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161
Db 137 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 177

RESULT 14
US-10-684-109-91
; Sequence 91, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-91

Query Match      86.8%; Score 737; DB 16; Length 234;
Best Local Similarity 88.2%; Pred. No. 2.4e-46;
Matches 142; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPKAPKSLIYAASLSQ 60
Db 17 GSRCDIQMTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPKAPKSLIYAASLSQ 76
Qy 61 GVPKPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 120
Db 77 GVPKPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 136
Qy 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161
Db 137 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 177

RESULT 15
US-10-693-629-66
; Sequence 66, Application US/10693629
; Publication No. US20040120948A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: MIKAYAMA, Toshifumi
; APPLICANT: YOSHIDA, Hitoshi
; APPLICANT: FORCE, Walker, R.
; APPLICANT: CHEN, Xingjie
; APPLICANT: TAKAHASHI, Nobuaki
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
; FILE REFERENCE: 021286-0306473
; CURRENT APPLICATION NUMBER: US/10/693,629
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP2001/142482
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: JP2001/310535
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US10/040,244
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-693-629-66

Query Match      86.7%; Score 736; DB 16; Length 223;
Best Local Similarity 88.2%; Pred. No. 2.7e-46;
Matches 142; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
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Qy	1	GIRLDIQLTQSPSSLSASVGDVRTITCRASQGISIYLAWFQORPGKAPKSLIYAASSLQS	60
Db	19	GSRCDIQMTQSPSSVSGVGDVRTITCRASQGISIYLAWFQORPGKAPKSLIYAASSLQS	78
Qy	61	GVPSKFSGSGGTDFTLTISLQPEDFATYYCOQYNSYPFTFGPGTKVDIKRTVAAPSVF	120
Db	79	GVPSRFSGSGGTDFTLTISLQPEDFATYYCOQYNSYPFTFGPGTKVDIKRTVAAPSVF	138
Qy	121	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG	161
Db	139	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG	179

Search completed: March 8, 2005, 07:15:30  
Job time : 134 secs



Result No.	Score	Query Match	Length	DB	ID	Description	
1	753	88.7	214	4	US-09-472-087-71	Sequence 71, Appl	
2	751	88.5	236	4	US-09-859-053-30	Sequence 30, Appl	
3	729	85.9	236	1	US-08-157-101A-5	Sequence 5, Appl	
4	720	84.8	431	4	US-10-011-125A-2	Sequence 2, Appl	
5	715	84.2	233	2	US-07-934-373C-25	Sequence 25, Appl	
6	715	84.2	233	3	US-08-437-642B-25	Sequence 25, Appl	
7	715	84.2	233	4	US-08-146-206C-25	Sequence 25, Appl	
8	715	84.2	233	4	US-09-705-686-25	Sequence 25, Appl	
9	715	84.2	233	4	US-09-705-392A-25	Sequence 25, Appl	
10	715	84.2	233	4	US-09-705-398-25	Sequence 25, Appl	
11	715	84.2	233	5	PCT-US93-0783-25	Sequence 25, Appl	
12	713	84.0	233	4	US-08-030-175-43	Sequence 43, Appl	
13	713	84.0	234	4	US-09-740-002-24	Sequence 24, Appl	
14	711	83.7	224	4	US-09-456-090A-48	Sequence 48, Appl	
15	711	83.7	224	4	US-09-453-234-48	Sequence 48, Appl	
16	710	83.6	214	2	US-07-934-373C-39	Sequence 39, Appl	
17	710	83.6	214	3	US-08-437-642B-39	Sequence 39, Appl	
18	710	83.6	214	5	PCT-US93-0783-39	Sequence 39, Appl	
19	709.5	83.6	233	3	US-08-812-586-45	Sequence 45, Appl	
20	709.5	83.6	233	4	US-09-535-832A-42	Sequence 42, Appl	
21	709	83.5	218	2	US-08-887-352B-13	Sequence 13, Appl	
22	709	83.5	218	3	US-08-466-151-9	Sequence 9, Appl	
23	709	83.5	218	3	US-09-109-207C-13	Sequence 13, Appl	
24	709	83.5	218	3	US-09-496-005-13	Sequence 13, Appl	
25	709	83.5	218	3	US-08-466-163B-9	Sequence 9, Appl	
26	709	83.5	218	4	US-09-920-171-13	Sequence 13, Appl	
27	709	83.5	218	4	US-09-802-096-9	Sequence 9, Appl	

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; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-859-053-30

Query Match      88.5%; Score 751; DB 4; Length 236;
Best Local Similarity 90.1%; Pred. No. 4e-59; Indels 0; Gaps 0;
Matches 145; Conservative 8; Mismatches 8;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFOQRPQKAPKSLIYAASLSQS 60
Db 19 GSRCDIQMTQSPSSLSASVGDRTVITTCRASQGISRLLAWYQKPGKAPKLLIYVASSLSQS 78

Qy 61 GVPSKFGSGSGDTFTLTISLQPEDPATYVCOQYNSYPFTFGTGKVDIKRTVAAPSVF 120
Db 79 GVPSRFSGSGGTFTLTISLQPEDPATYVCOQANSFPWTFGGTKVEIKRTVAAPSVF 138

Qy 121 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 139 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 179

RESULT 3
US-08-157-101A-5
; Sequence 5, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
```

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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-157-101A-5

Query Match      85.9%; Score 729; DB 1; Length 236;
Best Local Similarity 85.7%; Pred. No. 3.6e-57;
Matches 138; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFOQRPQKAPKSLIYAASLSQS 60
Db 19 GSRCDIQMTQSPSSLSASVGDRTVITTCRASQGISIYLVWFQKPGKAPKLLIYAASLSQS 78

Qy 61 GVPSKFGSGSGDTFTLTISLQPEDPATYVCOQYNSYPFTFGTGKVDIKRTVAAPSVF 120
Db 79 GVPSRFSGSGGTFTLTISLQPEDPATYVCLHNNYPLSFGGKVEIKRTVAAPSVF 138

Qy 121 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 139 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 179

RESULT 4
US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
; US-10-011-125A-2

Query Match      84.8%; Score 720; DB 4; Length 491;
Best Local Similarity 88.5%; Pred. No. 5.2e-56;
Matches 139; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 5 DIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFOQRPQKAPKSLIYAASLSQSVPS 64
Db 24 DIQLTQSPSSLSASVGDRTVITTCRASQDISNYLNWYQKPGKAPKLLIYFTSSLHSGVPS 83

Qy 65 KFGSGSGGTFTLTISLQPEDPATYVCOQYNSYPFTFGTGKVDIKRTVAAPSVFIFPP 124
Db 84 RFGSGSGGTFTLTISLQPEDPATYVCOQYNSYPFTFGTGKVDIKRTVAAPSVFIFPP 143

Qy 125 SDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 144 SDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 180

RESULT 5
US-07-934-373C-25
; Sequence 25, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
```

```
;
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-07-934-373C-25
;
; Query Match 84.2%; Score 715; DB 2; Length 233;
; Best Local Similarity 85.7%; Pred. No. 6.2e-56;
; Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
;
; QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASOGISIVLAWFOQRGKAPKSLIYAASLIQS 60
; DB 16 GVHSDIQMTQSPSSLSASVGDRTVITCRASODINNLYNWYQQRGKAPKLLIYTTSLHS 75
;
; QY 61 GVPKFSGSGGTDTLTITISLQPEDPATYCCQYNSYPFTFGTKVDIKRTVAAPSVF 120
; DB 76 GVPKFSGSGGTDTLTITISLQPEDPATYCCQYNSYPFTFGTKVDIKRTVAAPSVF 135
;
; QY 121 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSG 161
; DB 136 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSG 176
;
; RESULT 6
; US-08-437-642B-25
; Sequence 25, Application US/08437642B
; Patent No. 6054297
;
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
;
; US-07-934-373C-25
; Query Match 84.2%; Score 715; DB 2; Length 233;
; Best Local Similarity 85.7%; Pred. No. 6.2e-56;
; Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
;
; QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASOGISIVLAWFOQRGKAPKSLIYAASLIQS 60
; DB 16 GVHSDIQMTQSPSSLSASVGDRTVITCRASODINNLYNWYQQRGKAPKLLIYTTSLHS 75
;
; QY 61 GVPKFSGSGGTDTLTITISLQPEDPATYCCQYNSYPFTFGTKVDIKRTVAAPSVF 120
; DB 76 GVPKFSGSGGTDTLTITISLQPEDPATYCCQYNSYPFTFGTKVDIKRTVAAPSVF 135
;
; QY 121 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSG 161
; DB 136 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSG 176
;
; RESULT 7
; US-08-146-206C-25
; Sequence 25, Application US/08146206C
; Patent No. 6407213
;
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-437-642B-25
;
; Query Match 84.2%; Score 715; DB 3; Length 233;
; Best Local Similarity 85.7%; Pred. No. 6.2e-56;
; Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
;
; QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASOGISIVLAWFOQRGKAPKSLIYAASLIQS 60
; DB 16 GVHSDIQMTQSPSSLSASVGDRTVITCRASODINNLYNWYQQRGKAPKLLIYTTSLHS 75
;
; QY 61 GVPKFSGSGGTDTLTITISLQPEDPATYCCQYNSYPFTFGTKVDIKRTVAAPSVF 120
; DB 76 GVPKFSGSGGTDTLTITISLQPEDPATYCCQYNSYPFTFGTKVDIKRTVAAPSVF 135
;
; QY 121 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSG 161
; DB 136 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSG 176
;
; RESULT 7
; US-08-146-206C-25
; Sequence 25, Application US/08146206C
; Patent No. 6407213
;
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
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QY 1 GIRDILQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIYAASLSQS 60  
 Db 16 GVHSDIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNWYQORPGKAPKSLIYTTSLHS 75  
 QY 61 GVPSKFGSGSGDTFTLTISLQPEDPATYCCQYNSYPTFGPTKVDIKRTVAAPSVF 120  
 Db 76 GVPSRFGSGSGDTYTLTISLQPEDPATYCCQGNLTPTTFGGTKVEIKRTVAAPSVF 135

QY 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161  
 Db 136 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 176

## RESULT 10

US-09-705-398-25  
 ; Sequence 25, Application US/09705398  
 ; Patent No. 6800738  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carter, Paul J.  
 ; TITLE OF INVENTION: Method for Making Humanized Antibodies  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/705.398  
 FILING DATE: 02-Nov. 6800738-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/146206  
 FILING DATE: 17-NOV-1993  
 APPLICATION NUMBER: 07/715272  
 FILING DATE: 14-JUN-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER: 40,378  
 REFERENCE/DOCKET NUMBER: P0709P1D2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1994  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 233 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-705-398-25  
 Query Match 84.2%; Score 715; DB 4; Length 233;  
 Best Local Similarity 85.7%; Pred. No. 6.2e-56;  
 Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 GIRDILQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIYAASLSQS 60  
 Db 16 GVHSDIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNWYQORPGKAPKSLIYTTSLHS 75  
 QY 61 GVPSKFGSGSGDTFTLTISLQPEDPATYCCQYNSYPTFGPTKVDIKRTVAAPSVF 120  
 Db 76 GVPSRFGSGSGDTYTLTISLQPEDPATYCCQGNLTPTTFGGTKVEIKRTVAAPSVF 135  
 QY 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161  
 Db 136 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 176

## RESULT 11

PCT-US93-07832-25  
 ; Sequence 25, Application PC/TUS9307832  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc.  
 ; TITLE OF INVENTION: Immunoglobulin Variants  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/07832  
 FILING DATE: 19930820  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/715272  
 FILING DATE: 14-JUN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/05126  
 FILING DATE: 15-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/934373  
 FILING DATE: 21-AUG-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME:  
 REGISTRATION NUMBER:  
 REFERENCE/DOCKET NUMBER: 709P2PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE:  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 233 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 PCT-US93-07832-25

Query Match 84.2%; Score 715; DB 5; Length 233;  
 Best Local Similarity 85.7%; Pred. No. 6.2e-56;  
 Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 GIRDILQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIYAASLSQS 60  
 Db 16 GVHSDIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNWYQORPGKAPKSLIYTTSLHS 75  
 QY 61 GVPSKFGSGSGDTFTLTISLQPEDPATYCCQYNSYPTFGPTKVDIKRTVAAPSVF 120  
 Db 76 GVPSRFGSGSGDTYTLTISLQPEDPATYCCQGNLTPTTFGGTKVEIKRTVAAPSVF 135  
 QY 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161  
 Db 136 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 176

## RESULT 12

US-08-030-175-43  
 ; Sequence 43, Application US/08030175  
 ; Patent No. 6767996  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gorman, Scott D.  
 ; APPLICANT: Clark, Michael R.



APPLICANT: GenPharm International  
TITLE OF INVENTION: Human Antibodies  
FILE REFERENCE: 020015-000110US  
CURRENT APPLICATION NUMBER: US/09/453,234  
CURRENT FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: US 60/157,415  
PRIOR FILING DATE: 1999-10-02  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 48  
LENGTH: 224  
TYPE: PRT  
ORGANISM: Homo sapiens  
OTHER INFORMATION: MI-21L  
US-09-453-234-48

Query Match 83.7%; Score 711; DB 4; Length 224;  
Best Local Similarity 89.7%; Pred. No. 1.3e-55;  
Matches 140; Conservative 5; Mismatches 11; Indels 0; Gaps 0;  
Qy 6 IQLTQSPSSLASVGDRTTTCRASQGISIYLAWFQORPGKAPKSLIYAASSLQSGVPSK 65  
Db :::  
2 IRMTQSPSFLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSR 61  
Qy 66 FSGSGSGTDFTLTSSISLPEDFATYCCQYNISYPTFGPGTKVDIKRTVAAPSVFIFPPS 125  
Db :::  
62 FVSGSGGTDLTITSSISLPEDFATYCCQGYSTPTFGPGTKVDIKRTVAAPSVFIFPPS 121  
Qy 126 DEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSG 161  
Db :::  
122 DEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSG 157

Search completed: March 8, 2005, 07:06:35  
Job time : 43 secs

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